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Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 4
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SEQUENCE, 15 unordered pieces.
AC024029
AC024029.3 GI:7230916
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 155668)
Waterston,R.H.
REFERENCE
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 155668)
REFERENCE Waterston,R.H.
JOURNAL Direct Submission
AUTHORS Submitted (20-FEB-2000) Genome Sequencing Center, Washington
TITLE University School of Medicine, 4444 Forest Park Parkway, St. Louis,
JOURNAL MO 63108, USA
COMMENT On Mar 13, 2000 this sequence version replaced gi:7109555.
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0167N04
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 146450 bases at least Q40
Consensus quality: 149629 bases at least Q30
Consensus quality: 151087 bases at least Q20
Insert size: 16800; agarose-fp
Insert size: 154268; sum-of-contigs
Quality coverage: 3.98 in Q20 bases; sum-of-contigs
Quality coverage: 4.38 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1806: contig of 1806 bp in length
* 1807 1906: gap of unknown length
* 1907 4798: contig of 2892 bp in length
* 4799 4898: gap of unknown length
* 4899 7312: contig of 2414 bp in length
* 7313 7412: gap of unknown length
* 7413 11277: contig of 3865 bp in length
* 11278 11377: gap of unknown length
* 11378 14368: contig of 2991 bp in length
* 14369 14468: gap of unknown length
* 14469 20130: contig of 5662 bp in length
* 20131 20230: gap of unknown length
* 20231 25513: contig of 5283 bp in length
* 25514 25613: gap of unknown length
* 25614 30765: contig of 5152 bp in length
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*	77124	77223: gap of unknown length
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Best Local Similarity	99.4%	Pred. No. 2e-48		
Matches 175; Conservative	0	Mismatches 1	Indels 0	Gaps 0

QY	1	ACCTGTAATTCACGACTGCTAGAGATCCGAGGTCAGAGACCTGCTTGAGGCCAGGATTC	60
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Db 163478 GCTTAGTGCTCATCCCTGTGTCCTCCAGCTACTAGGAGGACAGATGAGACTGCT 163533
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RESULT 7
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LOCUS Homo sapiens genomic DNA, chromosome 11q clone:RP11-535C12,
DEFINITION complete sequences.
ACCESSION AP003531
VERSION AP003531.2 GI:20334341
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
AUTHORS 1
Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Homo sapiens genomic DNA
JOURNAL Published Only in Database (2001)
REFERENCE 2 (bases 1 to 19384)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
JOURNAL Submitted (18-APR-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Shuhiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
On Apr 26, 2002 this sequence version replaced gi:13699094.

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Best Local Similarity 99.4%; Pred. No. 2e-48; Mismatches 0; Gaps 0;
Matches 175; Conservative 0; Indels 1; Indels 0; Gaps 0;
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RESULT 8
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LOCUS Pan troglodytes BAC clone RP43-2801 from 7, complete sequence.
DEFINITION AC146263
ACCESSION AC146263.2 GI:47498252
VERSION AC146263.2
KEYWORDS HTG.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.
On May 19, 2004 this sequence version replaced gi:13699094.

AUTHORS Griffin, M., Bielicki, L. and Haakenson, W.
TITLE The sequence of Pan troglodytes BAC clone RP43-2801
JOURNAL Unpublished (2001)
REFERENCE 2 (bases 1 to 141252)
AUTHORS Wilson, R.K.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 3 (bases 1 to 141252)
AUTHORS Wilson, R.K.
TITLE Direct Submission
JOURNAL Submitted (19-MAY-2004) Washington University School of Medicine,
Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO
63108, USA
On May 19, 2004 this sequence version replaced gi:33387216.

COMMENT
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@wustl.wustl.edu
----- Summary Statistics
Center project name: C_PT028001

NOTICE:
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu

SOURCE INFORMATION:
The RPI-43 BAC Library has been constructed by Chung-Li Shu. DNA
was isolated from white blood cells obtained from a male chimpanzee
(Pan troglodytes, 'Cint', Yerkes #C0471; birthdate: 6-6-80). The
clone and detailed information can be obtained from Resgen
(http://www.resgen.com) or Pieter de Jong and co-workers at
http://www.bacpac.chori.org.

NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/chromosome="7"
/map="7"
/clone="RP43-2801"
/clone_11b="RPI-43"

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Best Local Similarity 79.5%; Pred. No. 5.e-28; Mismatches 136; Conservative 0; Indels 35; Indels 0; Gaps 0;
Matches 136; Conservative 0; Indels 35; Indels 0; Gaps 0;
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Db 76117 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGCTGAGAGAGCTGTTGAGGCCAGGAGTTTC 76058
|||||

QY 61 AAGAGCAGCTTGACACACAGAGGAGACCTGTCTACTCAAAAGATTAATTAATTAGCCAG 120
|||||
Db 76057 AAGAGCAGCTTGACACACAGAGGAGACCTGTCTACTCAAAAGATTAATTAATTAGCCAG 75998
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* 9791 9890: gap of unknown length
* 9891 13294: contig of 3404 bp in length
* 13295 13394: gap of unknown length
* 13395 16584: contig of 3190 bp in length
* 16585 16684: gap of unknown length
* 16685 20753: contig of 4069 bp in length
* 20754 20854: gap of unknown length
* 20854 24326: contig of 3473 bp in length
* 24327 24427: gap of unknown length
* 24427 28594: contig of 4168 bp in length
* 28595 28694: gap of unknown length
* 28695 32625: contig of 3931 bp in length
* 32626 32725: gap of unknown length
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* 39440 39540: gap of unknown length
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* 44815 44915: gap of unknown length
* 44915 52189: contig of 7275 bp in length
* 52190 52290: gap of unknown length
* 52290 58734: contig of 6445 bp in length
* 58735 58834: gap of unknown length
* 58835 66484: contig of 7650 bp in length
* 66485 66584: gap of unknown length
* 66585 74428: contig of 7844 bp in length
* 74429 74528: gap of unknown length
* 74529 84369: contig of 9841 bp in length
* 84370 84469: gap of unknown length
* 84470 91569: contig of 7100 bp in length
* 91570 91670: gap of unknown length
* 91670 101447: contig of 9778 bp in length
* 101448 101547: gap of unknown length
* 101548 119545: contig of 17998 bp in length
* 119546 119645: gap of unknown length
* 119646 137645: contig of 18000 bp in length
* 137646 162701: gap of unknown length
* 137746 162701: contig of 24956 bp in length.
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FEATURES

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313. 3508
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7523. 9790
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ORIGIN

Query Match 64.3%; Score 114.2; DB 12; length 162701;
Best Local Similarity 78.3%; Pred. No. 1.1e-27;
Matches 137; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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QY 62 AGAGCAGCTGACACACAGGAGACTGTCTACTACAAAGATAATTAATGACGAG 121
DB 133706 AGACGAGCTGGCGCAGCATGTGTAAACCGCTCTACTATAAAATACAAATACGACGAG 133765
QY 122 CTTAGGTGCTACCTCTGTGTGTCCGACTTACCTAGGAGGACGAGAGTACGCTCT 176
DB 133766 CATAGTGGCAAAATGCTGTATCTCCAGCTACTGCGAGGCTGAGGAGAACTGCT 133820

RESULT 11
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LOCUS Homo sapiens chromosome 11, clone RP11-2C23, complete sequence.
AC015684
AC015684.11 GI:18129440
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,B., Allen,N., Anderson,M.,
TITLE Homo sapiens chromosome 11, clone RP11-2C23, complete sequence.
JOURNAL
AUTHORS Unpublished
2 (bases 1 to 183939)
1 (bases 1 to 183939)
Homo sapiens chromosome 11, clone RP11-2C23
2 (bases 1 to 183939)
Birren,B., Linton,L., Nusbaum,C., Lander,B., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Bouhassal,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cook,P., Dearliano,K., Dewar,K., Domino,M., Donelan,D., Doyle,M.,
Ferreira,P., Fitzhugh,M., Forrest,C., Funke,R., Gage,D., Horton,L.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heathford,A., Klein,J.,
Howland,J.C., Johnson,R., Jones,C., Kam,L., Karatas,A., Klein,J.,
Lehoczky,J., Liew,C., Locke,K., MacDonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tessfay,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 183939)
Birren,B., Linton,L., Nusbaum,C., Lander,B., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Bouhassal,B.,
Brown,A., Camarata,J., Campiano,A., Chang,J., Chararo,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cook,P., Dearliano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,M., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Illie,I., Johnson,R., Jones,C.,
Karatas,A., Karatas,A., Kells,C., Lacroque,K., Lamazares,R.,
Lander,B., Lehoczky,J., Levine,R., Liu,G., Maclean,A.,
Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Meldrum,J., Menais,L., Mhova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Niccol, R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunthang,P., Pierre,N., Pollara,V., Raymond,C.,
Reeta,R., Riebeck,M., Riley,R., Rhee,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupbach,N.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Stroas,N., Subramanian,A., Talamas,J., Tessfay,S., Theodora,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (01-FEB-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jan 11, 2002 this sequence version replaced gi:1874886.
All repeats were identified using RepeatMasker:
Smt, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1331
Center clone name: 2_C_23

FEATURES
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10087..10291
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complement(10211..10235)
/note="<30 qual SNGT region"

* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 114750: contig of 114750 bp in length
* 114751 114850: gap of 100 bp
* 114851 115820: contig of 970 bp in length
* 115821 115920: gap of 100 bp
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* 116623 116722: gap of 100 bp
* 116723 116775: contig of 953 bp in length
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* 118387 118486: gap of 100 bp
* 118487 119466: contig of 980 bp in length
* 119467 119566: gap of 100 bp
* 119567 120382: contig of 816 bp in length
* 120383 120482: gap of 100 bp
* 120483 121110: contig of 628 bp in length
* 121111 121210: gap of 100 bp
* 121211 121906: contig of 696 bp in length
* 121907 122006: gap of 100 bp
* 122007 122708: contig of 702 bp in length
* 122709 122808: gap of 100 bp
* 122809 123427: contig of 619 bp in length
* 123428 123527: gap of 100 bp
* 123528 124282: contig of 755 bp in length
* 124283 124382: gap of 100 bp
* 124383 125443: contig of 1061 bp in length
* 125444 125543: gap of 100 bp
* 125544 126291: contig of 748 bp in length
* 126292 127418: contig of 1027 bp in length
* 127419 127518: gap of 100 bp
* 127519 128462: contig of 944 bp in length
* 128463 128562: gap of 100 bp
* 128563 129834: contig of 1272 bp in length
* 129835 129934: gap of 100 bp
* 129935 130942: contig of 1008 bp in length
* 130943 131042: gap of 100 bp
* 131043 132120: contig of 1078 bp in length
* 132121 132220: gap of 100 bp
* 132221 133078: contig of 858 bp in length
* 133079 133178: gap of 100 bp
* 133179 133944: contig of 766 bp in length
* 133945 134044: gap of 100 bp
* 134045 135404: contig of 1360 bp in length
* 135405 135504: gap of 100 bp
* 135505 136755: contig of 1251 bp in length
* 136756 136855: gap of 100 bp
* 136856 137656: contig of 801 bp in length
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* 137757 138886: contig of 1130 bp in length
* 138887 138986: gap of 100 bp
* 138987 140043: contig of 1057 bp in length
* 140044 140143: gap of 100 bp
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* 140941 141040: gap of 100 bp
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* 142653 142752: gap of 100 bp
* 142753 144004: contig of 1252 bp in length
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* 144105 145485: contig of 1381 bp in length
* 145486 145585: gap of 100 bp
* 145586 146820: contig of 1235 bp in length
* 146821 146920: gap of 100 bp
* 146921 148400: contig of 1480 bp in length
* 148401 148500: gap of 100 bp
* 148501 149509: contig of 1009 bp in length
* 149510 149609: gap of 100 bp
* 149610 151355: contig of 1746 bp in length
* 151356 151455: gap of 100 bp

* 151456 153113: contig of 1658 bp in length
* 153114 153213: gap of 100 bp
* 153214 154844: contig of 1631 bp in length
* 154845 154944: gap of 100 bp
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FEATURES Location/Qualifiers

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/db_xref="taxon:9606"

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vector_side:left"

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Best Local Similarity 80.2%; Pired. No. 1.1e-27;
Matches 134; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

5 GTATTTCAGTACTGTGAGAGTCCGAGAGTCCAGAGACTGCTTAGAGCCAGAGTTCAAGA 64

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Db	54146	CCAGCCGACGACCAATGAGCAAGAGACTGTCTCTACTAAGATATCATTAATTTAGCAGGACAT	54205
Qy	125	AGTAGCTTCATCCCTGTGTGCTCCAGACTCTTAGGAGAGCAGAACTAGAGA	171
Db	54206	GCTGGCACATGCTCTGTATTCCTCCAGACTTACTTTGGAGGCTGAGGACAGA	54252
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LOCUS	BV190642	401 bp	DNA linear STS 10-UTN-2004
DEFINITION	sqm167865 Human DNA (Sequenom) Homo sapiens STS genomic, sequence		
ACCESSION	BV190642		
VERSION	BV190642.1	GI:48032193	
KEYWORDS	STS.		
ORGANISM	Homo sapiens (human)		
SOURCE	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
TITLE	Hominidae; Homo.		
JOURNAL	1 (bases 1 to 401)		
COMMENT	Nelson,R.M., Manneillo,G., Kammerer,S., Hoyal,C.R., Shi,M.M., Cantor,C.R. and Braun,A. Large-Scale Validation of Single Nucleotide Polymorphisms in Gene Regions Genome Res. (2004) In press		
FEATURES			
source	Contact: Andreas Braun Pharmaceuticals division Sequenom, Inc. 3595 John Hopkins Court, San Diego, CA 92121, USA Tel.: 18582028018 Fax: 18582029020 Email: abraun@sequenom.com Primer A: No primer sequence submitted Primer B: No primer sequence submitted STS size: 401		
ORIGIN	STS		
Query Match	64.8%; Score 114; DB 7; Length 401;		
Best Local Similarity	79.4%; Pred. No. 6e-28;		
Matches 135; Conservative	0; Mismatches 35; Indels 0; Gaps 0;		
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Qy	62	AGAGACCCCTTGAGACACACAGGAGAGACTTGTCACTACAAAGATTAATTAATTTAGCCAG	121
Db	180	AGACACACCTTGAGACACACATGAGAACCCCTCTCTTTTAAATAATTAATTTAGCCAG	239
Qy	122	CTTAGTGGCTCATCCCTGTGTGCTCCAGACTACTAGGAGGCGAGAACTAGAGA	171
Db	240	CTTAGTGGCGCACCTGTAGTCCCACTTATTGGAGGCTGAGGCGAGAA	289
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DEFINITION	Homo sapiens chromosome 18 clone RP11-886011 map 18q11.2, WORKING		
	DRAFT SEQUENCE, 19 unordered pieces.		

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ACCESSION      AP001277.2  GI:8117670
VERSION        AP001277.2
KEYWORDS       HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mamalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE          Hominiidae; Homo
JOURNAL        1 (bases 1 to 132966)
REFERENCE      Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
AUTHORS        Fujiiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE          Homo sapiens 132,966 genomic DNA of 19q11.2
JOURNAL        2 (bases 1 to 132966)
REFERENCE      Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
AUTHORS        Fujiiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE          Direct Submission
JOURNAL        Submitted (23-FEB-2000) Masahira Hattori, The Institute of Physical
REFERENCE      and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
AUTHORS        Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
TITLE          Japan (E-mail:hattori@gsc.riken.go.jp,
JOURNAL        URL:http://hnp.gsc.riken.go.jp/, Tel:81-42-778-9923,
REFERENCE      Fax:81-42-778-9924)
AUTHORS        On May 31, 2000 this sequence version replaced gi:7106155.
COMMENT        ----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hnp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: Humdrat18
Center clone name: RP11-886011
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 122160 bases at least Q40
Consensus quality: 127107 bases at least Q30
Consensus quality: 129558 bases at least Q20
Insert size: 131166; sum-of-coverage
Quality coverage: 5.73x in Q20 bases; sum-of-coverage
-----
NOTE: This is a 'working draft' sequence. It currently consists of
19 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved
1
18533 18432 contig of 18432 bp in length
31839 contig of 13307 bp in length
31940 46961 contig of 15022 bp in length
47062 58376 contig of 11315 bp in length
58477 68787 contig of 10311 bp in length
68888 76179 contig of 7292 bp in length
76280 82148 contig of 5669 bp in length
82249 86877 contig of 4629 bp in length
86978 94001 contig of 7024 bp in length
94102 100574 contig of 6473 bp in length
100675 106683 contig of 6009 bp in length
106784 111994 contig of 5211 bp in length
112095 117429 contig of 5335 bp in length
117530 121564 contig of 4035 bp in length
121665 125145 contig of 3481 bp in length
125246 127781 contig of 2536 bp in length
127882 129887 contig of 2006 bp in length
129988 131384 contig of 1397 bp in length
131485 132966 contig of 1482 bp in length

```


JOURNAL

COMMENT

Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 24, 2001 this sequence was replaced by: 13376505.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) RepeatMasker.html
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center -----

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIRB

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information -----

Center Project name: L12674

Center clone name: 886 O. 11

----- Summary Statistics -----

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 134241 bases at least Q40

Consensus quality: 135346 bases at least Q30

Consensus quality: 135810 bases at least Q20

Insert size: 14500; agarose-fp

Insert size: 136113; sum-of-contigs

Quality coverage: 7.9 in Q20 bases; agarose-fp

Quality coverage: 8.5 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 62832: contig of 62832 bp in length
* 62833 62932: gap of 100 bp
* 62933 65665: contig of 2733 bp in length
* 65666 65765: gap of 100 bp
* 65766 69250: contig of 3485 bp in length
* 69251 69350: gap of 100 bp
* 69351 74656: contig of 5306 bp in length
* 74657 74757: gap of 100 bp
* 74757 84084: contig of 9328 bp in length
* 84085 84184: gap of 100 bp
* 84185 136613: contig of 52429 bp in length.

FEATURES

Source

1. 136613

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="18"

/map="18"

/clone="RP11-886011"

/clone_id="RP11-886011 Human Male BAC"

1. 62832

/note="assembly_fragment"

clone_end:SP6

vector_side:left"

62833. 62932

/estimated_length=100

62933. 65665

/note="assembly_fragment"

65666. 65765

/estimated_length=100

65766. 69250

/note="assembly_fragment"

69251. 69350

/estimated_length=100

69351. 74656

/note="assembly_fragment"

74657. 74756

/estimated_length=100

74757. 84084

/note="assembly_fragment"

84085. 84184

/estimated_length=100

84185. 136613

/note="assembly_fragment"

clone_end:T7

vector_side:right"

ORIGIN

Query Match

Best Local Similarity 79.4%; Pred. No. 1.2e-27;

Matches 135; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTGAGAGGCGCAGAGTTCA 61

Db 131226 CCTGTAATTCAGAGACTTTGAGAGCGGAGGTGGCGGATCATTGATCAGAGTTCA 131167

QY 62 AGAGCAGCTGAGACACAGGAGAGCTGTCTACTACAAAGATTAATTATTTGCCAGG 121

Db 131166 AGACCAAGCTGCGCAACATGTGTAAACCGTCTTATTAATAAATAATTAGCCAGG 131107

QY 122 CTTAGTGGCTCATCCCTGTGTGTCCTCCAGCTACTAGGAGGAGGAAGTAGGA 171

Db 131106 CTTAGTGGCGCACACCTGTAGTCCAGCTATTGGAGGCTGAGGCAGAA 131057

Search completed: June 5, 2006, 22:27:04

Job time : 1201.56 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:15:11 ; Search time 153.125 Seconds
(Without alignments)
8013.826 Million cell updates/sec

Title: US-09-869-098a-1_COPY_255_430

Perfect score: 176
Sequence: 1 acctgtattccagctactgt.....gagcgagaagtagactgtc 176

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: N_Geneseq_8:*
2: geneeqn1980s:*
3: geneeqn1990s:*
4: geneeqn2000s:*
5: geneeqn2001as:*
6: geneeqn2001bs:*
7: geneeqn2002as:*
8: geneeqn2003as:*
9: geneeqn2003bs:*
10: geneeqn2003cs:*
11: geneeqn2003ds:*
12: geneeqn2004as:*
13: geneeqn2004bs:*
14: geneeqn2005s:*
15: geneeqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	176	100.0	3505	3	AAA62932	Aaa62932 DNA conta
2	112.6	64.0	185035	6	ABT10147	Abt10147 Human bre
3	112.6	64.0	185035	8	ACA64951	Aca64951 Human PEN
4	112.6	64.0	185035	12	ADQ20284	Adq20284 Human sof
5	112.4	63.9	3521	12	ADQ62996	Adq62996 Novel hum
6	112	63.6	2312	14	ADM02195	Adm02195 Human CDN
7	112	63.6	2312	14	ABC85125	Aec85125 Human CDN
8	110.8	63.0	13001	4	AAK82979	Aak82979 Human imm
9	110.8	63.0	38653	12	ADH26544	Adh26544 Human hea
10	109.4	62.2	81099	11	ACN45018	Actn45018 Human gen
11	109.4	62.0	620	12	ADN12517	Adn12517 Human pro
12	109.2	62.0	31116	11	ACN44954	Actn44954 Human gen
13	109.2	62.0	31279	14	ADA02540	Ada02540 Human can
14	109.2	62.0	58832	9	ADA02540	Ada02540 Human TCO
15	109.2	62.0	58832	9	ADA02540	Ada02540 Human TCO
16	109.2	62.0	58832	10	ADB72278	Adb72278 Human TCO
17	109.2	62.0	58832	10	ADB72278	Adb72278 Human TCO
18	109.2	62.0	58832	10	ADe95788	Ad95788 Human TCO

C	19	109.2	62.0	58832	10	ADe95788	Ad95788 Human TCO
C	20	108.2	61.5	310268	13	ABD32548	Abd32548 Human can
C	21	108	61.4	135005	12	ADQ19501	Adq19501 Human sof
C	22	107.8	61.2	1480	6	AA142843	Aa142843 Human NF-
C	23	107.8	61.2	1890	6	AA142845	Aa142845 Human NF-
C	24	107.6	61.1	2136	4	AAH18289	Aah18289 Human CDN
C	25	107.6	61.1	285020	11	ACN44958	Actn44958 Human gen
C	26	107.6	61.1	322885	13	ADe93537	Ad93537 Human MRC
C	27	107	60.8	201	13	ADe93537	Ad93537 Human aut
C	28	107	60.8	39265	6	ABL52838	Ab152838 Polynucle
C	29	107	60.8	57502	12	ADQ97092	Adq97092 Human can
C	30	107	60.8	149671	6	ABK84797	Abk84797 Human CDN
C	31	107	60.8	149671	9	ADB70361	Adb70361 Moesin cd
C	32	107	60.8	149671	12	ADJ37140	Adj37140 Human mal
C	33	107	60.8	158417	13	ADe93537	Ad93537 Human aut
C	34	106.8	60.7	312477	12	ADP69744	Adp69744 Human ROC
C	35	106.2	60.3	832	4	AA188238	Aa188238 Human pol
C	36	106.2	60.3	1793	4	AAH17207	Aah17207 Human CDN
C	37	106.2	60.3	101961	14	ABD18616	Abd18616 Fibrotic
C	38	106.2	60.3	114596	14	ADZ70593	Adz70593 Human CDN
C	39	106.2	60.3	128117	14	ABD18395	Abd18395 Fibrotic
C	40	106.2	60.3	157230	14	ABD89424	Abd89424 Human bre
C	41	106.2	60.3	170508	14	ABD89422	Abd89422 Human bre
C	42	106.2	60.3	173115	14	ABD89425	Abd89425 Human bre
C	43	106.2	60.3	226475	9	ADDe8279	Ad8279 Human tum
C	44	106	60.2	2575	4	AAK82973	Aak82973 Human imm
C	45	106	60.2	2918	14	ADY15885	Ady15885 DNA encod

ALIGNMENTS

RESULT 1
AAA62932 standard; DNA; 3505 BP.
ID AAA62932
AC AAA62932;
XX
XX
XX 02-NOV-2000 (first entry)
XX
XX
XX DNA containing human uncoupling protein-2 (UCP-2) promoter region.
XX
XX
XX Promoter; human; uncoupling protein-2; UCP-2; obesity; diabetes;
XX
XX hypotensive; hyperlipidaemia; anti-pyretic; ds.
XX
XX Homo sapiens.
XX
XX
XX WO200039315-A1.
XX
XX 06-JUL-2000.
XX
XX
XX 22-DEC-1999; 99WO-JP007198.
XX
XX
XX 24-DEC-1998; 98JP-00366719.
XX
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Toyoda Y, Kobayashi M, Igaki S;
XX
XX WPI; 2000-452407/39.
XX
XX
XX DNA with promoter region containing regulator sequence of uncoupling
XX protein-2 (UCP-2), applicable in screening anti-obesity, anti-diabetic,
XX hypotensive, anti-hyperlipidemic and anti-pyretic drugs for use in
XX therapy.
XX
XX
XX Claim 4; Fig 1-6; 43pp; Japanese.
XX
XX This invention relates to DNA comprising a promoter region containing the
XX regulatory sequences of human uncoupling protein-2 (UCP-2). Included in
XX the invention are a recombinant vector containing the DNA sequence, cells
XX transformed by the vector, and a method for screening for compounds or
XX salts that can promote or inhibit the UCP-2 promoter activity using the

CC transformants. The DNA and cells transformed using it can be used to
CC screen for anti-obesity, anti-diabetic, hypotensive, anti-hyperlipidaemic
CC and anti-pyretic drugs. The present sequence represents DNA containing
CC the UCP-2 promoter sequences

XX
SQ Sequence 3505 BP; 671 A; 1053 C; 894 G; 887 T; 0 U; 0 Other;

Query Match 100.0%; Score 176; DB 3; Length 3505;
Best Local Similarity 100.0%; Pred. No. 3e-48;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGTAATTCAGTACTGTAGAGTCCGAGGCTCAGAGACTGCTTGAAGCCAGAGTTTC 60
DB 255 ACCTGTAATTCAGTACTGTAGAGTCCGAGGCTCAGAGACTGCTTGAAGCCAGAGTTTC 314
QY 61 AAGAGCAGCTGGACAAACAGGAGAGCCTGTCACTACAAAGATTAATTAATTAAGCCAG 120
DB 315 AAGAGCAGCTGGACAAACAGGAGAGCCTGTCACTACAAAGATTAATTAATTAATTAAGCCAG 374
QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGCTACTAGGAGGACAGAACTAGACTGCT 176
DB 375 GCTTAGTGCTCATCCCTGTGTGCCAGCTACTAGGAGGACAGAACTAGACTGCT 430

RESULT 2
ABT10147/c
ID ABT10147 standard; cDNA; 185035 BP.

XX ABT10147;

DT 04-DEC-2002 (first entry)

DE Human breast cancer associated coding sequence SEQ ID NO: 281.

KM Human; breast specific gene; breast cancer; differential expression;
KW cytosolic; gene therapy; gene; ss.

OS Homo sapiens.

PN MO200259271-A2.

PD 01-AUG-2002.

PF 25-JAN-2002; 2002MO-US002176.

PR 25-JAN-2001; 2001US-0263757P.

PR 25-APR-2001; 2001US-0286090P.

PR 23-MAY-2001; 2001US-0292517P.

XX (GENE-) GENE LOGIC INC.

PI Orr MS, Nation M, Diggs J, Zeng W;

DR WPI; 2002-674803/72.

XX
PT Diagnosing breast cancer in a patient comprises detecting the level of
PT gene expression in cell or tissue samples, where a differential gene
PT expression is indicative of breast cancer.

XX
PS Claim 1; SEQ ID NO 281; 260pp + Sequence Listing; English.

XX
CC The present invention relates to methods of diagnosing breast cancer in a
CC patient, which comprise detecting the level of expression in a tissue
CC sample of two or more genes selected from those shown in ABT09867-
CC ABT1112, where a differential expression of the genes indicates breast
CC cancer. The methods are useful in diagnosing, treating, detecting the
CC progression, and in monitoring treatment of breast cancer in patients.
CC The methods are also useful as a screening tool for agents that modulate
CC the onset or progression of breast cancer. The breast cancer genes may be
CC used as diagnostic markers for the prediction or identification of the
CC malignant state of breast tissue, for confirming the type and progression
CC of cancer, and for drug screening and assays. The present sequence is a
CC coding sequence of the invention. Note: The sequence data for this patent

CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 185035 BP; 42256 A; 51727 C; 51210 G; 39842 T; 0 U; 0 Other;

Query Match 64.0%; Score 112.6; DB 6; Length 185035;
Best Local Similarity 82.5%; Pred. No. 2.1e-26;
Matches 141; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 2 CCTGTAATTCAGTACTGTAGAGTCCGAGGCTCAGAGACTGCTTGAAGCCAGAGTTTC 61
DB 150502 CCTGTAATTCAGTACTGTAGAGTCCGAGGCTCAGAGACTGCTTGAAGCCAGAGTTTC 150443
QY 62 AAGAGCAGCTGGACAAACAGGAGAGCCTGTCACTACAAAGATTAATTAATTAAGCCAG 120
DB 150442 AAGAGCAGCTGGACAAACAGGAGAGCCTGTCTACAAAATTAATTAATTAAGCCAG 150383
QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGCTACTAGGAGGACAGAACTAGAGA 171
DB 150382 GCATGTGGACATGCTGTGACCCAGCTACTTGGAGAGCTGAGGTAGAGA 150332

RESULT 3
ACA64951/c
ID ACA64951 standard; DNA; 185035 BP.

XX ACA64951;

DT 27-JUN-2003 (first entry)

DE Human FEN1 DNA corresponding to AC004770.

KM Human; chronic inflammatory joint disease; infection; tumour;
KW antiinflammatory; cytosolic; antirheumatic; antineumatic;
KW immunosuppressive; gene therapy; etiological pathogenicity; ds.

OS Homo sapiens.

PN DE10127572-A1.

PD 05-DEC-2002.

PF 30-MAY-2001; 2001DE-01027572.

PR 30-MAY-2001; 2001DE-01027572.

PA (PATR-) PATHOARRAY GMBH.

PI Haepfl T, Ungethuem U, Blaess S;

DR WPI; 2003-240797/24.

XX
PT Reagents for diagnosis, study and therapy of chronic inflammatory joint
PT and other diseases, comprises any of many specified genes or derived
PT proteins.

XX
PS Claim 1; Page; 12pp; German.

XX
CC This invention describes a novel reagent for diagnosis, molecular
CC definition and therapy of chronic inflammatory joint diseases, and other
CC inflammatory disorders, infective or tumour diseases in humans. The
CC products of the invention have antiinflammatory, cytosolic,
CC antirheumatic, antineumatic and immunosuppressive activity and can be
CC used for gene therapy. The reagent of the invention and any proteins and
CC antibodies derived from it, are used (i) for analysing tissue and blood
CC samples for medical diagnosis; (ii) for diagnosis and characterisation of
CC chronic joint diseases, on the basis of molecular characterisation, and
CC determining the etiological pathogenicity principle of as yet
CC uncharacterised inflammatory diseases, also monitoring progression and/or
CC treatment of disease, and optimisation of therapy and (iii) for
CC developing treatments for inflammatory diseases, particularly of joints,
CC infections and tumours. ACA64801-ACA64965 represent human polynucleotides

CC used in the method of the invention
XX Sequence 185035 BP; 42256 A; 51727 C; 51210 G; 39842 T; 0 U; 0 Other;
SQ

Query Match 64.0%; Score 112.6; DB 8; Length 185035;
Best Local Similarity 82.5%; Pred. No. 2.1e-26;
Matches 141; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 2 CCTGTATTCCAGTACTGTAGAGTCCGAGGTCCAGAGCTGTGAGGCCAGAGTTCA 61
DB 150502 CCTGTATTCCAGTACTGTGAGGCCGAGGTGAGAGATTGCTTGAGGCCAGAGTTTG 150443

QY 62 AGAGCAGCCTTGAGCAACACAGGAGGAG-CTGTCACTCAAAAGATTAATTAATTAAGCCAG 120
DB 150442 AGACACAGCCTTGAGCAACATAGTAGAGCCCTGTCTCAAAAAAATAATTAAGCCAA 150383

QY 121 GCTTAGTGCTCATCCCTGTGTGTCCTCACTACTAGGAGCAGAGATGAGA 171
DB 150382 GCATGTGTGACATGTGCTGTGACCCAGCTACTTGGAGGCTGAGTAGGA 150332

RESULT 4
ADQ20284/C
ID ADQ20284 standard; DNA; 185035 BP.
XX
XX ADQ20284;
XX
XX 26-AUG-2004 (first entry)
XX
XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 3104.
XX
XX soft tissue sarcoma; cytoskeletal; gene therapy; vaccine; screening; human;
XX
XX de.
XX
XX Homo sapiens.
XX
XX WO2004048938-A2.
XX
XX 10-JUN-2004.
XX
XX 26-NOV-2003; 2003WO-US038193.
XX
XX 26-NOV-2002; 2002US-0429739P.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Aziz N, Ginsburg WM, Zlotnick A;
XX
XX WPI; 2004-441208/41.
XX
XX
XX Early detection of soft tissue sarcoma comprises determining expression
XX of a gene in a first soft tissue sample and a normal soft tissue sample
XX and comparing the gene expression, also useful in treating soft tissue
XX sarcoma.
XX
XX Example 2; SEQ ID NO 3104; 210pp; English.

CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytoskeletal applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
XX Sequence 185035 BP; 42256 A; 51727 C; 51210 G; 39842 T; 0 U; 0 Other;
SQ

Query Match 64.0%; Score 112.6; DB 12; Length 185035;
Best Local Similarity 82.5%; Pred. No. 2.1e-26;
Matches 141; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

QY 2 CCTGTATTCCAGTACTGTAGAGTCCGAGGTCCAGAGCTGTGAGGCCAGAGTTCA 61
DB 150502 CCTGTATTCCAGTACTGTGAGGCCGAGGTGAGAGATTGCTTGAGGCCAGAGTTTG 150443

QY 62 AGAGCAGCCTTGAGCAACACAGGAGGAG-CTGTCACTCAAAAGATTAATTAATTAAGCCAG 120
DB 150442 AGACACAGCCTTGAGCAACATAGTAGAGCCCTGTCTCAAAAAAATAATTAAGCCAA 150383

QY 121 GCTTAGTGCTCATCCCTGTGTGTCCTCACTACTAGGAGCAGAGATGAGA 171
DB 150382 GCATGTGTGACATGTGCTGTGACCCAGCTACTTGGAGGCTGAGTAGGA 150332

RESULT 5
ADQ62996/C
ID ADQ62996 standard; cDNA; 3521 BP.
XX
XX ADQ62996;
XX
XX 07-OCT-2004 (first entry)
XX
XX
XX Novel human cDNA sequence #157.
XX
XX ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian;
XX cytoskeletal; gene therapy; diagnostic marker; morbid state; osteoporosis;
XX neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
XX cancer.
XX
XX Homo sapiens.
XX
XX EP1440981-A2.
XX
XX 28-JUL-2004.
XX
XX 21-JAN-2004; 2004EP-00001196.
XX
XX 21-JAN-2003; 2003JP-00102206.
XX
XX 09-MAY-2003; 2003JP-00131392.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isegai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX Yamamoto J, Isono Y, Nagai K, Irie R;
XX
XX WPI; 2004-535376/52.
XX
XX P-PsDB; ADQ65184.
XX
XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
XX Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
XX Claim 1; SEQ ID NO 157; 2449pp; English.

CC The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a nucleotide
CC sequence of the invention.
XX
XX
XX Sequence 3521 BP; 727 A; 1051 C; 919 G; 824 T; 0 U; 0 Other;
SQ

Query Match 63.9%; Score 112.4; DB 12; Length 3521;
Best Local Similarity 78.8%; Pred. No. 6e-27;
Matches 134; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 2 CCTGTATTCCAGTACTGTAGAGTCCGAGGTCCAGAGCTGTGAGGCCAGAGTTCA 61

```
DB 910 CCTGTAATCCCAACACTTTGGAGGCTGAGGAGGAGGATTTGTTAGGCGCAGAGCTTCA 851
OY 62 AGAGCAGCCTTGACACACACAGGAGACTGTCTACTACTAAAGATTAATTAATTAAGCCAG 121
DB 850 AAGACGAGCTGGGCAACATAGAGAGCCCTGTCTCTCAAAAATTTTAAATTAATTAAGCTGG 791
OY 122 CTTAGTGCTCATCCTCTGTGTGTCACGCTACTAGAGGAGCAGAGTAAAGTA 171
DB 790 CGGTGTGGGCGCATGCTGTAGTTCCAGCTACTTGGGAAACAGAGTGGGA 741

RESULT 6
ADM02195
ID ADM02195 standard; cDNA; 2312 BP.
XX
XX
AC ADM02195;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Human cDNA of the invention SEQ ID NO:880.
XX
XX KM ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.
XX
XX OS Homo sapiens.
XX
XX PN EP1347046-A1.
XX
XX PD 24-SEP-2003.
XX
XX PF 12-APR-2002; 2002EP-00008400.
XX
XX PR 22-MAR-2002; 2002JP-00137785.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX PA Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;
XX
XX DR WPI: 2003-723558/69.
XX
XX P-PSDB; ADM04638.
XX
XX PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
XX PS Claim 1; SEQ ID NO 880; 305bp; English.
XX
XX CC The invention relates to a novel human polynucleotide and the encoded
XX polypeptide. A polynucleotide of the invention may have a use in gene
XX therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
XX as a primer for synthesizing the polynucleotide or as a probe for
XX detecting the polynucleotide. The polynucleotides ADM03136-ADM03758 are
XX useful in gene therapy, for developing a diagnostic marker or medicines
XX for regulating their expression and activity, or as a target of gene
XX therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
XX are useful as pharmaceutical agents. The present sequence represents a
XX cDNA sequence of the invention.
XX
XX SQ Sequence 2312 BP; 609 A; 493 C; 563 G; 647 T; 0 U; 0 Other;

Query Match 63.6%; Score 112; DB 11; Length 2312;
Best Local Similarity 82.0%; Pred. No. 7e-27;
Matches 141; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

OY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGTTGAGGCCAGAGATTC 60
DB 1142 ACCTGTAATTCGCGCACTTTGGAGGCTGAGGTGAGAGACTGTTGAGTCCAGAGATTC 1201
OY 61 AAGAGCAGCCTTGACACACACAGGAGAGC-CTGTCACTACAAAGATTAATTAATTAAGCA 119
DB 1202 AAGACGAGCTGGGCAACATAGTAGACTTTGCTCTCAAAAATTTTAAATTAATTAAGCTG 1261
```

```
OY 120 GCGTTAGTGGCTCATCCTCTGTGTGTCACGCTACTAGAGGAGGCAAGTAAGGA 171
DB 1262 GCGATGTGGCAGACATGCTGTGGTCCAGCTACTTGGGAGGCGCAAGCAGAGA 1313

RESULT 7
AEC85125
ID AEC85125 standard; cDNA; 2312 BP.
XX
XX AC AEC85125;
XX
XX DT 01-DEC-2005 (first entry)
XX
XX DE Human cDNA clone FEBRA20093520, SEQ ID 880.
XX
XX KM Osteopathic; Cytostatic; Antiinflammatory; Gastrointestinal-Gen.;
XX Antulcer; Gene Therapy; Osteoporosis; cancer; inflammation; gastritis;
XX Stomach ulcer; gastrointestinal ulcer; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1580263-A1.
XX
XX PD 28-SEP-2005.
XX
XX PF 12-APR-2002; 2004EP-00027348.
XX
XX PR 22-MAR-2002; 2002JP-00137785.
XX
XX PR 12-APR-2002; 2002EP-00008400.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX PA Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;
XX
XX DR WPI: 2005-667421/69.
XX
XX P-PSDB; AEC87568.
XX
XX PT New full-length cDNA sequences, useful for treating diseases, e.g.
PT osteoporosis, cancer, inflammation, gastritis, or gastroduodenal ulcer.
XX
XX PS Example 3; SEQ ID NO 880; 296bp; English.
XX
XX CC The present invention relates to novel human cDNAs (AEC84246-AEC86688)
XX encoding proteins AEC86689-AEC89131. The cDNAs are useful for analyzing
XX the functions of the proteins, and for developing medicines for diseases
XX e.g. osteoporosis, cancer, inflammation, gastritis, or gastroduodenal
XX ulcer. Note: The sequence data for this patent did not form part of the
XX printed specification but was obtained in electronic format directly from
XX EPO.
XX
XX SQ Sequence 2312 BP; 609 A; 493 C; 563 G; 647 T; 0 U; 0 Other;

Query Match 63.6%; Score 112; DB 14; Length 2312;
Best Local Similarity 82.0%; Pred. No. 7e-27;
Matches 141; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

OY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGTTGAGGCCAGAGATTC 60
DB 1142 ACCTGTAATTCGCGCACTTTGGAGGCTGAGGTGAGAGACTGTTGAGTCCAGAGATTC 1201
OY 61 AAGAGCAGCCTTGACACACACAGGAGAGC-CTGTCACTACAAAGATTAATTAATTAAGCA 119
DB 1202 AAGACGAGCTGGGCAACATAGTAGACTTTGCTCTCAAAAATTTTAAATTAATTAAGCTG 1261
OY 120 GCGTTAGTGGCTCATCCTCTGTGTGTCACGCTACTAGAGGAGCAGAAAGTAAGGA 171
DB 1262 GCGATGTGGCAGACATGCTGTGTGTCACGCTACTTGGGAGGCGCAAGCAGAGA 1313

RESULT 8
```

AAK82979/c
ID AAK82979 standard; DNA; 13001 BP.
XX
AC AAK82979;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37791.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234977P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235464P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236337P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239355P.
PR 13-OCT-2000; 2000US-0239357P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.

PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251899P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 DR WPI; 2001-483426/52.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 useful for preventing, diagnosing and/or treating cancers and metastasis.
 XX
 PS Disclosure; SEQ ID NO 37791; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
 amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 activity, and can be used in gene therapy and vaccine production. (I)
 proteins and polynucleotides may be used in the prevention, diagnosis and
 treatment of diseases associated with inappropriate (I) expression. For
 example, they may be used to treat disorders associated with decreased
 expression by rectifying mutations or deletions in a patient's genome
 that affect the activity of (I) by expressing inactive proteins or to
 supplement the patient's own production of (I). Additionally, (I)
 polynucleotides may be used to produce the secreted (I), by inserting the
 nucleic acids into a host cell and culturing the cell to express the
 protein. (I) proteins and polynucleotides may be used to prevent,
 diagnose and treat immune/haematopoietic-related diseases, especially
 cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 to AAK87694 represent human immune/haematopoietic antigen genomic
 sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 13001 BP; 2839 A; 3915 C; 3680 G; 2567 T; 0 U; 0 Other;
 Query Match 63.0%; Score 110.8; DB 4; Length 13001;
 Best Local Similarity 78.2%; Pred. No. 3.3e-26;
 Matches 133; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
 QY 2 CCTGTAATTCGACTACTGTGAGAGTCCGAGGTCAGAGACTGTTGAGCCAGAGTTCA 61
 DB 1517 CCTGTAATTCGACTACTGTGAGAGTCCGAGGTCAGAGACTGTTGAGCCAGAGTTCA 1458
 QY 62 AGAGCAGCCTGGAACAACAGGAGACCTGTCACTACAAAGAAATTAATTAGCCAGG 121
 DB 1457 AGAGCAGCCTGGAACAACAGGAGACCTGTCTCTCAAAAATTTAAAAAATAGCCGG 1398
 QY 122 CTTAGTGCTCATTCCTGTGCTCCAGCTACTAGGAGGAGCAAGTAGCA 171
 DB 1397 CGTAGTGCTGTGCTGTGCTGATTCAGCTACTTGGAGAGCAAGTAGGGA 1348
 RESULT 9
 ADR26544
 ID ADR26544 standard; DNA; 38653 BP.
 XX
 AC ADR26544;
 XX
 DT 11-MAR-2004 (first entry)
 DE Human heart failure-associated gene hUNC93B1.
 XX
 KM Human; heart failure-associated gene; hUNC93B1; de; gene;
 KM chromosome 11q13; SNP; single nucleotide polymorphism; heart failure;
 KM 12 transmembrane transporter; left ventricular diastolic heart failure;
 KM systolic heart failure.

XX Homo sapiens.
 OS
 XX Key
 FH variation
 FT Location/Qualifiers
 FT 24801
 FT /tag= A
 FT /standard_name= "Single nucleotide polymorphism"
 FT /label= A,G
 FT 24941
 FT /tag= b
 FT /standard_name= "Single nucleotide polymorphism"
 FT /label= T,C
 FT 26157..38653
 FT /tag= d
 FT 26157..26252
 FT /tag= c
 FT 26253..26401
 FT /tag= e
 FT 26402..26543
 FT /tag= f
 FT 26544..27024
 FT /tag= g
 FT 27025..27178
 FT /tag= h
 FT 27179..30519
 FT /tag= i
 FT 27645
 FT /tag= j
 FT /standard_name= "Single nucleotide polymorphism"
 FT /label= C,G
 FT 30520..30681
 FT /tag= k
 FT 30682..30894
 FT /tag= l
 FT 30895..31027
 FT /tag= m
 FT 31028..31747
 FT /tag= n
 FT 31748..31841
 FT /tag= o
 FT 31842..32400
 FT /tag= p
 FT 32163
 FT /tag= q
 FT /standard_name= "Single nucleotide polymorphism"
 FT /label= A,C
 FT 32401..32528
 FT /tag= r
 FT 32529..33414
 FT /tag= s
 FT 32614
 FT /tag= t
 FT /standard_name= "Single nucleotide polymorphism"
 FT /label= A,G
 FT 33415..33597
 FT /tag= u
 FT 33598..34314
 FT /tag= v
 FT 34315..34588
 FT /tag= w
 FT 34589..36404
 FT /tag= x
 FT 36405..36523
 FT /tag= y
 FT 36524..38341
 FT /tag= z
 FT 38342..38653
 FT /tag= aa
 XX
 PN US6528268-B1.
 XX
 PD 04-MAR-2003.
 XX

PF		03-AUG-2001; 2001US-00922445.	
XX			
PR		03-AUG-2001; 2001US-00922445.	
XX			
PA	(SECU-)	SEQUENOM GEMINI LTD.	
PI	Andersson MK,	Berglund LGT,	Reneland RH, Adam GIR;
DR	WPI; 2004-088115/09.		
XX			
XX			
PT	Diagnosing predisposition to left ventricular diastolic heart failure in		
PT	a human comprises detecting the presence or absence of an allelic variant		
PT	at position 24941 of hUNC93B1 gene.		
XX			
PS	Claim 1; SEQ ID NO 1; 53bp; English.		
CC	The invention relates to diagnosing predisposition to left ventricular		
CC	diastolic heart failure in a human comprises detecting the presence or		
CC	absence of an allelic variant at position 24941 of the heart failure		
CC	associated gene appearing as ADH26544(hUNC93B1, encoding a possible 12		
CC	transmembrane receptor protein) in the sample, where the presence or		
CC	absence of the allelic variant is indicative of a predisposition to left		
CC	ventricular diastolic heart failure in the human. The method further		
CC	comprises determining the genotype of the human at position 24941 of		
CC	ADH26544. The method is useful for diagnosing predisposition to left		
CC	ventricular diastolic and systolic heart failure. The hUNC93B1 gene is		
CC	located on chromosome 11q13. The present sequence is the human heart		
CC	failure associated gene hUNC93B1.		
XX			
SQ	Sequence 38653 BP; 7944 A; 10836 C; 11667 G; 8201 T; 0 U; 5 Other;		
	Query Match	63.0%; Score 110.8; DB 12; Length 38653;	
	Best Local Similarity	78.2%; Pred. No. 4.9e-26;	
	Matches 133; Conservative 0; Mismatches 37; Indels 0; Gaps 0;		
OY	2 CCTGTAAATTCACGACTGTGAGAGCTCCGAGTGTCAGAGACTGTTNAGGCCAGAGATTCA	61	
DB	37583 CCTGTAAATCCCACACACTTTGGGAGGCTGAGAGCGAGGAGATTGCTTAGAGCCAGGAGTTCA	37642	
OY	62 AGAGCAGCGCTGGACAACACACAGGGGAGACCCTGTCACTACAAAGAATAAATTAGCCAGG	121	
DB	37643 AGACCAAGCCTGGGACAACTAGAGAACCCCTCTCTCTCAAAAAAATTAAAATAAGCTGGG	37702	
OY	122 CTTATGGGCTCATCCCTGTGGTCCCACTACTAGAGGAGGCAGAAAGTAGGA	171	
DB	37703 CGTAGTGGCGGTGTCCTGTAGTTCCAGCTACTTTGGGAGACTGAAGTGGGA	37752	
RESULT 10			
ACN45018/C			
ID	ACN45018 standard; DNA; 81099 BP.		
XX			
AC	ACN45018;		
XX			
DT	18-NOV-2004 (first entry)		
XX			
DE	Human genomic sequence hCG17395.		
KM	Cytosstatic; carcinoma; lymphoma; cancer; human; gene; ss.		
OS	Homo sapiens.		
PN	WO2003073826-A2.		
PD	12-SEP-2003.		
PF	28-FEB-2003; 2003WO-US006235.		
PR	01-MAR-2002; 2002US-00087192.		
PA	(SAGR-) SAGRES DISCOVERY.		
PI	Morris DW;		

XX	WP1: 2003-328604/31.
DR	
XX	Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT	comprises a nucleotide sequence.
XX	
PS	Claim 1; SEQ ID NO 1756; Opp; English.
XX	
CC	The present invention relates to novel DNA and protein sequences which
CC	are associated with carcinomas. The sequences are useful for: (i) for
CC	screening drug candidates; (ii) for screening of bioactive agent capable
CC	of binding to CarcinoMa Associated Protein (CAP); (iii) for screening of
CC	a bioactive agent capable of modulating the activity of CAP; (iv) for
CC	evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC	carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC	carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC	(x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC	determining CarcinoMa Associated (CA) gene copy number. In addition, the
CC	CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC	carcinoma including Lymphoma. The present sequence is one such CA coding
CC	sequence. Note: This patent is an equivalent to basic patent
CC	US2002182586m1, for which no sequence data was published
XX	
SEQ	Sequence 81099 BP; 20015 A; 18716 C; 19786 G; 22439 T; 0 U; 143 Other;
Query Match	62.2%; Score 109.4; DB 11; Length 81099;
Best Local Similarity	76.6%; Pred. No. 1.9e-25;
Matches 134; Conservative	0; Mismatches 41; Indels 0; Gaps 0;
OY	2 CCTGTATTTCCTAGTACTGTGAGAGCTCCAGAGTCAGAGACCTCTTAGGCCAGAGTTCA 61
DB	18811 CCTGAAATTCCTACACACTTGTGGAGGCCAAGGACGAGAGACTCTTAGGCCAGAGTTCC 18752
OY	62 AGAGCAGCCTGAGCAACAACAGGAGACCTGTCACTACAAAGAATAATTAATTAAGCCAGG 121
DB	18751 AGACCACTCTGGGCAACATGAAAGACCTTCATCTACAAAAATAAAAAATTTAGCCAGG 18692
OY	122 CTTAGTGCTCATCTCCTGTGTGTCCTCAAGCTTACATAGGAGGCAAGATGAGACTGCT 176
DB	18691 CGGTGTCTCTACGCGCTGTAGTCCAGACTACAGAGAGGCTGAAGTGGAGGAGACT 18637
RESULT 11	
ADN12517	
ID	ADN12517 standard; cDNA; 620 BP.
XX	
AC	ADN12517;
XX	
DT	29-JUL-2004 (first entry)
XX	
DE	Human prostate/colon/lung/breast cancer-related cDNA 32, SEQ:32.
XX	
KW	Human; cancer; tumour; prostate cancer; colon cancer; lung cancer;
KW	breast cancer; drug screening; diagnosis; prognosis; prevention;
KW	gene mapping; tissue typing; tissue profiling; cytostatic; gene therapy;
XX	89.
XX	
OS	Homo sapiens.
XX	
PM	WO2004039943-A2.
XX	
PD	13-MAY-2004.
XX	
PE	16-MAY-2003; 2003WO-US015465.
XX	
PR	17-MAY-2002; 2002US-0381533P.
XX	
PR	04-FEB-2003; 2003US-0445222P.
XX	
PA	(CHIR) CHIRON CORP.
XX	
PI	Scott EM, Lamson G, Kassam A, Zhang G, Sakamoto D, Garcia PD;
XX	
DR	WP1; 2004-376173/35.

XX New isolated polynucleotides, useful for gene mapping or tissue typing or
PT profiling, as diagnostic reagents, and for preventing or treating cancer,
XX e.g. prostate, colon, or breast cancer.

PS Claim 2; SEQ ID NO 32; 190pp; English.

XX The invention relates to nucleic acids (ADN12486-ADN13970) isolated from
CC human prostate, colon, lung and breast cancer cDNA libraries, and to 57
CC proteins (ADN13971-ADN14027) encoded by a subset of these cDNA sequences
CC (ADN13914-ADN13970). The invention also relates to vectors and host cells
CC comprising a nucleic acid of the invention; a method for the recombinant
CC production of a protein of the invention; an antibody specific for a
CC protein of the invention; a polynucleotide library comprising at least
CC one nucleic acid sequence of the invention; a method for detecting a
CC cancerous cell by PCR or probe hybridization; inhibiting a cancerous
CC phenotype (particularly aberrant proliferation) of a cell; a method of
CC identifying an agent that modulates the biological activity of a gene
CC product differentially expressed in a cancerous cell compared with a
CC normal cell; and a method of treating a cancer patient using the agent
CC identified. The nucleic acids and polypeptides can be used to diagnose,
CC prognose, treat or prevent cancers such as prostate, colon, lung or
CC breast cancer, and can also be used to screen for drugs for the treatment
CC of cancer. The nucleic acids can also be used for gene mapping, tissue
CC typing and tissue profiling. The present sequence represents a
CC specifically claimed cancer-related cDNA of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 620 BP; 177 A; 139 C; 162 G; 142 T; 0 U; 0 Other;

XX Query Match 62.0%; Score 109.2; DB 12; Length 620;
Best Local Similarity 77.6%; Pred. No. 3.8e-26;
Matches 132; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGCTCAGAGAGCTGTTGAGCCAGAGTTCA 61

DB 290 CTTGTAATCCAGTACTGTTGAGAGCTGAGTGAATGATCAGCTGAGGTCAAGAGTTCA 349

QY 62 AGAGCAGCCTGGACACACAGGAGAGCTGTCTCACTCAAGAAATAAATTAATTAAGCCAGG 121

DB 350 AGACCAAGCCTGGCCAAATGTAATCTTCTACTTAAATAATCAAAAATTAAGCCAGG 409

QY 122 CTTAGTGCTCATCCCTGTGTGTCCTCAGCTACTAGGAGGAGAGATAGGA 171

DB 410 TGTGTGTGCGACGTGCTGTATCTCAGCTACTGCGAGAGGCTGAAGCAGA 459

RESULT 12

ACN44954
ID ACN44954 standard; DNA; 3116 BP.

AC ACN44954;

DT 18-NOV-2004 (first entry)

DE Human genomic sequence hCG38622.

XX Cytoskeletal; carcinoma; lymphoma; cancer; human; gene; ss.

OS Homo sapiens.

PN MO2003073826-A2.

PD 12-SEP-2003.

PF 28-FEB-2003; 2003WO-US006235.

PR 01-MAR-2002; 2002US-00087192.

PA (SAGR-) SAGRES DISCOVERY.

PI Morris DW;

DR WPI; 2003-328604/31.

XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma

PT comprises a nucleotide sequence.

PS Claim 1; SEQ ID NO 1660; Opp; English.

XX The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) as a biochip;
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US200212586A1, for which no sequence data was published

XX Sequence 31116 BP; 7214 A; 8217 C; 7722 G; 7963 T; 0 U; 0 Other;

XX Query Match 62.0%; Score 109.2; DB 11; Length 31116;
Best Local Similarity 77.6%; Pred. No. 1.5e-25;
Matches 132; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGCTCAGAGAGCTGTTAAGCCAGAGTTCA 61

DB 24557 CCGCAATCCAGCAGCTTTGGAGGCTGAGCGGTGGATGTGTTAAGCCAGAGTTCA 24616

QY 62 AGAGCAGCCTGGACACACAGGAGAGCTGTCTCACTCAAGAAATAAATTAATTAAGCCAGG 121

DB 24617 AGACCAAGCCTGGCCAAATGTAATCTTCTTCACTTAAATAATCAAAAATTAAGCTGG 24676

QY 122 CTTAGTGCTCATCCCTGTGTGTCCTCAGCTACTAGGAGGAGCAAGATAGGA 171

DB 24677 GATGTGTGTGACAGCCTGTGTGTCCTCAGCTATTGCGGAGCTGAAGCAGA 24726

RESULT 13

ADZ13255
ID ADZ13255 standard; DNA; 31279 BP.

AC ADZ13255;

DT 16-JUN-2005 (first entry)

DE Human cancer-associated genomic DNA #63.

XX Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;

XX cytoskeletal; gene; ds.

OS Homo sapiens.

PN MO2005031001-A2.

PD 07-APR-2005.

PF 23-SEP-2004; 2004WO-US031617.

PR 23-SEP-2003; 2003US-00669920.

PA (CHIR) CHIRON CORP.

PI Morris DW, Malandro MS;

DR WPI; 2005-273395/28.

XX Nucleic acid array useful for detecting cancer associated nucleic acid,

PT comprises two or more nucleic acid probes.
XX
PS Disclosure; SEQ ID NO 775; 198bp; English.
XX
CC The invention relates to a nucleic acid array for detecting a cancer
CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
CC The invention also relates to a peptide array comprising two or more
CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
CC that binds to a polypeptide, an isolated antibody or its fragment which
CC binds to a polypeptide, which is prepared by immunizing a host animal
CC with a composition comprising the polypeptide or its antigen binding
CC fragment and collecting cells from the host expressing antibodies against
CC the antigen or its antigen binding fragment, a composition comprising the
CC antibody and a carrier, a method of screening for anticancer activity, a
CC method of detecting a CA nucleic acid, a method of diagnosing cancer,
CC method of treating cancer and a method of inhibiting expression of a CA
CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
CC nucleic acid. The antibody is useful for detecting the presence or
CC absence of cancer cells in an individual which involves contacting cells
CC from the individual with the antibody and detecting a complex of a CA
CC protein from the cancer cells and the antibody, where the detection of
CC the complex correlates with the presence of cancer cells in the
CC individual. The composition is useful for inhibiting growth of cancer
CC cells in an individual or for delivering a therapeutic agent to cancer
CC cells in an individual. The invention is also useful for diagnosing
CC cancer, for treating cancer and for inhibiting expression of a CA gene in
CC a cell. This sequence represents human cancer-associated genomic DNA of
CC the invention.
XX
SQ Sequence 31279 BP; 7246 A; 8268 C; 7755 G; 8010 T; 0 U; 0 Other;
Query Match 62.0%; Score 109.2; DB 14; Length 31279;
Best Local Similarity 77.6%; Pred. No. 1.5e-25;
Matches 132; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 2 CCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCCAGAGACTGTTGAGCCAGAGTTCA 61
DB 24713 CTTGCATATCCAGACATTTGGGAGCTGAGCGCGGTGGATTGTAAGCCAGAGTTCA 24772
QY 62 AGAGCAGCCTGGACAACACAGGAGACCTGTCTACTACAAAGAAATTAATTATTCAGCAG 121
DB 24773 AGACCACTCTGGGCAACATAGTGTAGACCTGTCTTACAAATAATTAATTATTCAGCAG 24832
QY 122 CTTAGTGCTCATCTCTGTGGTCCAGCTACTAGAGAGGAGAGTATGGA 171
DB 24833 GATGTGTGTGACGCCCTGTGTGTCCAGCTATTGTGGGGGCTGAAGCAAGA 24882
RESULT 14
ADA02540
ID ADA02540 standard; DNA; 58822 BP.
XX
AC ADA02540;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human TCOF1 carcinoma associated gene, SEQ ID NO:1058.
XX
KW Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
KW prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003057146-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041414.
XX
PR 26-DEC-2001; 2001US-00035832.
XX
PA (SAGR-) SAGRES DISCOVERY.

XX
PI Morris DW;
XX
DR WPI; 2003-587068/55.
XX
PT New recombinant nucleic acid encoding carcinoma associated protein,
XX useful for preparing compositions for treating carcinomas.
PS Claim 1; SEQ ID NO 1058; 245pp; English.
XX
CC The invention relates to recombinant carcinoma associated (CA) nucleic
CC acid sequences from mouse and human (ADA01482-ADA03094), and to
CC recombinant carcinoma associated proteins (CAP) encoded by them. The
CC invention also encompasses expression vectors and host cells comprising a
CC CA nucleic acid, a polypeptide (especially an antibody) that specifically
CC binds to the protein, and a biochip comprising CA nucleic acid or
CC fragments thereof. The sequences of the invention were identified using
CC oncogenic retroviruses, which insert into the genome of the host organism
CC at random. Many of these do not carry transduced host oncogenes or
CC pathogenic trans-acting viral genes, meaning that cancer incidence is a
CC direct consequence of the effects of proviral integration into host
CC protooncogenes. The CA nucleic acid sequences can be used to diagnose
CC carcinoma (especially breast cancer, prostate cancer, lymphoma or
CC leukaemia) or a propensity to carcinoma by determination of the sequence
CC of a CA gene, or by determination of CA gene expression in particular
CC tissues. CA nucleic acids, proteins and antibodies are also useful as
CC therapeutic agents and in screening and evaluating drug candidates. The
CC present sequence represents a specifically claimed human CA nucleic acid
CC sequence of the invention. Note: The complete sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 58822 BP; 14199 A; 14875 C; 15625 G; 13656 T; 0 U; 467 Other;
Query Match 62.0%; Score 109.2; DB 9; Length 58822;
Best Local Similarity 77.6%; Pred. No. 1.9e-25;
Matches 132; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 2 CCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCCAGAGACTGTTGAGCCAGAGTTCA 61
DB 740 CTTGTAAATTCAGACATTTGAGGGCTGAGGGTGGTGTATCATTGTGAGCCAGAGTTCA 799
QY 62 AGAGCAGCCTGGACAACACAGGAGACCTGTCTACTACAAAGAAATTAATTATTCAGCAG 121
DB 800 AGACCACTCTGGGCAACATAGTGTAGAACCATCTCTTACAAATAATTAATTATTCAGCAG 859
QY 122 CTTAGTGCTCATCTCTGTGGTCCAGCTACTAGAGAGGAGAGTATGGA 171
DB 860 CATGTGTGTGACATGCTGTAGTCCAGCTACTCGGAGGCTGAGGACAGGA 909
RESULT 15
ADA02540/C
ID ADA02540 standard; DNA; 58822 BP.
XX
AC ADA02540;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human TCOF1 carcinoma associated gene, SEQ ID NO:1058.
XX
KW Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
KW prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003057146-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041414.

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:39:00 ; Search time 1218.72 Seconds
(without alignments)
8075.514 Million cell updates/sec

Title: US-09-869-098a-1_COPY_255_430

Perfect score: 176
Sequence: 1 acctgtaaccagctactgtc.....gagcgagaagtagactgct 176

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	113.4	64.4	1209	3	BU182693	BU182693 AGENCOURT
C 2	112	63.6	881	14	DU798537	DU798537 Fv01 fP0
C 3	110.8	63.0	282	1	AI244764	AI244764 q197h07.x
C 4	110.6	62.8	465	11	AQ713218	AQ713218 HS_5393
C 5	109.2	62.0	447	1	AA699702	AA699702 2140607.s
C 6	109.2	62.0	541	1	AA225358	AA225358 nc24402.s
C 7	109.2	62.0	554	11	AQ784105	AQ784105 HS_3250
C 8	108.6	61.7	388	1	AA228270	AA228270 nc38b02.x
C 9	108.6	61.7	494	1	AI354333	AI354333 qt78e11.x
C 10	108.6	61.7	578	11	AQ15010	AQ15010 RPCI11-9
C 11	108.2	61.5	754	5	CD652416	CD652416 AGENCOURT
C 12	107.8	61.2	749	8	CN417549	CN417549 170006001
C 13	107.6	61.1	826	11	AQ747017	AQ747017 HS_5338
C 14	107.2	60.9	536	11	AQ314458	AQ314458 RPCI11-1
C 15	107	60.8	434	11	B42135	B42135 HS-1055-A2
C 16	107	60.8	689	14	AG088851	AG088851 Pan t10g
C 17	107	60.8	787	4	CB988735	CB988735 AGENCOURT
C 18	107	60.8	808	4	CD109864	CD109864 AGENCOURT
C 19	107	60.8	939	4	CB990645	CB990645 AGENCOURT

20	106.6	60.6	236	10	H81788
21	106.6	60.6	705	14	AG013775
22	106.2	60.3	270	4	CA774055
23	106.2	60.3	271	1	AA366936
24	106.2	60.3	314	1	AA484256
25	106.2	60.3	459	1	A1917132
26	106.2	60.3	617	14	AG070727
27	106.2	60.3	968	7	BF345228
28	106.2	60.2	348	8	CN269051
29	106.2	60.2	361	11	AQ194840
30	106.2	60.2	412	11	AY760888
31	106.2	60.2	450	9	DB360062
32	106.2	60.2	521	1	AA837027
33	106.2	60.2	552	9	DB302779
34	106.2	60.2	652	8	CN271031
35	106.2	60.2	669	1	AF075373
36	106.2	60.2	669	1	A1110874
37	106.2	60.2	707	1	AV713579
38	106.2	60.2	807	5	CD644267
39	106.2	60.2	893	1	AL521749
40	106.2	60.2	954	2	BG723587
41	105.4	59.9	2412	6	CR859663
42	105.4	59.9	352	1	AA736557
43	105.4	59.9	400	1	AA728939
44	105.4	59.9	428	1	A1000825
45	105.4	59.9	549	9	DB326947

ALIGNMENTS

RESULT 1
BU182693 1209 bp mRNA linear EST 04-SEP-2002
AGENCOURT_7931720 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6150589
LOCUS
DEFINITION
5', mRNA sequence.

ACCESSION
BU182693
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM

REFERENCE
1 (bases 1 to 1209)
AUTHORS
TITLE
JOURNAL
COMMENT
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM13485 row: h column: 14
High quality sequence stop: 330.
Location/Qualifiers

FEATURES

source
1..1209
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6150589"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. primer: oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

AA225358 541 bp mRNA linear EST 20-AUG-1997
LOCUS nc24d02.s1 NCI CGAP Pr1 Homo sapiens cDNA clone IMAGE:1009059
DEFINITION similar to contains Alu repetitive element; contains element PFR5
repetitive element ;, mRNA sequence.
ACCESSION AA225358
VERSION AA225358.1 GI:1846696
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 541)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapdb@remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuquí,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNT at:
www.bio.linn.gov/bdrip/image/image.html
Insert Length: 467 Std Error: 0.00
Seq primer: -41m13 fwd. RT from Amerisham
High quality sequence stop: 434.
Location/Qualifiers
1. 541
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1009059"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pr1"
/note="Vector: PAMF10; Site_1: Not1; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into PAMF10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."

ORIGIN
Query Match 62.0%; Score 109.2; DB 1; Length 541;
Best Local Similarity 77.6%; Pred. No. 2,7e-16;
Matches 132; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 2 CCTGTATTCCACTGTCGAGAGTCGAGGTCAGAGAGCTGCTTGAGGCCAGAGTTCA 61
Db 100 CCTGTATTCCAGACCTTTGGAGGCTTAAGCCGAGAGATGACTTGAAGCCAGAGTTGG 159
QY 62 AGAGCAGCCTGGAACAACAGGAGAGACTGTCTACTCAAAAGAAATAAATTATGCCAGG 121
Db 160 AGACCAAGCCTGGCAACATGTAACCTGTCTCTACTTAATAAATAATTAGCTCG 219
QY 122 CTTAGTGGCTCATCCCTGTGTGCTCCAGCTACTAGGAGGAGCAAGTAGGA 171
Db 220 CGTGTGTGGACACCTGTATCCCACTACTCGGAGGCTGAGGACGGA 269

LOCUS AQ784105 554 bp DNA linear GSS 03-AUG-1999
DEFINITION HS_3250_A2_H10_T7C CTT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3250 Col=20 Row=0, genomic survey
sequence.
ACCESSION AQ784105
VERSION AQ784105.1 GI:5691729
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 554)
AUTHORS Mahairas,G.G., Wallace,J.C., Sutch,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLES Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3867
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htec.washington.edu>
Plate: 3250 row: 0 column: 20
Seq primer: T7
Class: BAC ends
High quality sequence stop: 554.
Location/Qualifiers
1. 554
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3250 Col=20 Row=0"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"

ORIGIN
Query Match 62.0%; Score 109.2; DB 1; Length 554;
Best Local Similarity 77.6%; Pred. No. 2,7e-16;
Matches 132; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 2 CCTGTATTCCACTGTCGAGAGTCGAGGTCAGAGAGCTGCTTGAGGCCAGAGTTCA 61
Db 140 CCTGTATTCTAGACCTTTGGAGGCGGAGTGCGGATTACTTGAAGTCAGAGTTCA 199
QY 62 AGAGCAGCCTGGAACAACAGGAGAGCTGTCTACTCAAAAGAAATAAATTATGCCAGG 121
Db 200 AGACCAAGCCTGGCAACATGTAACCTGTCTCTACTTAATAAATAATTAGCTCG 259
QY 122 CTTAGTGGCTCATCCCTGTGTGCTCCAGCTACTAGGAGGAGCAAGTAGGA 171
Db 260 TGTGTGTGGACATGCTGTATCCCACTACTCAGAGAGGCTGAGGACGGA 309

RESULT 8
AA228270 388 bp mRNA linear EST 21-AUG-1997
LOCUS nc38b02.r1 NCI CGAP Pr2 Homo sapiens cDNA clone IMAGE:1010379
DEFINITION similar to contains Alu repetitive element; mRNA sequence.
ACCESSION AA228270
VERSION AA228270.1 GI:1849841
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 388)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuqui,

M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.illn.gov/bbrp/image/image.html
Insert Length: 551 Std Error: 0.00
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 378.

FEATURES

source

1..388
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1010379"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/clone_id="NCI_CGAP_P12"
/note="Vector: PAMPI0; Site 1: NotI; Site 2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into PAMPI0 by the UIC-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."

ORIGIN

Query Match 61.7%; Score 108.6; DB 1; Length 388;
Best Local Similarity 77.2%; Pred. No. 3.9e-16;

Matches 132; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGCACTGCTGAGCCGAGAGTTC 60
|||||
Db 127 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGCACTGCTGAGCTTGAAGATTTC 186
|||||
QY 61 AAGAGCAGCTTGACACACAGGAGACCTGTCACTCAAAAGATTAATAATTAGCCAG 120
|||||
Db 187 AAGACCGGTCTGGGCAACATGTAACCTGTCTCAAAAAATTAATAATTAGCCAG 246
|||||
QY 121 GCTTAGTGCTCATCTCTGTGTCTCCAGCTACTAGGAGGAGAGAGTAGGA 171
|||||
Db 247 GTGTGTGGGCGACGCTATGTCTCCAGCTACTGGGAGGCTGAGATGGGA 297
|||||

RESULT 9

AI354333/c

LOCUS AI354333 494 bp mRNA linear EST 15-FEB-1999
DEFINITION [gt78e11.x1](http://www.ncbi.nlm.nih.gov/ncicgap) NCI CGAP Es02 Homo sapiens cDNA clone IMAGE:1961420 3'
similar to contains Alu repetitive element;; mRNA sequence.

ACCESSION AI354333
VERSION AI354333.1 GI:4094486

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 494)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Nan Hu, M.D., Ph.D., Mark Roth, M.D., Phillip
Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.illn.gov/bbrp/image/image.html
Insert Length: 1028 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 411.

FEATURES

source

1..494
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1961420"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B"
/clone_id="NCI_CGAP_Es02"
/note="Organ: esophagus; Vector: pCMV-SportE; Site 1:
SalI; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.1 Kb. Life Technologies
catalog #: 11502-010"

ORIGIN

Query Match 61.7%; Score 108.6; DB 1; Length 494;
Best Local Similarity 77.2%; Pred. No. 3.8e-16;

Matches 132; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 2 CCTGTATTCAGTACTGTGAGAGTCCGAGGTCAGAGCACTGCTTGAAGCCGAGATTCA 61
|||||
Db 280 CCTGTATTCAGTACTGTGAGAGTCCGAGGTCAGAGCACTGCTTGAAGCTTGAAGATTTC 221
|||||
QY 62 AAGACAGCTTGACACACAGGAGACCTGTCACTCAAAAGATTAATAATTAGCCAG 121
|||||
Db 220 AAGACAGCTTGACACACAGGAGACCTGTCACTCAAAAGATTAATAATTAGCCAG 161
|||||
QY 122 CTTAGTGCTCATCTCTGTGTCTCCAGCTACTAGGAGGAGAGTAGGAAC 172
|||||
Db 160 CATGTGTGTCATCTCTGTATTCCTGAGCTTGGGAGGCTGAGGAGGAGAC 110
|||||

RESULT 10

AQ315010/c

LOCUS AQ315010 578 bp DNA linear GSS 04-MAY-1999
DEFINITION R0111-9404.TV R011-11 Homo sapiens genomic clone R011-9404,
genomic survey sequence.

ACCESSION AQ315010
VERSION AQ315010.1 GI:4046473

KEYWORDS GSS.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE

AUTHORS

1 (bases 1 to 578)
Adams,M.D., Rounsley,S.D., Zhao,S., Baes,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeet@igf.org
 Clones are derived from the human BAC library RPCL1-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (http://resgen.com). BAC end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
 Seq primer: T7
 Class: BAC ends.

FEATURES

source

Location/Qualifiers

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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GDB:7536051"
 /db_xref="taxon:9606"
 /clone="RPCL1-11-9404"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_1ib="RPCL1-11"
 /note="Vector: PBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCL11 Human Male BAC Library"

ORIGIN

Query Match 61.7%; Score 108.6; DB 11; Length 578;
 Best Local Similarity 77.2%; Pred. No. 3.8e-16;
 Matches 122; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 ACTGTAAATCCAGTACTGTGAGAGTCCGAGTCCAGAGACCTGTGAGCCGAGAGTTC 60
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 DB 462 ACCGTAAATCCAGCCTTTGAGAGGCTGGGCGGAGATCATTGAGGTCTGAGAGTTT 403
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 QY 61 AAGAGAGCCTGACACACAGAGGAGACCTGTCACTACAAAGATAATTAATTAGCCAG 120
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 DB 402 CAGACCAAGCTGGCCAAACATGTGAACCTGTCTTCTTAAATACAAAATTTTCCAG 343
 |||||
 QY 121 GCTTAAGTGTCAATCCCTGTGTGCCAGCTACTAGGAGGACAGAAATGAGA 171
 |||||
 DB 342 GCGTGGTGGCAGATGCTGTAAATCCAGCTACTTGGGAGGCTGAGGACAGA 292
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RESULT 11
 CD652416 754 bp mRNA linear EST 18-JUN-2003
 LOCUS CD652416
 DEFINITION (long) Homo sapiens cDNA clone IMAGE:30427894 5', mRNA sequence.
 ACCESSION CD652416 GI:31889779
 VERSION CD652416
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 754)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@nci.nih.gov
 Tissue Procurement: Irene Glins and Mahendra Rao, NIA
 CDNA Library Preparation: Julian Piao and Minoru Ko
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC c
 can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: NDAMS16 row: a column: 23
 High quality sequence stop: 348.

FEATURES

source

Location/Qualifiers

1..754
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30427894"
 /issue_type="Embryonic Stem cells"
 /cell_line="WA01"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_1ib="NIA Human H1 Embryonic Stem Cell cDNA Library (long)"

/note="Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI;
 This is a long-transcript enriched cDNA library (Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]) from WA01 cell line. Undifferentiated human ES cell line WA01/H1 was obtained from WiCell Research Institute, Inc., Madison, WI, cultured according to their instructions, on MEF feeders. They formed round colonies with defined edges and were positive for alkaline phosphatase, SSEA-4, OCT3, OCT4, REX1, UTF, TERT, SOX2, CX43 and CX45. They are negative for GATA2, GATA4, PDX1, NCM, MSX1, FLT3, SSEA-1, TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days after plating), the ES cells from 4 X 6cm dishes were treated with 1 mg/ml collagenase, type IV (Invitrogen/GIBCO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with TRIzol Reagent from Invitrogen. Protocol ref: Genome Res. 11: 1553-1558 (2001). [PMID:11544199] Double-stranded cDNAs were synthesized with an oligo(dT) primer (Invitrogen: 5'-pACTGTTCTAGATCGCAGCGCCCTTTTCTTTT-3') from 3.4g of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Loxe-linker L1-Sal1, purified by phenol/chloroform extraction, and separated from free linkers by Centricon-100 column. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal1-5 for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The average insert size is about 3.6kb."

ORIGIN

Query Match 61.5%; Score 108.2; DB 5; Length 754;
 Best Local Similarity 77.5%; Pred. No. 4.6e-16;
 Matches 131; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 3 CTGTAAATCCAGTACTGTGAGAGTCCGAGTCCAGAGACCTGTGAGCCGAGAGTTCA 62
 |||||
 DB 282 CTGTAAATCCAGCCTTTGAGAGGCTGGGCGGAGATCCTCCTGAGGTCAAGAGTTGA 223
 |||||
 QY 63 GAGCAGCCTGGACACACAGAGGAGACCTGTCACTACAAAGATAATTAATTAGCCAGG 122
 |||||
 DB 222 GACCAGCCTGGCCAAACATGTGAACCTCTGCTACTTAAATACAAAATTTGCGGGC 163
 |||||
 QY 123 TTAGTGTCTATCCCTGTGTGCCAGCTACTAGGAGGACAGAAATGAGA 171
 |||||
 DB 162 GTGTGGCACACACCTGTGTCCAGCTACTCGGAGGCTGGAAGACAGA 114
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RESULT 12
 CN417549 749 bp mRNA linear EST 16-MAY-2004
 LOCUS CN417549
 DEFINITION 1700600171981 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN417549
 VERSION CN417549.1 GI:47405143
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:58:22 ; Search time 45.0864 Seconds
(without alignments)
7304.087 Million cell updates/sec

Title: US-09-869-098a-1_COPY_255_430
Perfect score: 176
Sequence: 1 accgtgaattccagctgt.....gagcgcaagtagactgt 176

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /EMC_Celerra_SIDS3/prodata/2/ina/7-COMB.seq:*
6: /EMC_Celerra_SIDS3/prodata/2/ina/H-COMB.seq:*
7: /EMC_Celerra_SIDS3/prodata/2/ina/PCTOS-COMB.seq:*
8: /EMC_Celerra_SIDS3/prodata/2/ina/RE-COMB.seq:*
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10: /EMC_Celerra_SIDS3/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	174.4	99.1	11808	3	US-09-949-016-15281 Sequence 15281, A
2	174.4	99.1	39754	3	US-09-949-016-14689 Sequence 14689, A
3	115	65.3	601	3	US-09-949-016-17686 Sequence 17686, A
4	115	65.3	148609	3	US-09-949-016-12860 Sequence 12860, A
5	115	65.3	148609	3	US-09-949-016-16787 Sequence 16787, A
6	112.4	63.9	49401	3	US-09-949-016-17080 Sequence 17080, A
7	111	63.1	119981	3	US-09-949-016-11984 Sequence 11984, A
8	111	63.1	119981	3	US-09-949-016-13606 Sequence 13606, A
9	110.8	63.0	38653	3	US-09-922-445-1 Sequence 1, Appl1
10	109.8	62.4	601	3	US-09-949-016-150302 Sequence 150302, A
11	109.8	62.4	17607	3	US-09-949-016-43162 Sequence 43162, A
12	107.6	61.1	601	3	US-09-949-016-43164 Sequence 43164, A
13	107.6	61.1	601	3	US-09-949-016-43164 Sequence 43164, A
14	107.6	61.1	601	3	US-09-949-016-43165 Sequence 43165, A
15	107.6	61.1	601	3	US-09-949-016-43351 Sequence 43351, A
16	107.6	61.1	601	3	US-09-949-016-43393 Sequence 43393, A
17	107.6	61.1	601	3	US-09-949-016-43394 Sequence 43394, A
18	107.6	61.1	601	3	US-09-949-016-43620 Sequence 43620, A
19	107.6	61.1	601	3	US-09-949-016-43622 Sequence 43622, A
20	107.6	61.1	601	3	US-09-949-016-43623 Sequence 43623, A
21	107.6	61.1	601	3	US-09-949-016-56159 Sequence 56159, A
22	107.6	61.1	12113	3	US-09-949-016-15144 Sequence 15144, A
23	107.6	61.1	40641	3	US-09-949-016-13376 Sequence 13376, A

C	24	107.6	61.1	55130	3	US-09-949-016-11850	Sequence 11850, A
C	25	107.6	61.1	157866	3	US-09-949-016-12982	Sequence 12982, A
C	26	107.6	61.1	157866	3	US-09-949-016-12983	Sequence 12983, A
C	27	107.6	61.1	157866	3	US-09-949-016-12984	Sequence 12984, A
C	28	107.6	61.1	192956	3	US-09-949-016-14382	Sequence 14382, A
C	29	107.2	60.9	601	3	US-09-949-016-43163	Sequence 43163, A
C	30	107.2	60.9	601	3	US-09-949-016-43392	Sequence 43392, A
C	31	107.2	60.9	601	3	US-09-949-016-43621	Sequence 43621, A
C	32	107.2	60.9	601	3	US-09-949-016-158924	Sequence 158924, A
C	33	106.2	60.3	38961	3	US-09-949-016-12143	Sequence 12143, A
C	34	106.2	60.3	38961	3	US-09-949-016-14474	Sequence 14474, A
C	35	106	60.2	601	3	US-09-949-016-30683	Sequence 30683, A
C	36	106	60.2	601	3	US-09-949-016-140077	Sequence 140077, A
C	37	106	60.2	601	3	US-09-949-016-182090	Sequence 182090, A
C	38	106	60.2	2923	2	US-08-480-449-1	Sequence 1, Appl1
C	39	106	60.2	2923	2	US-08-660-544-1	Sequence 1, Appl1
C	40	106	60.2	2923	3	US-08-479-603-1	Sequence 1, Appl1
C	41	106	60.2	2923	3	US-08-939-107-1	Sequence 1, Appl1
C	42	106	60.2	2923	3	US-08-931-764-1	Sequence 1, Appl1
C	43	106	60.2	2923	3	US-09-591-992-1	Sequence 1, Appl1
C	44	106	60.2	2923	3	US-09-067-447B-1	Sequence 1, Appl1
C	45	106	60.2	2923	3	US-08-479-620-1	Sequence 1, Appl1

ALIGNMENTS

```
RESULT 1
US-09-949-016-15281
Sequence 15281, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTNER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15281
LENGTH: 11808
TYPE: DNA
ORGANISM: Human
US-09-949-016-15281

Query Match 99.1%; Score 174.4; DB 3; Length 11808;
Best Local Similarity 99.4%; Pred. No. 3.3e-51;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACCTGAATTCGAGTCTGAGAGTCCGAGGCTGAGGACGCTGAGGCGCAGGATTC 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 23 ACCTGAATTCGAGTCTGAGAGTCCGAGGCTGAGGACGCTGAGGCGCAGGATTC 82
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 61 AAGAGCAGCTGAGCAACAGAGGAGCCTGTCACTACCAAGATTAATTAATTAAGCAG 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 83 AAGAGCAGCTGAGCAACAGAGGAGCCTGTCACTACCAAGATTAATTAATTAAGCAG 142
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 121 GCTTAGTGGCTCATCTCCCTGTGCTCCAGCTACTAGGAGGAGGAGGAGGAGGAGTCT 176
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 143 GCTTAGTGGCTCATCTCCCTGTGCTCCAGCTACTAGGAGGAGGAGGAGGAGGAGTCT 198
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
US-09-949-016-14689
Sequence 14689, Application US/09949016
Patent No. 6812339
```

```

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14689
; LENGTH: 39754
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(39754)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14689

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Query Match          99.1%; Score 174.4; DB 3; Length 39754;
Best Local Similarity 99.4%; Pred. No. 5.5e-51;
Matches 175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGGACTGTTGAGCCAGAGTTTC 60
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DB 27938 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGGACTGTTGAGCCAGAGTTTC 27997
    |||||||
QY 61 AAGAGCAGCTGACAAACACAGAGAGCTGTCTACTCAATCAAGATATTAATTAGCCAG 120
    |||||||
DB 27998 AAGAGCAGCTGACAAACACAGAGAGCTGTCTACTCAATCAAGATATTAATTAGCCAG 28057
    |||||||
QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGTACTAGGAGGACAGAGTACTGCT 176
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DB 28058 GCTTAGTGCTCATCCCTGTGTGCCAGTACTAGGAGGACAGAGTACTGCT 28113
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RESULT 3
US-09-949-016-176686
; Sequence 176686, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176686
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-176686

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Query Match          65.3%; Score 115; DB 3; Length 601;
Best Local Similarity 79.5%; Pred. No. 9.4e-31;
Matches 136; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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```

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGGACTGTTGAGCCAGAGTTTC 60
    |||||||

```

```

DB 14 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGGACTGTTGAGCCAGAGTTTC 73
    |||||||
QY 61 AAGAGCAGCTGACAAACACAGAGAGCTGTCTACTCAATCAAGATATTAATTAGCCAG 120
    |||||||
DB 74 GAGACAGCTGGGCAACCTAGGAGACTGTCTCTACAAAAATTAATAATTAGCCAG 133
    |||||||
QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGTACTAGGAGGACAGAGTACTAGA 171
    |||||||
DB 134 GTGTGTAGCACACGCTGTGTGCCAGTACTAGGAGTGTGACATGGGA 184
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```

```

RESULT 4
US-09-949-016-12860
; Sequence 12860, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12860
; LENGTH: 148609
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12860

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Query Match          65.3%; Score 115; DB 3; Length 148609;
Best Local Similarity 79.5%; Pred. No. 9.6e-30;
Matches 136; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGGACTGTTGAGCCAGAGTTTC 60
    |||||||
DB 30046 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGGACTGTTGAGCCAGAGTTTC 30105
    |||||||
QY 61 AAGAGCAGCTGACAAACACAGAGAGCTGTCTACTCAATCAAGATATTAATTAGCCAG 120
    |||||||
DB 30106 GAGACAGCTGGGCAACCTAGGAGACTGTCTCTACAAAAATTAATAATTAGCCAG 30165
    |||||||
QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGTACTAGGAGGACAGAGTACTAGA 171
    |||||||
DB 30166 GTGTGTAGCACACGCTGTGTGCCAGTACTAGGAGTGTGACATGGGA 30216
    |||||||

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RESULT 5
US-09-949-016-16787
; Sequence 16787, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16787

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LENGTH: 148609
TYPE: DNA
ORGANISM: Human
US-09-949-016-16787

Query Match
Best Local Similarity 79.5%; Score 115; DB 3; Length 148609;
Matches 136; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

1 ACCTGTAATTCAGTCTGTGAGAGTCCGAGTCCAGAGCACTGTGAGGCCAGAGTTTC 60
30046 ACCTGTAATTCAGTCTGTGAGAGTCCGAGTCCAGAGCACTGTGAGGCCAGAGTTTG 30105
61 AAGAGCAGCTTGACAAACAGGAGAGCTGTCTACTACAAAGATTAATAATTAGCCAG 120
30106 GAGACAGGCTGGGCAACGAGGAGAGCTGTCTCTACAAAATAATTAATTAAGCCAG 30165
121 GCTTATGCTCATCCCTGTGTCCAGCTACTAGGAGGAGGAGAGTAGGA 171
30166 GTGTGAGTACACAGGCTGTGTCCAGCTACTTGGGATGCTGACATGGGA 30216

RESULT 6

US-09-949-016-17080/c
Sequence 17080, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17080
LENGTH: 49401
TYPE: DNA
ORGANISM: Human
US-09-949-016-17080

Query Match
Best Local Similarity 78.8%; Score 112.4; DB 3; Length 49401;
Matches 134; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

2 CCTGTAAATTCAGTCTGTGAGAGTCCGAGTCCAGAGCACTGTGAGGCCAGAGTTTCA 61
40664 CCTGTAAATTCAGTCTGTGAGAGTCCGAGTCCAGAGCACTGTGAGGCCAGAGTTTCA 40605
62 AAGAGCAGCTTGACAAACAGGAGAGCTGTCTACTACAAAGATTAATAATTAGCCAG 121
40604 AAGAGCAGCTTGAGCAACAGGAGAGCTGTCTACTACAAAGATTAATAATTAGCCAG 40545
122 CTTAGTGTCTATCCCTGTGTCCAGCTACTAGGAGGAGGAGGAGTAGGA 171
40544 TTTGTGTGTGATGCTGTCTATCTAGCTACTAGGAGGAGGAGGAGTAGGA 40495

RESULT 7

US-09-949-016-11844/c
Sequence 11844, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11844
LENGTH: 119981
TYPE: DNA
ORGANISM: Human
US-09-949-016-11844

Query Match
Best Local Similarity 81.9%; Score 111; DB 3; Length 119981;
Matches 140; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

2 CCTGTAAATTCAGTCTGTGAGAGTCCGAGTCCAGAGCACTGTGAGGCCAGAGTTTCA 61
26713 CCTGTAAATTCAGTCTGTGAGAGTCCGAGTCCAGAGCACTGTGAGGCCAGAGTTTCA 26654
62 AAGAGCAGCTTGACAAACAGGAGAGCTGTCTACTACAAAGATTAATAATTAGCCAG 120
26653 AAGAGCAGCTTGAGCAACAGGAGAGCTGTCTACTACAAAGATTAATAATTAGCCAG 26594
121 GCTTATGCTCATCCCTGTGTCCAGCTACTAGGAGGAGGAGAGTAGGA 171
26593 GCATGTGATATGCTGTGTCCAGCTACTTGGGATGCTGACATGGGA 26543

RESULT 8

US-09-949-016-13606/c
Sequence 13606, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13606
LENGTH: 119982
TYPE: DNA
ORGANISM: Human
US-09-949-016-13606

Query Match
Best Local Similarity 81.9%; Score 111; DB 3; Length 119982;
Matches 140; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

2 CCTGTAAATTCAGTCTGTGAGAGTCCGAGTCCAGAGCACTGTGAGGCCAGAGTTTCA 61
26713 CCTGTAAATTCAGTCTGTGAGAGTCCGAGTCCAGAGCACTGTGAGGCCAGAGTTTCA 26654
62 AAGAGCAGCTTGACAAACAGGAGAGCTGTCTACTACAAAGATTAATAATTAGCCAG 120
26653 AAGAGCAGCTTGAGCAACAGGAGAGCTGTCTACTACAAAGATTAATAATTAGCCAG 26594
121 GCTTATGCTCATCCCTGTGTCCAGCTACTAGGAGGAGGAGGAGTAGGA 171
26593 GCATGTGATATGCTGTGTCCAGCTACTTGGGATGCTGACATGGGA 26543

```

RESULT 9
US-09-922-445-1
Sequence 1, Application US/09922445
Patent No. 6528268
GENERAL INFORMATION:
APPLICANT: Andersson, Maria K.
APPLICANT: Berglund, Lars G. T.
APPLICANT: Reneland, Rikard H.
APPLICANT: Adam, Gail I. R.
TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
FILE REFERENCE: CG126US
CURRENT APPLICATION NUMBER: US/09/922.445
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 38653
TYPE: DNA
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: 5' UTR
LOCATION: (1)..(26156)
OTHER INFORMATION:
NAME/KEY: misc feature
LOCATION: (24801)..(24801)
OTHER INFORMATION: nucleotide 24801 is a single nucleotide polymorphism which can be
NAME/KEY: misc feature
LOCATION: (24941)..(24941)
OTHER INFORMATION: nucleotide 24941 is a single nucleotide polymorphism which can be
OTHER INFORMATION: T or C
NAME/KEY: exon
LOCATION: (26157)..(26252)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (26253)..(26401)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (26402)..(26543)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (26544)..(27024)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (27025)..(27178)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (27179)..(30519)
OTHER INFORMATION:
NAME/KEY: misc feature
LOCATION: (27645)..(27645)
OTHER INFORMATION: nucleotide 27645 is a single nucleotide polymorphism which can be
OTHER INFORMATION: C or G
NAME/KEY: exon
LOCATION: (30520)..(30681)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (30682)..(30894)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (30895)..(31027)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (31028)..(31747)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (31748)..(31841)
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (31842)..(32400)
OTHER INFORMATION:

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NAME/KEY : misc feature
LOCATION : (32163) ..(32163)
OTHER INFORMATION : nucleotide 32163 is a single nucleotide polymorphism which can bc
OTHER INFORMATION : A or C
NAME/KEY : exon
LOCATION : (32401) ..(32528)
OTHER INFORMATION :
NAME/KEY : Intron
LOCATION : (32529) ..(33414)
OTHER INFORMATION :
NAME/KEY : misc feature
LOCATION : (32614) ..(32614)
OTHER INFORMATION : nucleotide 32614 is a single nucleotide polymorphism which can bc
OTHER INFORMATION : A or G
NAME/KEY : exon
LOCATION : (33415) ..(33597)
OTHER INFORMATION :
NAME/KEY : Intron
LOCATION : (33598) ..(34314)
OTHER INFORMATION :
NAME/KEY : exon
LOCATION : (34315) ..(34588)
OTHER INFORMATION :
NAME/KEY : Intron
LOCATION : (34589) ..(36404)
OTHER INFORMATION :
NAME/KEY : exon
LOCATION : (36405) ..(36523)
OTHER INFORMATION :
NAME/KEY : Intron
LOCATION : (36524) ..(38341)
OTHER INFORMATION :
NAME/KEY : exon
LOCATION : (38342) ..(38653)
OTHER INFORMATION :
PUBLICATION INFORMATION :
DATABASE ACCESSION NUMBER : Genbank/AC004923
ENTRY DATE : 1999-12-21
RELEVANT RESIDUES : (1) ..(38653)
US-09-922-445-1

Query Match      63.0% ; Score 110.8 ; DB 3 ; Length 38653 ;
Best Local Similarity 78.2% ; Pred. No. 1.7e-28 ;
Matches 133 ; Conservative 0 ; Mismatches 37 ; Indels 0 ; Gaps 0 ;

QY      2 CCTGTAATTCAGACTCTGTGAGAGTCCGAGGTCAAGAGAACTGTTGAGGCCAGAGATTCA 61
DB      37583 CCTGTAATTCAGAACACTTTGGGAGGCTGAAGCAGAGAGATGCTTGAGGCCAGAGAGTTCA 37642

QY      62 AGAGCAGCTCGACAACAACAAGGAGAGACTGTCTACTAACAAGAATAAATAATTAGCCAG 121
DB      37643 AGACCAGCTCGGCACACATAGGAGAGACCTGTCTCTCAAAAAAATTTAAAATAATAGCTGGG 37702

QY      122 CTTAGGGCTCATCCCTGTGTGTCGCCAGCTACTAGGGAGGCGAAGTAGAGA 171
DB      37703 CGTAGGGCTGTGCTGTGTAATTCAGACTTGGGAGACTGAAGTGGGA 37752

RESULT 10
US-09-949-016-150302
; Sequence 150302, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
```

```

: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: PARSSEQ for Windows Version 4.0.
: SEQ ID NO 150302
:
: LENGTH: 601
:
: TYPE: DNA
:
: ORGANISM: Human
:
: OS-949-016-150302

```

Query Match:	62.4%	Score 109.8:	DB 3,	Length 601,
Best Local Similarity:	78.1%	Pred. No. 6.5e-29,		
Matches 132, Conservative	0,	Mismatches 37,	Indels 0,	Gaps 0.

Qy 3 CTGTAATTCAGTAACGTGTAGAGTCCGAGGTCAAGAGACTGCTTAGGCGCAGAGTTCAA 62

Db 82 CTGTAATTCAGCACTTTGGAGAGGCCAAGGTGGGTGATCCGTTAGGTCAAGAGTTCGA 141

Qy 63 GACGAGCTTGACAAACACAGGAGACTGTCTACTCAAAAGATATAATTAATTAGCCAGGC 122

Db 142 GACCAAGCTTGCCAAAGAGTGAAACCATCTCTACTAAAAATACAAAAATTTAGCCAGAC 201

Qy 123 TTAGTGGCTTATCCCTGTGGTCCAGAGTACTAGGAGGCGAGAAATGAGA 171

Db 202 ATGTGTGCACTGCTCTGTAATCCAGCTACTTTGGAGGCGAGAGGAGGA 250

RESULT 11
US-09-949-016-15968/c
; Sequence 15968, Application US/09949016

```

? APPLICANT: IENSTER, J. Craig et al.
? TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
? TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
? FILE REFERENCE: CLO011307
? CURRENT APPLICATION NUMBER: US/09/949,016
? CURRENT FILING DATE: 2000-04-14
? PRIOR APPLICATION NUMBER: 60/241,755
? PRIOR FILING DATE: 2000-10-20
? PRIOR APPLICATION NUMBER: 60/237,768
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: fastSeq for Windows Version 4.0
? SEQ ID NO 15968
? LENGTH: 17607
? TYPE: DNA
? ORGANISM: Human
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1)...(17607)
? OTHER INFORMATION: n = A,T,C or G
? IS-09-949-016-15968

```

Query Match	62.4%;	Score 109.8;	DB 3;	Length 17607;
Best Local Similarity	78.1%;	Pred. No. 2.7e-28;		
Matches 132; Conservative	0;	Mismatches 37;	Indels 0;	

QY	3	CTGTAATTCAGTACTGTGAGAGTCCAGGTCAGAGAGACTGTGAGGCCAGGAGTTCAA	62
Db	13804	CTGTAATTCAGACTTTGGGAGGCCAAGTGGGTGGATCGCTTGAGGTACAGGAGTTCCA	13745
QY	63	GAGAGGCTGGGACAAACACAGGAGACCTGTCACTACAAAGAAATTAATTTTGGCCAGGC	122
Db	13744	GACCAGGCTGGGCCAACAGGTGAATCCCATCTCTAATTAATAATACAAATTTTGGCCAGAC	13685
QY	123	TTAAGTGCCTATCCCTGTGGTCCCAAGCTACTAGGAGGCGCAGAAATGAGA	171
Db	13684	ATGGTGGCACATGCTCTGTAATCCCAAGCTACTCTGGGAGGCGCAGAGAGAGA	13636

RESULT 12
US-09-949-016-43162
; Sequence 43162, Application US/09949016
; Patent No. 6812339

```

1  APPLICANT: VENTER, J. Craig et al.
2  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
3  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
4  FILE REFERENCE: C0001307
5  CURRENT APPLICATION NUMBER: US/09/949,016
6  CURRENT FILING DATE: 2000-04-14
7  PRIOR APPLICATION NUMBER: 60/241,755
8  PRIOR FILING DATE: 2000-10-20
9  PRIOR APPLICATION NUMBER: 60/237,768
10 PRIOR FILING DATE: 2000-10-03
11 PRIOR APPLICATION NUMBER: 60/231,498
12 PRIOR FILING DATE: 2000-09-08
13 NUMBER OF SEQ ID NOS: 207012
14 SOFTWARE: FastSeq for Windows Version 4.0
15 SEQ ID NO 43162
16 LENGTH: 601
17 TYPE: DNA
18 ORGANISM: Human
19 US-09-949-016-43162

```

Query Match	61.1%	Score 107.6	DB 3	Length 601
Best Local Similarity	77.1%	Pred. No. 3.9e-28		
Matches 131, Conservative	0	Mismatches 39	Indels 0	Gaps 0

Qy	2	CCGTGAATTCAGATCTGTGAGAGTCCAGAGTCAGAGACCTGTGAGGCCAGGAGTTCA	61
	117	CCGTATATCCACGACTTTGGGAGGCCAGAGCGAATGTGATCCTGAGGTCCAGAGTTGG	176
Db			
Qy	62	AGAGCAGCCTGGACAACACAGGGAACCTGTCACTACCAAGATTAATTAATTGACGAG	121
Db	177	AGACGAGCCTAGCACAATGGTGAACCCGCTCTACTAAATAATACAAAATTCAGCAGG	236
Qy			
	122	CTTAAGAGCGTCATCCCTGTGGTCCGAGCACTTAGGAGGACGAGAGTAGGA	171
Db	237	CATGGTGGCAATCCCTGCATCCCAAGCTACCTGGGAAGCTGAAGCAGGA	286

RESULT 13
US-09-949-016-43164
; Sequence 43164, Application US/09949016

```

1  APPLICANT: VENTER, J. Craig et al.
2  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
3  TITLE OR INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
4  FILE REFERENCE: C1001307
5  CURRENT APPLICATION NUMBER: US/09/949,016
6  CURRENT FILING DATE: 2000-04-14
7  PRIOR APPLICATION NUMBER: 60/241,755
8  PRIOR FILING DATE: 2000-10-20
9  PRIOR APPLICATION NUMBER: 60/237,768
10 PRIOR FILING DATE: 2000-10-03
11 PRIOR APPLICATION NUMBER: 60/231,498
12 PRIOR FILING DATE: 2000-09-08
13 NUMBER OF SEQ ID NOS: 207012
14 SOFTWARE: FASTSEQ for Windows Version 4.0
15 SEQ ID NO 43164
16 LENGTH: 601
17 TYPE: DNA
18 ORGANISM: Human
19 OS-09-949-016--43164

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Query Match	61.1%	Score 107.6;	DB 3;	Length 601;
Best Local Similarity	77.1%	Pred. No. 3.9e-28;		
Matches 131;	Conservative	0;	Mismatches 39;	Indels 0;
Gaps	0;			

2	CCGCTATTCCAGTCTGTGAGAGTCCGAGGTGAGAGACTGCTTGAAGCCAGAGTTCA	61

2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGGACTGCTTTGAGGCCAGAGTTCA 61

```
Db 400 CCTGTGATCCAGCACTTTGGAGGCCGGAAGTGAATCAGCTGAGGTGAGGAGTTGG 459
QY 62 AGAGCAGCCTGGACAACAAGGAGAGCTGTCTACTCAAAAGATAATTAATTAGCCAGG 121
Db 460 AGACCAAGCCTTAGGCAACATGTGTGAACCCGTCTCTACTTAATAAATACAAAATCAGCCAGG 519
QY 122 CTTAGTGCTCATCCCTGTGTGTCCTCCAGCTACTAGGAGGAGGAGGAGTAAGA 171
Db 520 CATGTGGGACATCCCTGCAATCCAGCTACTGAGGAGGCTGAAGCAGGA 569

RESULT 14
US-09-949-016-43165
; Sequence 43165, Application US/09949016
; Patent No. 6812339
; ORGANISM: Human
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 43165
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-43165

Query Match 61.1%; Score 107.6; DB 3; Length 601;
Best Local Similarity 77.1%; Pred. No. 3.9e-28;
Matches 131; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 2 CCTGTAAATTCAGTAAGTCCGAGTCCAGAGTCAAGTCTGAGGCGCAGAGTTCA 61
Db 408 CCTGTATCCAGCACTTTGGAGGCCGAGGCAAGTGAATCCTGAGGTGAGGAGTTGG 467
QY 62 AGAGCAGCCTGGACAACAAGGAGAGCTGTCTACTCAAAAGATAATTAATTAGCCAGG 121
Db 468 AGACCAAGCCTTAGGCAACATGTGTGAACCCGTCTCTACTTAATAAATACAAAATCAGCCAGG 527
QY 122 CTTAGTGCTCATCCCTGTGTGTCCTCCAGCTACTAGGAGGAGGAGTAAGA 171
Db 528 CATGTGGGACATCCCTGCAATCCAGCTACTGAGGAGGCTGAAGCAGGA 577

RESULT 15
US-09-949-016-43391
; Sequence 43391, Application US/09949016
; Patent No. 6812339
; ORGANISM: Human
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 43391
```

```
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-43391

Query Match 61.1%; Score 107.6; DB 3; Length 601;
Best Local Similarity 77.1%; Pred. No. 3.9e-28;
Matches 131; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 2 CCTGTAAATTCAGTAAGTCCGAGTCCAGAGTCAAGTCTGAGGCGCAGAGTTCA 61
Db 117 CCTGTATCCAGCACTTTGGAGGCCGAGGCAAGTGAATCAGCTGAGGTGAGGAGTTGG 176
QY 62 AGAGCAGCCTGGACAACAAGGAGAGCTGTCTACTCAAAAGATAATTAATTAGCCAGG 121
Db 177 AGACCAAGCCTTAGGCAACATGTGTGAACCCGTCTCTACTTAATAAATACAAAATCAGCCAGG 236
QY 122 CTTAGTGCTCATCCCTGTGTGTCCTCCAGCTACTAGGAGGAGGAGTAAGA 171
Db 237 CATGTGGGACATCCCTGCAATCCAGCTACTGAGGAGGCTGAAGCAGGA 286
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Search completed: June 5, 2006, 22:39:34
Job time : 49.0864 secs

RESULT 2
US-10-301-480-688929
; Sequence 688929, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 688929
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-688929

Query Match 65.6%; Score 115.4; DB 12; Length 463;
Best Local Similarity 80.2%; Pred. No. 3,4e-29;
Matches 134; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

QY 5 GTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGCACTGTTAGGCCAGAGTTCAAGA 64
DB 21 GTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGCACTGTTAGGCCAGAGTTCAAGA 80
QY 65 GCAGCTTGACACACAGGAGAGCTGTCTACTCAAAAGATAATTAATTAGCCAGGCTT 124
DB 81 CCAGCCCAAGCAATGAGCAAGACCTGTCTACTCAAAAGATAATTAATTAGCCAGGCAAT 140
QY 125 AGTGGCTCATCCTGTGTGTCCTCCAGCTACTAGGAGGACAGAGTAGGA 171
DB 141 GGTGGCAATGCTGTATTCCTCCAGCTACTAGGAGGCTGAGGAGGA 187

RESULT 3
US-10-027-632-235356
; Sequence 235356, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235356
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235356

Query Match 65.6%; Score 115.4; DB 6; Length 494;
Best Local Similarity 80.2%; Pred. No. 3,4e-29;
Matches 134; Conservative 1; Mismatches 32; Indels 0; Gaps 0;
QY 5 GTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGCACTGTTAGGCCAGAGTTCAAGA 64
DB 52 GTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGCACTGTTAGGCCAGAGTTCAAGA 111
QY 65 GCAGCTTGACACACAGGAGAGCTGTCTACTCAAAAGATAATTAATTAGCCAGGCTT 124
DB 112 CCAGCCCAAGCAATGAGCAAGACCTGTCTACTCAAAAGATAATTAATTAGCCAGGCAAT 171
QY 125 AGTGGCTCATCCTGTGTGTCCTCCAGCTACTAGGAGGACAGAGTAGGA 171
DB 172 GGTGGCAATGCTGTATTCCTCCAGCTACTAGGAGGCTGAGGAGGA 218

RESULT 4
US-10-027-632-235356
; Sequence 235356, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 235356
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235356

Query Match 65.6%; Score 115.4; DB 7; Length 494;
Best Local Similarity 80.2%; Pred. No. 3,4e-29;
Matches 134; Conservative 1; Mismatches 32; Indels 0; Gaps 0;

QY 5 GTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGCACTGTTAGGCCAGAGTTCAAGA 64
DB 52 GTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGCACTGTTAGGCCAGAGTTCAAGA 111
QY 65 GCAGCTTGACACACAGGAGAGCTGTCTACTCAAAAGATAATTAATTAGCCAGGCTT 124
DB 112 CCAGCCCAAGCAATGAGCAAGACCTGTCTACTCAAAAGATAATTAATTAGCCAGGCAAT 171
QY 125 AGTGGCTCATCCTGTGTGTCCTCCAGCTACTAGGAGGACAGAGTAGGA 171
DB 172 GGTGGCAATGCTGTATTCCTCCAGCTACTAGGAGGCTGAGGAGGA 218

RESULT 5
US-10-027-632-235357
; Sequence 235357, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
US-10-027-632-235356

;; TITLE OF INVENTION: Identification and Mapping of Single
;; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
;; CURRENT APPLICATION NUMBER: US/09/925,065A
;; PRIOR FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: US 60/243,096
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: US 60/252,147
;; PRIOR FILING DATE: 2000-11-20
;; PRIOR APPLICATION NUMBER: US 60/250,092
;; PRIOR FILING DATE: 2000-11-30
;; PRIOR APPLICATION NUMBER: US 60/261,766
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/289,846
;; PRIOR FILING DATE: 2001-05-09
;; NUMBER OF SEQ ID NOS: 957086
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 48526
;; LENGTH: 1333
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-925-065A-48526

Query Match 65.1%; Score 114.6; DB 5; Length 1333;
Best Local Similarity 78.9%; Pred. No. 8,7e-29;
Matches 135; Conservative 1; Mismatches 35; Indels 0; Gaps 0;

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGACTGTTGAGGCCAGAGATTC 60
DB 184 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGACTGTTGAGGCCAGAGATTC 243
QY 61 AAGAGCAGCTGAGCAACACAGGAGAGACTGTGCTACCAAAAGATAATTAATTAGCCAG 120
DB 244 GAGACCAAGCTTGAGCAACGTAAGGAGAGACTGTGCTACCAAAAGATAATTAATTAGCCAG 303
QY 121 GCTTAGTGCTCATCCCTGTGTGTCCTCCAGCTACTAGGAGGACAGAGTAGGA 171
DB 304 GTGTGTAGACACAGCTGTGTGTCCTCCARCTTAGGATGCTGACATGGGA 354

RESULT 9
US-10-301-480-149764
; Sequence 149764, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149764
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-149764

Query Match 65.1%; Score 114.6; DB 12; Length 1333;
Best Local Similarity 78.9%; Pred. No. 8,7e-29;
Matches 135; Conservative 1; Mismatches 35; Indels 0; Gaps 0;

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGACTGTTGAGGCCAGAGATTC 60
DB 184 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGACTGTTGAGGCCAGAGATTC 243
QY 61 AAGAGCAGCTGAGCAACACAGGAGAGACTGTGCTACCAAAAGATAATTAATTAGCCAG 120

DB 244 GAGACCAAGCTTGAGCAACGTAAGGAGAGCTGTCTCTACCAAAAGATAATTAATTAGCCAG 303
QY 121 GCTTAGTGCTCATCCCTGTGTGTCCTCCAGCTACTAGGAGGACAGAGTAGGA 171
DB 304 GTGTGTAGACACAGCTGTGTGTCCTCCARCTTAGGATGCTGACATGGGA 354

RESULT 10
US-10-301-480-763173
; Sequence 763173, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 763173
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-763173

Query Match 65.1%; Score 114.6; DB 12; Length 1333;
Best Local Similarity 78.9%; Pred. No. 8,7e-29;
Matches 135; Conservative 1; Mismatches 35; Indels 0; Gaps 0;

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGACTGTTGAGGCCAGAGATTC 60
DB 184 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGACTGTTGAGGCCAGAGATTC 243
QY 61 AAGAGCAGCTGAGCAACACAGGAGAGACTGTGCTACCAAAAGATAATTAATTAGCCAG 120
DB 244 GAGACCAAGCTTGAGCAACGTAAGGAGAGACTGTGCTACCAAAAGATAATTAATTAGCCAG 303
QY 121 GCTTAGTGCTCATCCCTGTGTGTCCTCCAGCTACTAGGAGGACAGAGTAGGA 171
DB 304 GTGTGTAGACACAGCTGTGTGTCCTCCARCTTAGGATGCTGACATGGGA 354

RESULT 11
US-10-301-480-75521
; Sequence 75521, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75521
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-75521

Query Match 64.9%; Score 114.2; DB 12; Length 463;
Best Local Similarity 80.2%; Pred. No. 8,7e-29;
Matches 134; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 5 GTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGTCTGTGAGCCGAGATTCAAGA 64
| | | | |
| | | | |
Db 21 GTAATTCAGTACTGTGAGAGTCCGAGTCCGAGTCTGTGAGCCGAGATTCAAGA 80
| | | | |
| | | | |
QY 65 GCAGCTCGAGACAACAGAGGAGACCTGTCTACTACAAAGATTAATTAATTTGCCAGGCTT 124
| | | | |
| | | | |
Db 81 CCAGCCCAAGCCCAACATGCGACAGACCTGTCTACTACAAAGATTAATTAATTTGCCAGGCTT 140
| | | | |
| | | | |
QY 125 AGTGGCTCATCCCTGTGTCCTCCAGCTACTAGGAGGAGGAGAGTGA 171
| | | | |
| | | | |
Db 141 GCTGGCACAATGCTCTGTATCCAGCTACTTGGAGGCTGAGGCGAGGA 187
| | | | |
| | | | |

RESULT 12

US-10-301-480-688930
; Sequence 688930, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 688930
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-688930

Query Match 64.9%; Score 114.2; DB 12; Length 463;
Best Local Similarity 80.2%; Pred. No. 8.7e-29;
Matches 134; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 5 GTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGTCTGTGAGCCGAGATTCAAGA 64
| | | | |
| | | | |
Db 21 GTAATTCAGTACTGTGAGAGTCCGAGTCCGAGTCTGTGAGCCGAGATTCAAGA 80
| | | | |
| | | | |
QY 65 GCAGCTCGAGACAACAGAGGAGACCTGTCTACTACAAAGATTAATTAATTTGCCAGGCTT 124
| | | | |
| | | | |
Db 81 CCAGCCCAAGCCCAACATGCGACAGACCTGTCTACTACAAAGATTAATTAATTTGCCAGGCTT 140
| | | | |
| | | | |
QY 125 AGTGGCTCATCCCTGTGTCCTCCAGCTACTAGGAGGAGGAGAGTGA 171
| | | | |
| | | | |
Db 141 GCTGGCACAATGCTCTGTATCCAGCTACTTGGAGGCTGAGGCGAGGA 187
| | | | |
| | | | |

RESULT 13

US-09-925-065A-48525
; Sequence 48525, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289, 846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48525
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-48525

Query Match 64.4%; Score 113.4; DB 4; Length 1333;
Best Local Similarity 78.9%; Pred. No. 2.3e-28;
Matches 135; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGTCTGTGAGCCGAGATTTC 60
| | | | |
| | | | |
Db 184 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGTCTGTGAGCCGAGATTTC 243
| | | | |
| | | | |
QY 61 AAGAGCAGCTCGACAACAACAGAGGAGACCTGTCTACTACAAAGATTAATTAATTTAGCCAG 120
| | | | |
| | | | |
Db 244 GAGACCAAGCTCGGCAACGTAAGGAGACTTGTCTCTACAAAATAAATAATTTAGCCAG 303
| | | | |
| | | | |
QY 121 GCTTAGTGCATCCCTGTGTCCTCCAGCTACTACTAGGAGGAGAGTAAGGA 171
| | | | |
| | | | |
Db 304 GTGTGTAGACACAGCCTGTGTCTCCACTACTTGGAGATGTCGACATGGGA 354
| | | | |
| | | | |

RESULT 14

US-09-925-065A-48527
; Sequence 48527, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289, 846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48527
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-48527

Query Match 64.4%; Score 113.4; DB 4; Length 1333;
Best Local Similarity 78.9%; Pred. No. 2.3e-28;
Matches 135; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGTCTGTGAGCCGAGATTTC 60
| | | | |
| | | | |
Db 184 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGTCTGTGAGCCGAGATTTC 243
| | | | |
| | | | |
QY 61 AAGAGCAGCTCGACAACAACAGAGGAGACCTGTCTACTACAAAGATTAATTAATTTAGCCAG 120
| | | | |
| | | | |
Db 244 GAGACCAAGCTCGGCAACGTAAGGAGACTTGTCTCTACAAAATAAATAATTTAGCCAG 303
| | | | |
| | | | |
QY 121 GCTTAGTGCATCCCTGTGTCCTCCAGCTACTACTAGGAGGAGAGTAAGGA 171
| | | | |
| | | | |
Db 304 GTGTGTAGACACAGCCTGTGTCTCCACTACTTGGAGATGTCGACATGGGA 354
| | | | |
| | | | |

```
RESULT 15
US-09-925-065A-48528
; Sequence 48528, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48528
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-48528

Query Match      64.4%; Score 113.4; DB 4; Length 1333;
Best Local Similarity 78.9%; Pred. No. 2.3e-28;
Matches 135; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY      1  ACCGTAAATTCAGTCTGTGAGAGTCCGAGGTCAGAGCACTGTGAGGCCAGAGATTC 60
      184  ACCGTAAATTCAGCACTTGGAGGCTGAGGCAAGCGATTGCTTGAGCCCGAGAGTTG 243
QY      61  AAGAGCAGCCTGGACAACACAGGAGACCTGTCACTACAAAGAATAATTAATTAGCCAG 120
      244  GAGACCAAGCCTGGCAACGTAAGGAGACTGTCTTACAAAATAAATAAATTAGCCAG 303
QY      121  GCTTAGTGCTCATCCCTGTGTGCCAGCTACTAGGAGGCGAGAGTAGGA 171
      304  GTGTGCTAGACACGCGCTGTGTCCCACTACTTGGGATGTGCATGCGA 354
DB
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Search completed: June 6, 2006, 00:20:56
Job time : 352.008 secs

November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: IDENTITY_NIC

Gapop 10.0, Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Published Applications NA New:
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2: /EMC_Celerra_SIDS3/prodata/1/pubpna/US06_NEW_PUB.seq:
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4: /EMC_Celerra_SIDS3/prodata/1/pubpna/US08_NEW_PUB.seq:
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8: /EMC_Celerra_SIDS3/prodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	ID	Description
1	112	63.6	2312	US-11-293-697-880	Sequence 880, App
2	103	58.5	3550	US-11-293-697-509	Sequence 509, App
3	103	58.5	5515	US-10-524-021-1	Sequence 1, Appl
4	101.4	57.6	1947	US-11-293-697-1980	Sequence 1980, App
5	99.8	56.7	2218	US-11-293-697-2254	Sequence 2254, App
6	99.6	56.6	3178	US-10-505-928-277	Sequence 277, App
7	98.2	55.8	138941	US-10-489-730-10	GENERAL INFORMATI
8	98	55.7	2561	US-11-293-697-1616	Sequence 1616, Ap
9	98	55.7	2789	US-11-293-697-2050	Sequence 2050, Ap
10	97.6	55.5	1935	US-11-293-697-2208	Sequence 2208, App
11	97.6	55.5	2374	US-11-293-697-441	Sequence 441, App
12	96.6	54.9	2849	US-11-293-697-1604	Sequence 1604, App
13	96.4	54.8	2143	US-11-293-697-1607	Sequence 1607, App
14	96.4	54.8	2252	US-11-293-697-1292	Sequence 1292, Ap
15	96.4	54.8	2389	US-11-293-697-2013	Sequence 2013, Ap
16	96	54.5	2387	US-11-293-697-1487	Sequence 1487, Ap
17	95.8	54.4	3564	US-11-293-697-639	Sequence 639, App
18	95.8	54.4	128361	US-10-505-928-151	Sequence 151, App
19	95.2	54.1	2915	US-11-293-697-59	Sequence 59, Appl
20	95	54.0	2017	US-11-293-697-2207	Sequence 2207, App
21	95	54.0	2460	US-11-293-697-595	Sequence 595, App
22	95	54.0	2800	US-11-293-697-23	Sequence 23, Appl
23	95	54.0	4086	US-11-301-554-1801	Sequence 1801, App
24	95	54.0	54550	US-11-318-813-42	Sequence 42, Appl
25	95	54.0	394191	US-10-506-549-3	Sequence 3, Appl

C 26	94.8	53.9	2909	US-11-293-697-1113	Sequence 1113, Ap
C 27	94.8	53.9	128361	US-10-505-928-151	Sequence 151, Appl
C 28	94.4	53.6	2836	US-11-293-697-30	Sequence 30, Appl
C 29	94.2	53.5	138941	US-10-489-730-10	GENERAL INFORMATI
C 30	93.6	53.2	2607	US-11-293-697-608	Sequence 608, App
C 31	93.4	53.1	1977	US-11-293-697-2303	Sequence 2303, App
C 32	93.4	53.1	2140	US-11-293-697-513	Sequence 513, App
C 33	93.4	53.1	2342	US-11-293-697-1268	Sequence 1268, App
C 34	93.4	53.1	2682	US-11-293-697-1324	Sequence 1324, App
C 35	93.4	53.1	2731	US-11-293-697-1412	Sequence 1412, App
C 36	93.4	53.1	2782	US-11-293-697-1729	Sequence 1729, App
C 37	92.8	52.7	1733	US-11-293-697-1577	Sequence 1577, App
C 38	92.6	52.6	2237	US-11-293-697-1855	Sequence 1855, App
C 39	92.6	52.6	2856	US-11-293-697-1116	Sequence 1116, App
C 40	92.4	52.5	2462	US-11-293-697-2214	Sequence 2214, App
C 41	91.8	52.2	391	US-10-511-937-583	Sequence 583, App
C 42	91.8	52.2	1177	US-10-196-749-381	Sequence 381, App
C 43	91.8	52.2	1177	US-11-101-316-129	Sequence 129, App
C 44	91.8	52.2	1981	US-11-293-697-443	Sequence 443, App
C 45	91.8	52.2	2067	US-11-293-697-2313	Sequence 2313, App

ALIGNMENTS

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RESULT 1
US-11-293-697-880
; Sequence 880, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length CDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293.697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108.260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 880
; LENGTH: 2312
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-880

Query Match      63.6%; Score 112; DB 7; Length 2312;
Best Local Similarity 82.0%; Pred. No. 3.1e-24;
Matches 141; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

QY 1 ACCTGTAATCCAGTACTGTGAGATCCGAGCTGAGGCTTGTAGGCGCAGAGTTC 60
   |||||
Db 1142 ACCTGTAATCCGCGCACTTTGGAGGCTGAGGCTGAGGAGCTGTTGAGTCCAGAGTTC 1201
   |||||

QY 61 AAGACGAGCTTGACCAACACAGGAGAGC-CTGTCACTACCAAGAAATTAATTAGCCA 119
   |||||
Db 1202 AAGACGAGCTTGAGCAACATAGTAGAGCTTTGCTCTACAAATATATATTAATTACTG 1261
   |||||

QY 120 GGGTATGCTGCTATCCCTGTGTGCTCCAGCTACTAGGAGGCGAAGTAGAGA 171
   |||||
Db 1262 GGCATGCTGACATGCTGTGTGCTCCAGCTACTTGGAGGCGCAAGCAGAGA 1313
   |||||

RESULT 2
US-11-293-697-509/C
; Sequence 509, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length CDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293.697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108.260
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;; PRIOR FILING DATE: 2002-03-28
;; NUMBER OF SEQ ID NOS: 5458
;; SOFTWARE: PatentIn Ver. 2.1.1
;; SEQ ID NO 509
;; LENGTH: 3550
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-293-697-509

Query Match 58.5%; Score 103; DB 7; Length 3550;
Best Local Similarity 78.9%; Pred. No. 1.4e-21;
Matches 135; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGTTGAGGCCAGAGTTCA 61
DB 1837 CCTGTAATTCAGTACTGTGAGAGGCCGAGGCGGGTGTGATCACTTGAGGTCAAGAGTTCA 1778
QY 62 AGAGCAGCCTGGACAACAACAGGG-AGACCTGTCACTCAAAAGATAATTAATTAGCCAG 120
DB 1777 AGACCAAGCCTGGCAACATGGGGAGGCCCTGTCTCTACTAAATAACAAAATTAGCCAG 1718
QY 121 GCTTAGTGCTCATCCCTGTGTGTCAGACTAGGAGGAGCAAGTAGGA 171
DB 1717 GCGTGTGGCGGGTGCCTGTAATCCAGCTACTCAGAGGCTGAGGAGGA 1667

* RESULT 3

US-10-524-021-1
;; Sequence 1, Application US/10524021
;; Publication No. US2006099590A1
;; GENERAL INFORMATION:
;; APPLICANT: NAGOYA INDUSTRIAL SCIENCE RESEARCH INSTITUTE
;; APPLICANT: GIFU INTERNATIONAL INSTITUTE OF BIOTECHNOLOGY
;; APPLICANT: YAMADA, Yoshiiji
;; APPLICANT: YOKOTA, Mitsuhiro
;; TITLE OF INVENTION: Method for diagnosing a risk of restenosis after percutaneous cor
;; TITLE OF INVENTION: Intervention
;; FILE REFERENCE: C0200501
;; CURRENT APPLICATION NUMBER: US/10/524,021
;; CURRENT FILING DATE: 2005-02-09
;; PRIOR APPLICATION NUMBER: JP P2002-233041
;; PRIOR FILING DATE: 2002-08-09
;; NUMBER OF SEQ ID NOS: 67
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 1
;; LENGTH: 5515
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-524-021-1

Query Match 58.5%; Score 103; DB 6; Length 5515;
Best Local Similarity 78.9%; Pred. No. 1.6e-21;
Matches 135; Conservative 0; Mismatches 35; Indels 1; Gaps 1;
QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGTTGAGGCCAGAGTTCA 61
DB 2581 CCTGTAATTCAGTACTGTGAGAGGCCAAGGTGGAGATCACTTGAGGCCAGAGTTCA 2640
QY 62 AGAGCAGCCTGGACAACAACAGGGAGA-CCTGTCACTCAAAAGATAATTAATTAGCCAG 120
DB 2641 ACACCAAGCCTGGCAACATGTGTGAGCCCTGTCTCTACTAAATAACAAAATTAGCCAG 2700
QY 121 GCTTAGTGCTCATCCCTGTGTGTCAGACTAGGAGGAGCAAGTAGGA 171
DB 2701 GCAATGTGCCACACACCTGTGTCTCAGCTACTCAGAGGAGGCTGAGGAGGA 2751

RESULT 4

US-11-293-697-1980
;; Sequence 1980, Application US/11293697
;; Publication No. US20060105376A1
;; GENERAL INFORMATION:
;; APPLICANT: HELIX RESEARCH INSTITUTE

;; TITLE OF INVENTION: Novel full length cDNA
;; FILE REFERENCE: H1-A0106
;; CURRENT APPLICATION NUMBER: US/11/293,697
;; CURRENT FILING DATE: 2005-12-05
;; PRIOR APPLICATION NUMBER: US/10/108,260
;; PRIOR FILING DATE: 2002-03-28
;; NUMBER OF SEQ ID NOS: 5458
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1980
;; LENGTH: 1947
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-293-697-1980

Query Match 57.6%; Score 101.4; DB 7; Length 1947;
Best Local Similarity 75.4%; Pred. No. 3.6e-21;
Matches 126; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGTTGAGGCCAGAGTTCA 61
DB 1679 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGTTGAGGCCAGAGTTCA 1738
QY 62 AGAGCAGCCTGGACAACAACAGGGAGCCTGTCACTCAAAAGATAATTAATTAGCCAG 121
DB 1739 AGACCAAGCCTGGCAACATGTGTGAACCCATCTAATCAAAAATTAGCCAGG 1798
QY 122 CTTAGTGCTCATCCCTGTGTGTCAGACTAGGAGGAGCAAGTAG 168
DB 1799 TGTGTGTATGCACACCTGTATATCCAGCTACTCGGAGGCTGAGGCA 1845

RESULT 5

US-11-293-697-2254
;; Sequence 2254, Application US/11293697
;; Publication No. US20060105376A1
;; GENERAL INFORMATION:
;; APPLICANT: HELIX RESEARCH INSTITUTE
;; APPLICANT: HELIX RESEARCH INSTITUTE
;; TITLE OF INVENTION: Novel full length cDNA
;; FILE REFERENCE: H1-A0106
;; CURRENT APPLICATION NUMBER: US/11/293,697
;; CURRENT FILING DATE: 2005-12-05
;; PRIOR APPLICATION NUMBER: US/10/108,260
;; PRIOR FILING DATE: 2002-03-28
;; NUMBER OF SEQ ID NOS: 5458
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2254
;; LENGTH: 2218
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-11-293-697-2254

Query Match 56.7%; Score 99.8; DB 7; Length 2218;
Best Local Similarity 77.8%; Pred. No. 1.1e-20;
Matches 133; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGTTGAGGCCAGAGTTCA 61
DB 1014 CCTGTAATTCAGTACTGTGAGAGGCCAAGGTGGCGGATCACTTGAGGCCAGAGTTCC 1073
QY 62 AGAGCAGCCTGGACAACAACAG-GGAGACTGTCACTCAAAAGATAATTAATTAGCCAG 120
DB 1074 AGACCAAGCCTGGCAACATGTGTGAACCCCTGTCTCTAATAATAACAAAATTAGCTGG 1133
QY 121 GCTTAGTGCTCATCCCTGTGTGTCAGACTAGGAGGAGCAAGTAGGA 171
DB 1134 GCTGGGTGGCAATGCTGTATGTCAGCTACTCGGAGGCTGAGGAGGA 1184

RESULT 6

US-10-505-928-277/C
;; Sequence 277, Application US/10505928
;; Publication No. US20060088532A1
;; GENERAL INFORMATION:


```

? APPLICANT: Ludwig Institute for Cancer Research et al
? TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
? FILE REFERENCE: 28967/39178
? CURRENT APPLICATION NUMBER: US/10/505,928
? CURRENT FILING DATE: 2004-08-27
? PRIOR APPLICATION NUMBER: US 60/363,019
? PRIOR FILING DATE: 2002-03-07
? NUMBER OF SEQ ID NOS: 866
? SOFTWARE: PatentIn 3.2
? SEQ ID NO 277
?
? LENGTH: 3178
?
? TYPE: DNA
?
? ORGANISM: Homo sapiens
?
US-10-505-928-277

```

Query Match	56.6%	Score 99.6	DB 6	Length 3178
Best Local Similarity	74.1%	Pred. No. 1.4e-20		
Matches 126; Conservative	0;	Mismatches 44;	Indels 0;	Gaps 0;

Qy 2 CCTGTATTCACACTCTGTGAGAGTCCGAGGTCAAGAGACTCGTTAAGGCCAGAGATTCA 61
Dd 2096 CCTGTATTCACAGCACATTGGAGGCTGAGGTGGGTGCATCACCAGGTCAGAAGATTCA 20

QY	62	AGACGAGCCCTGGACAAACACAGGAGACCTGTCTACACAAAGAATAAATAATTGCGCAG	121
Db	2036	AGACCGAGTCTGGCCCAACAGGTGAACCCCTCTATATATAAAATTCAAAAATTTGCGCAG	1977

```

Oy      122  CTTAGTGGCTATCCCTGTGTCCTCCAGCTACTAGGGAGGCGAGAAGTAGGA 171
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1976 CGTGTAGTGTGTGCTGTATCCAGCTACTCGGGAAGCTGAAGCAGGA 1922

```

RESULT 7
US-10-489-730-10/C

APPLICANT: Melino, Gennaro
 APPLICANT: Hayes, Ian
 APPLICANT: de Laurenti, Vincenzo
 APPLICANT: Barcaroli, Daniela
 APPLICANT: Candi, Eleonora
 APPLICANT: Bernasola, Francesca
 APPLICANT: Tobler, Andreas
 APPLICANT: Novak, Urban
 TITLE OF INVENTION: Human Delta-N p73 Molecules and Uses Thereof
 FILE REFERENCE: 19319.002
 CURRENT APPLICATION NUMBER: US/10/489,730
 CURRENT FILING DATE: 2004-03-16
 PRIOR APPLICATION NUMBER: PCT/GB02/04238
 PRIOR FILING DATE: 2002-09-17
 PRIOR APPLICATION NUMBER: US 60/322,436
 PRIOR FILING DATE: 2001-09-17
 NUMBER OF SEQ ID NOS: 39
 OTHER INFORMATION: reverse complement of exons 14 through 1 as reported in GenBank #
 US-10-489-730-10

Query Match	55.8%	Score 98.2;	DB 6;	Length 138941;
Best Local Similarity	77.2%	Pred. No. 9e-20;		
Matches 132; Conservative	0;	Mismatches 38;	Indels 1;	Gaps 1;

Qy	2	CCTGTAATTCAGTACTGTGAGATGCCAGSTCAGAGACCTGCTTGAAGCCAGAGATTCA	61
Db	133671	CCTGTAATCCAGCACTTTGGAGGCGCAAGCTGCGATCATCTTGAACAAGAAATTCA	133612

QY	62	AGAGCAGCCTGGACAACACAGGAGAC-CCTGTCACTACCAAGAATTAATAATTGACCG	120
Db	133611	AGAGCAGTCTGGGCAACACGGTGAAACCCCATCTCTACCAAGAATTCAAAAATTACCGG	133552

Oy 121 GCTTAGTGCTCATCCCTGTGTCACGACTAGGGGAGCAGAATAGGA 171
 || | | | | | | | | | | | | | | | | | |
Db 13351 GCGTGTGTGCATGCTTTGTGTCGCCAGTACTTGGAGGCTGACGTAGGA 133501

RESULT 8

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US-11-293-697-1616
; Sequence 1616, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1616
; LENGTH: 2561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1616

```

Query Match	55.7%;	Score 98;	DB 7;	Length 2561;
Best Local Similarity	73.5%;	Pred. No. 3.8e-20;		
Matches 125;	Conservative	0;	Mismatches 45;	Indels 0;
				Gaps 0;

QY	2	CCGTAAATCCAGACTGTGAGAGTCCAGAGTCAGAGAGCTGTGAGGCACAGAGTTCA	61
Db	2302	CCATAATCCAGACCTTTGGATGCCAGAGTGGCAGATCACTTGAAGCTCAGAGATTCA	2365

QY 62 AGAGCAGCTGGACACACAGGAGACCTGTACTACAAGAAATATAATATGGCCAG 121

Db 2362 AGACCAGCTGGCCACATGTGTAAACCCGCTTACTTAAATAACAATAATTAGCTGG 2422

Db 2422 TGTGCTGGACATGCTCTGTAATCCACGCTACTCAGAGGCTGAGGCAGAA 2477

RESULT 9

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US-11-293-697-2050
? Sequence 2050, Application US/11293697
? Publication No. US20060105376A1
? GENERAL INFORMATION:
? APPLICANT: HELIX RESEARCH INSTITUTE
? TITLE OF INVENTION: Novel full length cDNA
? FILE REFERENCE: H1-A0106
? CURRENT APPLICATION NUMBER: US/11/293,697
? CURRENT FILING DATE: 2005-12-05
? PRIOR APPLICATION NUMBER: US/10/108,260
? PRIOR FILING DATE: 2002-03-28
? NUMBER OF SEQ ID NOS: 5458
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 2050
? LENGTH: 2799
? TYPE: DNA
? ORGANISM: Homo sapiens
US-11-293-697-2050

```

Query Match 55.7%; Score 98; DB 7; Length 2799;
Best Local Similarity 73.5%; Pred. NO. 3.9e-20;
Matches 125; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGCTCAGAGCACTGCCTTGAGGCCAGGATTCA 61
| | | | | | | | | | | | | | | | | | | | | |
Db 2540 CCTGTAATTCAGCACTTTGGAGGCGTGAAGGCACTGATACCTGAGAGCTCAGAGATTYTG 25

QY 62 AGAGCAGCGCTGGACAACACAGGAGACCTGTCACTACAAGANTAAATTAATGACCGG 121
Db 2600 AGACCAAGCTGGCAACATGTGTAACTGTCTACTCAAAAATACAAAATTAATGACCGG 2659

QY	122	CTTAACTGGCTCATCCCTGTGGTCCAGCTACTAGGAGCAGAAAGTAGGA	171
Db	2660	CGTGGTGGCGGGTGCCCTGTATCCTAGCTACTCAGGAGACTGAGCAGGA	2709

RESULT 10
US-11-293-697-2208/c
; Sequence 2208, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2208
; LENGTH: 1935
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-2208

Query Match 55.5%; Score 97.6; DB 7; Length 1935;
Best Local Similarity 76.7%; Pred. No. 4.6e-20;
Matches 132; Conservative 0; Mismatches 39; Indels 1; Gaps 1;

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGGCCAGAGTTTC 60
DB 1241 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGGCCAGAGTTTC 1182
QY 61 AAGAGCAGCTTGACACACAGGAGAG-CCTGTCACTACAAAGATTAATTAATTAAGCCA 119
DB 1181 GAGACGAGCTTGACACACAGGAGAG-CCTGTCTCTACTTAAATAAATAAATTAAGCTG 1122
QY 120 GCGTTAGTGGCTATCCCTGTGGTCCAGCTACTAGGAGGACGAAGTAGGA 171
DB 1121 GCGATGTGGACACACCTGTAGTCCAGCTACTTGGAGGCTGAGGACAGGA 1070

RESULT 11
US-11-293-697-441/c
; Sequence 441, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 441
; LENGTH: 2374
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-441

Query Match 55.5%; Score 97.6; DB 7; Length 2374;
Best Local Similarity 76.7%; Pred. No. 4.9e-20;
Matches 132; Conservative 0; Mismatches 39; Indels 1; Gaps 1;

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGGCCAGAGTTTC 60
DB 2139 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGGCCAGAGTTTC 2080
QY 61 AAGAGCAGCTTGACACACAGGAGAG-CCTGTCACTACAAAGATTAATTAATTAAGCCA 119
DB 2079 GAGACGAGCTTGACACACAGGAGAG-CCTGTCTCTACTTAAATAAATAAATTAAGCCA 2020
QY 120 GCGTTAGTGGCTATCCCTGTGGTCCAGCTACTAGGAGGACGAAGTAGGA 171
DB 2019 GCGATGTGGACACACCTGTAGTCCAGCTACTTGGAGGCTGAGGACAGGA 1968

RESULT 12
US-11-293-697-404/c
; Sequence 404, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 404
; LENGTH: 2849
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-404

Query Match 54.9%; Score 96.6; DB 7; Length 2849;
Best Local Similarity 76.6%; Pred. No. 1e-19;
Matches 131; Conservative 0; Mismatches 39; Indels 1; Gaps 1;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGGCCAGAGTTTC 61
DB 383 CCTGTAAGCCAGCAGTCTTGGAGGCTGAGGACATGATCACTTGAGGTCAAGAGTTTC 324
QY 62 AAGAGCAGCTTGACACACAGGAGAG-CCTGTCACTACAAAGATTAATTAATTAAGCCA 120
DB 323 AGACGAGCTTGACACACAGGAGAG-CCTGTCTCTACTTAAATAAATAAATTAAGCTG 264
QY 121 GCGTTAGTGGCTATCCCTGTGGTCCAGCTACTAGGAGGACGAAGTAGGA 171
DB 263 GCGATGTGGACACACCTGTAGTCCAGCTACTTGGAGGCTGAGGACAGGA 213

RESULT 13
US-11-293-697-1607
; Sequence 1607, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1607
; LENGTH: 2143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1607

Query Match 54.8%; Score 96.4; DB 7; Length 2143;
Best Local Similarity 72.9%; Pred. No. 1.1e-19;
Matches 124; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGGCCAGAGTTTC 61
DB 1884 CCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGGCCAGAGTTTC 1943
QY 62 AAGAGCAGCTTGACACACAGGAGAG-CCTGTCACTACAAAGATTAATTAATTAAGCCA 121
DB 1944 AGACGAGCTTGACACACAGGAGAG-CCTGTCTCTACTTAAATAAATAAATTAAGCCA 2003
QY 122 CTTAGTGGCTATCCCTGTGGTCCAGCTACTAGGAGGACGAAGTAGGA 171
DB 2004 TGAAGTGGCAGGCTGTAATCCAGCTACTGAGAGGCTGAGGACAGGA 2053

RESULT 14

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US-11-293-697-1292
; Sequence 1292, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1292
; LENGTH: 2252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1292
```

```
Query Match          54.8%; Score 96.4; DB 7; Length 2252;
Best Local Similarity 72.9%; Pred. No. 1,1e-19;
Matches 124; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
```

```
QY      2 CCTGTAAATCCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGTTCA 61
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      1891 CCTGTAAATCCAGCACTTTGGAGTGGAGGTGGCGGATCCTTGAGGTCAAGAGTTCA 1950
QY      62 AGAGCAGCCTGGAACAACAGGAGAGACCTGTCACTACAAGAATAAATAATTAGCCAGG 121
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      1951 AGACCAAGCCTGGCCACATGTGTAAACCGTCTCTACTTAACATACAAAGATTAGCTGG 2010
QY      122 CTTAGTGGCTCATTCCTGTGTCCTCCAGCTACTAGGAGGCGAAGTAGGA 171
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      2011 TGTGTGGCACAGGCGCTGTATCGACGCCCTTGGAAGGCCAAGGCAGGA 2060
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RESULT 15

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US-11-293-697-2013
; Sequence 2013, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2013
; LENGTH: 2389
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-2013
```

```
Query Match          54.8%; Score 96.4; DB 7; Length 2389;
Best Local Similarity 72.9%; Pred. No. 1,1e-19;
Matches 124; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
```

```
QY      2 CCTGTAAATCCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGTTCA 61
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      2116 CCTGTAAATCCAGCACTTTGGAGGCAAGGCGAGATCACCTTAAGTCAAGAGTTCA 2175
QY      62 AGAGCAGCCTGGAACAACAGGAGAGACCTGTCACTACAAGAATAAATAATTAGCCAGG 121
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB      2176 AGACCAAGCCTGGCCACATGTGTAAACCGTCTCTACTTAACATACAAAGATTAGCCAGG 2235
QY      122 CTTAGTGGCTCATTCCTGTGTCCTCCAGCTACTAGGAGGCGAAGTAGGA 171
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
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DB 2236 TGAGGTGGCAGGTGCTGTAAATCCAGCTACTAGAGAGGCTGAGGCAGGA 2285

Search completed: June 6, 2006, 00:22:28
Job time : 7.13032 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:15:46 ; Search time 3134.62 Seconds
(without alignments)
9445.379 Million cell updates/sec

Title: US-09-869-098a-1_COPY_255_717

Perfect score: 463
Sequence: 1 accgtgaattccgaactgtc.....attcttcctgttgcagacag 463

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
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9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_hcg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	463	100.0	3505	2 E54511	E54511 UCP-2 promo
2	461.4	99.7	3270	5 AF306570	AF306570 Homo sapi
3	461.4	99.7	12177	5 DQ087219	DQ087219 Homo sapi
4	461.4	99.7	155668	12 AC024029	AC024029 Homo sapi
5	461.4	99.7	156370	5 AP003717	AP003717 Homo sapi
6	461.4	99.7	197031	12 AC019121	AC019121 Homo sapi
7	461.4	99.7	199384	5 AP003531	AP003531 Homo sapi
8	327.8	70.8	3301	5 AF208500	AF208500 Homo sapi
9	158.4	34.2	168721	5 AC136431	AC136431 Homo sapi
10	158.4	34.2	173113	12 AC138962	AC138962 Homo sapi
11	158.4	34.2	175069	12 AC140895	AC140895 Homo sapi
12	158.4	34.2	175785	12 AC138897	AC138897 Homo sapi
13	158.4	34.2	189911	12 AC136434	AC136434 Homo sapi
14	158.4	34.2	211419	5 AC126760	AC126760 Homo sapi
15	158.4	34.2	235330	12 AC140522	AC140522 Homo sapi
16	158.2	34.2	66188	5 AL391136	AL391136 Human DNA
17	158.2	34.2	162820	5 AL138765	AL138765 Human DNA
18	156.8	33.9	133615	5 AC092326	AC092326 Homo sapi

19	156.8	33.9	170572	12 AC140894	AC140894 Homo sapi
20	156.8	33.9	173271	12 AC141623	AC141623 Homo sapi
21	156.8	33.9	173912	12 AC141075	AC141075 Homo sapi
22	156.8	33.9	174428	12 AC136441	AC136441 Homo sapi
23	156.8	33.9	180664	12 AC140896	AC140896 Homo sapi
24	156.8	33.9	189646	12 AC140909	AC140909 Homo sapi
25	156.8	33.9	195740	12 AC141269	AC141269 Homo sapi
26	156.4	33.8	13009	5 AC130468	AC130468 Homo sapi
27	156.4	33.8	198521	12 AC145723	AC145723 Homo sapi
28	155.8	33.7	190144	5 AL590080	AL590080 Human DNA
29	153.2	33.1	185511	5 AC093414	AC093414 Homo sapi
30	152.4	32.9	145414	5 HS78F24	AL022336 Human DNA
31	152.4	32.9	217292	5 AF288742	AF288742 Homo sapi
32	152.2	32.9	98569	5 HS209B9	AL035876 Human DNA
33	152	32.8	135005	5 HS860F19	AL035460 Human DNA
34	152	32.8	162701	12 AC073317	AC073317 Homo sapi
35	152	32.8	171860	5 AC010373	AC010373 Homo sapi
36	151.8	32.8	96559	5 AC079347	AC079347 Homo sapi
37	151.6	32.7	17688	5 CNS01D75	AL134640 Human chr
38	151.6	32.7	202521	12 AC146953	AC146953 Pongo pyg
39	151	32.6	171183	5 AL358876	AL358876 Human DNA
40	151	32.6	178820	5 AC020552	AC020552 Homo sapi
41	150.8	32.6	56912	5 AL160176	AL160176 Human DNA
42	150.6	32.5	184041	5 AC093496	AC093496 Homo sapi
43	150.6	32.5	187159	5 AC090941	AC090941 Homo sapi
44	150.4	32.5	23579	2 AX647373	AX647373 Sequence
45	150.4	32.5	115231	5 HS785G19	AL035458 Human DNA

ALIGNMENTS

RESULT 1
E54511
LOCUS E54511 UCP-2 promoter and use thereof.
DEFINITION UCP-2 promoter and use thereof.
ACCESSION E54511
VERSION E54511.1 GI:18629692
KEYWORDS JP 2000236886-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 3505)
AUTHORS Toyota, Y., Kobayashi, M. and Igaki, S.
TITLE UCP-2 promoter and use thereof
JOURNAL Patent: JP 2000236886-A 1 05-SEP-2000;
TAKEDA CHEM IND LTD
COMMENT
OS Homo sapiens (human)
PN JP 2000236886-A/1
PD 05-SEP-2000
PF 22-DEC-1999 JP 1999364724
PR
PI YUKIO TOYOTA, MAKOTO KOBAYASHI, SHIGERU IGAKI
PC C12N15/09, A61K45/00, A61P3/04, A61P3/06, A61P9/10, A61P9/12, PC
A61P29/00, C12N1/21,
PC C12N5/10, C12Q1/02, G01N33/15, G01N33/50//A61K31/711, A61K38/00,
PC A61K48/00,
PC (C12N15/09, C12R1:19), (C12N15/09, C12R1:91), (C12N1/21, C12R1:19),
PC (C12N5/10, C12R1:91), (C12N15/00, C12N5/00, A61K37/02, (C12N15/00,
PC C12R1:19),
PC (C12N15/00, C12R1:91), (C12N5/00, C12R1:91)

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FT Location/Qualifiers
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FT /mol_type='genomic DNA'
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ORIGIN

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Best Local Similarity	100.0%;	Pred. No. 2.2e-113;		
Matches 463;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

[illegible]

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RESULT 2
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LOCUS             Homo sapiens uncoupling protein 2 gene, promoter region and exon 1,
DEFINITION        nuclear gene for mitochondrial product.
ACCESSION         AF306570
VERSION           AF306570.1  GI:11037742
KEYWORDS
SOURCE
ORGANISM          Homo sapiens (human)
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                  Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                  Homnidae; Homo.
REFERENCE          1 (bases 1 to 3270)
AUTHORS           Schnetler,C., Oberkofler,H., Esterbauer,H. and Patsch,W.
TITLE             UCP2 promoter region and exon 1
JOURNAL           Unpublished
FEATURES          2 (bases 1 to 3270)
                  Schnetler,C., Oberkofler,H., Esterbauer,H. and Patsch,W.
                  Direct Submission
                  Submitted (18-SEP-2000) Laboratory Medicine, Landeskliniken
                  Salzburg, Mueller Hauptstr. 48, Salzburg A-5020, Austria
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ORIGIN

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Best Local Similarity	99.8%	Pred. No. 6e-113		
Matches 462; Conservative	0	Mismatches 1	Indels 0	Gaps 0

[illegible]

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ACCESSION	DQ087219				
VERSION	DQ087219.1	GI:67515418			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 12177) Livingston,R.J., Rieder,M.J., Shaffer,T., Bertucci,C., Baler,C.N., Raykumar,N., Wills,H.T., Daniels,M., Downing,T.K., Stanaway,I.B., Nguyen,G.P., Gildersleeve,H., Cassidy,C.M., Johnson,E.J., Swanson,J.E., McFarland,I., Yool,B., Park,C. and Nickerson,D.A. Direct Submission Submitted (07-JUN-2005) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA To cite this work please use: NIEHS-SNRs, Environmental Genome Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://esg.gs.washington.edu).				
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ORIGIN

Query Match 99.7%; Score 461.4; DB 12; Length 155668;
Best Local Similarity 99.8%; Pred. No. 2.6e-113;
Matches 462; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACCTGAATTCAGTACTGTGAGAGTCCGAGTCCAGAGGACTGCTTGAGCCAGAGATTC 60
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Db 70159 ACCTGAATTCAGTACTGTGAGAGTCCGAGTCCAGAGGACTGCTTGAGCCAGAGATTC 70100
QY 61 AAGAGAGCCTGGACACACAGAGGAGACTGCTGACTACCAAGATTAATTAATAGCCAG 120
Db 70099 AAGAGAGCCTGGACACACAGAGGAGACTGCTGACTACCAAGATTAATTAATAGCCAG 70040
QY 121 GCTTAGTGCTCAATCCCTGTGTGCTCCAGCTTACTAGGAGGACAGAGTGGACTGCTGTC 180
Db 70039 GCTTAGTGCTCAATCCCTGTGTGCTCCAGCTTACTAGGAGGACAGAGTGGACTGCTGTC 69980
QY 181 CCAGAGGTGAACACAGTGAAGTGAAGCCAGCCAGCCAGCTGATTCACCTGGGAGAC 240
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QY 241 AAAAGAGACCTGCTCAAAAAATAGTAAATTAATTAATTAATTAATTAATAGTTAAAC 300
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QY 301 CCTAAACACATCTCTCTTTTCAAGAGACTTCTTAAGACTTCATGCTGCTGTTG 360
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QY 361 ATCTCCACTTCCTTTTTCAGGCTCCACACTTTTAACAGTCTTTTGGCCAGATATA 420
Db 69799 ATCTCCACTTCCTTTTTCAGGCTCCACACTTTTAACAGTCTTTTGGCCAGATATA 69740
QY 421 AGTATATAGTTCTGGAATCCAGATTCCTGTTTGGACAG 463
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RESULT 5
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LOCUS Homo sapiens genomic DNA, chromosome 11q clone:RP11-167N4, complete
DEFINITION
ACCESSION AP003717
VERSION AP003717.3 GI:20334343
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Tocoli,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
Published Only in Database (2001)
2 (bases 1 to 156370)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Tocoli,Y., Watanabe,H. and Sakaki,Y.
Direct Submision
Submitted (04-JUN-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suenho-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel:81-45-503-9111, Fax:81-45-503-9170
On Apr 26, 2002 this sequence version replaced gi:16904692.
COMMENT
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ORIGIN

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Best Local Similarity 99.8%; Pred. No. 2.6e-113;
Matches 462; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 421 AGTATATAGTTTCTGGAATCAGATTCTTCCCTGTTTGACAG 463
Db 44453 AGTATATAGTTTCTGGAATCAGATTCTTCCCTGTTTGACAG 44411

RESULT 6
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LOCUS Homo sapiens chromosome 11 clone RP11-535C12, WORKING DRAFT
DEFINITION
SEQUENCE, 23 unordered pieces.
AC019121
AC019121.3 GI:8440022
VERSION HTG; HTGS PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 197031)
Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 197031)
Waterston, R.H.
Direct Submission
Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 10, 2000 this sequence version replaced gi:7105573.

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information -----
Center project name: H NH0535C12
----- Summary Statistics -----
Sequencing vector: M13, 55%
Sequencing vector: plasmid, 45%
Chemistry: Dye-primer ET, 55% of reads
Chemistry: Dye-terminator Big Dye, 45% of reads
Assembly program: Phrap, version 0.990119
Consensus quality: 182418 bases at least Q40
Consensus quality: 187565 bases at least Q30
Consensus quality: 190012 bases at least Q20

Insert size: 190000; agarose-fp
Insert size: 194831; sum-of-contigs
Quality coverage: 4.10 in Q20 bases; agarose-fp
Quality coverage: 4.05 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
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Best Local Similarity 99.8%; Pred. No. 2.5e-113;
Matches 462; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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          |||
Db      163478  GCTTAGTGCGTCATCCCTGGTGTCCCGACGTACTAGGAGGACAGAGTAAGACTGCTGTGTC 163537
QY      181  CCAAGAGGTCAAGACTGCTGAGTGAAGTGAAGCCAGCCTGCATTCCAGCTTGAGGCAAC 240
          |||
Db      163538  CCAAGAGGTCAAGACTGCTGAGTGAAGTGAAGCCAGCCTGCATTCCAGCTTGAGGCAAC 163597
QY      241  AAAAAAGACCTGTGTCTCAAAAAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAC 300
          |||
Db      163598  AAAAAAGACCTGTGTCTCAAAAAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAC 163657
QY      301  CCTAAACACATCTTCTTTTCAAAAGAGACTTCTTAAGACTTCATGCTGCTGCTGTG 360
          |||
Db      163658  CCTAAACACATCTTCTTTTCAAAAGAGACTTCTTAAGACTTCATGCTGCTGCTGTG 163717
QY      361  ATCTCCACTCCCTTTTTCAGCGTCCACACTTTTAACAGTCTCTTTGGCCAGAGATAATA 420
          |||
Db      163718  ATCTCCACTCCCTTTTTCAGCGTCCACACTTTTAACAGTCTCTTTGGCCAGAGATAATA 163777
QY      421  AGTATATAGTTTCTGGAATCCAGATTCTTCCTGTTTGAACAG 463
          |||
Db      163778  AGTATATAGTTTCTGGAATCCAGATTCTTCCTGTTTGAACAG 163820
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```
RESULT 7
AP003531/c      199384 bp      DNA      linear      PRI 27-APR-2002
LOCUS           Homo sapiens genomic DNA, chromosome 11q clone:RHL1-535c12,
DEFINITION      complete sequences.
ACCESSION      AP003531
VERSION        AP003531.2  GI:20334341
KEYWORDS       HTG.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homiidae; Homo.
REFERENCE
AUTHORS        Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
                Fujiyama,A., Yada,T., Torokiy,Y., Watanabe,H. and Sakaki,Y.
TITLE          Homo sapiens genomic DNA
JOURNAL        Published only in Database (2001)
REFERENCE      2 (bases 1 to 199384)
AUTHORS        Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
                Fujiyama,A., Yada,T., Torokiy,Y., Watanabe,H. and Sakaki,Y.
```

TITLE Direct Submission
JOURNAL Submitted (18-APR-2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shentaro-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://bgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Apr 26, 2002 this sequence version replaced gi:13699094.
FEATURES
source
1.199384
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q13"
/clone="RP11-535C12"
ORIGIN
Query Match 99.7%; Score 461.4; DB 5; Length 199384;
Best Local Similarity 99.8%; Pred. No.2:5e-113;
Matches 462; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGCACTGCTGAGGCCAGAGATTC 60
DB 182415 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCCAGAGCACTGCTGAGGCCAGAGATTC 182356
QY 61 AAGAGCAGCTGAGCAACACAGAGGAGACCTGTCACTCAAAAGTAATTAATTAGCCAG 120
DB 182355 AAGAGCAGCTGAGCAACACATAGGAGAGACCTGTCACTCAAAAGTAATTAATTAGCCAG 182296
QY 121 GCTTATGCTGCTATCCCTGTGCTCCAGCTACTAGGAGGAGCAAGTAGAGCACTGTGTC 180
DB 182295 GCTTATGCTGCTATCCCTGTGCTCCAGCTACTAGGAGGAGCAAGTAGAGCACTGTGTC 182236
QY 181 CCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCCACTGATTCAGCTGGGCAAC 240
DB 182235 CCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCCACTGATTCAGCTGGGCAAC 182176
QY 241 AAAAAGAGACCTGTCTCAAAAAATAATTAATTAATTAATTAATTAATTAATTAATTAAC 300
DB 182175 AAAAAGAGACCTGTCTCAAAAAATAATTAATTAATTAATTAATTAATTAATTAAC 182116
QY 301 CCTAAACACATCTCTTTTCAAGAGACTCTTAAGACTTCAGCTGCTGCTGCTG 360
DB 182115 CCTAAACACATCTCTTTTCAAGAGACTCTTAAGACTTCAGCTGCTGCTGCTG 182056
QY 361 ATCTCCACTTCCCTTTTTCAGCGTCCACACTTTTAACAGTCTCTTTGGCCAGGATATA 420
DB 182055 ATCTCCACTTCCCTTTTTCAGCGTCCACACTTTTAACAGTCTCTTTGGCCAGGATATA 181996
QY 421 AGTATATAGTTTCTGGAATCCAGATTCTTCCCTGTTTGAACAG 463
DB 181995 AGTATATAGTTTCTGGAATCCAGATTCTTCCCTGTTTGAACAG 181953
RESULT 8
AF208500 3301 bp DNA linear PRI 09-JAN-2000
LOCUS Homo sapiens uncoupling protein 2 (UCP2) gene, promoter and exon 1.
DEFINITION AF208500
ACCESSION AF208500
VERSION AF208500.1 GI:6684000
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
1 (bases 1 to 3301)
Tu,N., Chen,H., Winkler,U., Reinert,I., Marmann,G., Pirke,K.M. and
Lentes,K.U.
TITLE Molecular cloning and functional characterization of the promoter
JOURNAL region of the human uncoupling protein-2 gene
Biochem. Biophys. Res. Commun. 265 (2), 326-334 (1999)
PubMed 10558866

REFERENCE 2 (bases 1 to 3301)
AUTHORS Tu,N., Chen,H., Winkler,U., Reinert,I., Pirke,K.M. and Lentes,K.U.
TITLE Functional characterization of the 5'-flanking and promoter regions of the human UCP2 gene
JOURNAL Biochem. Biophys. Res. Commun. (2000) In press
REFERENCE 3 (bases 1 to 3301)
AUTHORS Lentes,K.U., Tu,N. and Chen,H.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-1999) Laboratory of Molecular Neurogenetics, Center for Psychobiological and Psychosomatic Research, University of Trier, Friedrich-Wilhelm-Strasse 23, Trier D-54290, Germany
FEATURES
source
1.3301
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q13"
/gene="UCP2"
/note="5' flanking region and promoter"
misc_feature
1.3297
/gene="UCP2"
3298..3301
/gene="UCP2"
mRNA
3298..3301
/gene="UCP2"
/product="uncoupling protein 2"
3298..3301
/gene="UCP2"
exon
/number=1
ORIGIN
Query Match 70.8%; Score 327.8; DB 5; Length 3301;
Best Local Similarity 92.3%; Pred. No.3:6e-77;
Matches 431; Conservative 0; Mismatches 26; Indels 10; Gaps 8;
QY 5 GTTAATTCAGTACTGTGAGAGT--CCGAGTCAAGAGTCTTGGAGCCAGAGTTC 62
DB 1320 GTTAATTCAGTACTGTGAGAGT--CCGAGTCAAGAGTCTTGGAGCCAGAGTTC 1379
QY 63 GAGCAGCTGAGCAACACAGAGGAGACCTGTCACTCAAAAGTAATTAATTAGCCAG 121
DB 1380 GAGCAGCTGAGCAACACATAGGAGAGACTGTCACTCAAAAGTAATTAATTAGCCAG 1438
QY 122 CTT-AGTGGCTCATCCCTGTGCTCCAGCTACTAGGAGGAGCAAGTAGAGTCTGTT 179
DB 1439 CTTAGTGGCTCATCCCTGTGCTCCAGCTACTAGGAGGAGCAAGTAGAGTCTGTT 1497
QY 180 CCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAG-CCAGCTGACCTCCAGCTGGGCA 238
DB 1498 CCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCCAGCTGACCTCCAGCTGGGCA 1557
QY 239 ACAAAAAGAGACCTGTCTCAAAAAATAATTAATTAATTAATTAATTAATTAATTA 298
DB 1558 ACAAAAAGAGACCTGTCTCAAAAAATAATTAATTAATTAATTAATTAATTAATTA 1617
QY 299 ACCCTAAACACATCTCTTTTCAAGAGGACTTTTAAGACTTCATGCTGCTGCTGT 358
DB 1618 ACCCTAAACACATCTCTTTTCAAGAGGACTTTTAAGACTTCATGCTGCTGCTGT 1677
QY 359 TGATCTCAGTCTCCCTTTTTCAGCGTCCACACTTTTAACAGTCTCTTTTTC-CCAAGATA 417
DB 1678 TGATCTCAGTCTCCCTTTTTCAGCGTCCACACTTTTAACAGTCTCTTTTTC-CCAAGATA 1737
QY 418 ATAAGTATATAGTTTCTGGAATCCAGATCTT-CCCTGTTTGAACAG 463
DB 1738 ATAAGTATATAGTTTCTGGAATCCAGATCTT-CCCTGTTTGAACAG 1784
RESULT 9
AC136431 168721 bp DNA linear PRI 21-DEC-2002
LOCUS Homo sapiens chromosome 16 clone RP11-148M17, complete sequence.
DEFINITION

ACCESSION AC136431
VERSION AC136431.3 GI:27356680
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (09-NOV-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE
AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (21-DEC-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Dec 21, 2002 this sequence version replaced gi:24819747.
COMMENT Draft Sequence Produced By DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www.shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.2.
FEATURES
source
1. .168721
location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-148M17"
ORIGIN
Query Match 34.2%; Score 158.4; DB 5; Length 168721;
Best Local Similarity 73.9%; Pred. No. 3.6e-32;
Matches 229; Conservative 0; Mismatches 76; Indels 5; Gaps 2;
2 CCTGTAATTCAGTGTGAGAGTCGAGGTGAGAGGCTTGAGGCGAGGTTCA 61
18726 CCTGTAATTCAGTGTGAGAGTCGAGGTGAGAGGCTTGAGGCGAGGTTTG 18785
62 AGAGCAGCCTGAGCAACACAGGAGACCTGTCACTAACAAGATTAATTAAGCCAG 121
18786 AGAGCAGCCTGAGCAACACAGGAGCTCATCTCTAATAAATAATTAAGCTAGG 18845
122 CTTAGTGGCTCATCCTGTGGTCCAGCTACTAGGAGGCAAGTGA---CTGCTT 177
18846 CCGTGTGGCAATGCCGTGTGCTCCAGCTACTAGGAGGCGCTGAGTGGGAGATGGCTTG 18905
178 GTCCGAGAGGCTCAAGCTCAGTGAAGTCCAGCCAGCCGATTCAGGCTGAGGCG 237
18906 AGCCCAAGAGGTGAGGATGAGTGAAGCCAGATTCAGCA-CTGCACTCAGGCTGGGT 18964
238 AACAAAAAGACCTGTCTCAAAAAATTAATTAAATTAATTAATTAATTAATTA 297
18965 GACAGAGCAAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTA 19024
298 AACCTTAAC 307
19025 ATCCCTAGAC 19034

RESULT 10
AC138962/c
LOCUS AC138962
DEFINITION Homo sapiens chromosome 16 clone RP11-906M12, WORKING DRAFT
SEQUENCE, 3 unordered pieces.
ACCESSION AC138962
KEYWORDS AC138962.1 GI:27805374
SOURCE HTGS_DRAFT; HTGS_ACTIVEFIN.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 16
JOURNAL Unpublished
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1642708
Center clone name: RPC1-11_906M12

Summary Statistics
Consensus quality: 171480 bases at least Q40
Consensus quality: 171615 bases at least Q30
Consensus quality: 171780 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Estimated insert size: 172913; sum-of-contigs estimation
Quality coverage: 15.53 in Q20 bases; agarose-fp estimation
Quality coverage: 16.17 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1119: contig of 1119 bp in length
* 1120 1219: gap of unknown length
* 1220 70508: contig of 69289 bp in length
* 70509 70608: gap of unknown length
* 70609 173113: contig of 102505 bp in length.
location/Qualifiers
1. .173113
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-906M12"
/clone_1ib="RP11 human BAC library 11"
1120. 1219
/estimated_length=unknown
70509. 70608
/estimated_length=unknown
ORIGIN
Query Match 34.2%; Score 158.4; DB 12; Length 173113;
Best Local Similarity 73.9%; Pred. No. 3.6e-32;
Matches 229; Conservative 0; Mismatches 76; Indels 5; Gaps 2;
2 CCTGTAATTCAGTGTGAGAGTCGAGGTGAGAGGCTTGAGGCGAGGTTCA 61

[illegible]

RESULT	11				
AC140895/c					
LOCUS					
DEFINITION	AC140895	175069 bp	DNA	linear	HTG 05-MAR-2003
ACCESSION	AC140895				
VERSION	AC140895.1	GI:28850006			
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEPIN.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Homnidae; Homo;				
REFERENCE	1 (bases 1 to 175069)				
AUTHORS	DOE Joint Genome Institute.				
TITLE	Sequencing of Human Chromosome 16				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 175069)				
AUTHORS	DOE Joint Genome Institute.				
TITLE	Direct Submission				
JOURNAL	Submitted (05-MAR-2003) Production Sequencing Facility, DOE Joint				
	Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA				
COMMENT	-----Genome Center				

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Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1554956
Center clone name: RPCT-11_678B4
-----

Summary Statistics
Consensus quality: 171558 bases at least Q40
Consensus quality: 172155 bases at least Q30
Consensus quality: 172672 bases at least Q20
Estimated insert size: 176000; agarose-1p estimation
Estimated insert size: 174269; sum-of-contigs estimation
Quality coverage: 6.48 in Q20 bases; agarose-1p estimation
Quality coverage: 6.44 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
    I 1231: contig of 1231 bp in length
    1232 1331: gap of unknown length

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FEATURES	Location/Qualifiers
*	1332 2506: contig of 1175 bp in length
*	2507 2606: gap of unknown length
*	2607 6130: contig of 3524 bp in length
*	6131 6230: gap of unknown length
*	6231 15102: contig of 8872 bp in length
*	15103 15202: gap of unknown length
*	15203 37238: contig of 22036 bp in length
*	37239 37338: gap of unknown length
*	37339 64159: contig of 26821 bp in length
*	64160 64259: gap of unknown length
*	64260 97134: contig of 32775 bp in length
*	97135 97035: gap of unknown length
*	97136 130745: contig of 33611 bp in length
*	130746 130845: gap of unknown length
*	130846 175069: contig of 44224 bp in length

FEATURES	source
location/Qualifiers	1..175069
	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/chromosome="16"
	/clone="RP11-678E4"
gap	1232..1331
	/clone_lib="RPC1 human BAC library 11"
gap	/estimated_length=unknown
gap	2507..2606
	/estimated_length=unknown
gap	6131..6230
	/estimated_length=unknown
gap	15103..15302
	/estimated_length=unknown
gap	37239..37338
	/estimated_length=unknown
gap	64160..64259
	/estimated_length=unknown
gap	97035..97134
	/estimated_length=unknown
gap	130746..130845
	/estimated_length=unknown

Query Match	Similarity	34.2%	Score 158.4	DB 12	Length 175069
Best Local	Similarity	73.9%	Pred. No. 3.6e-32		
Matches	229	Conservative	0	Mismatches	76
				Indels	5
				Gaps	2
Oy	2	CCTGTAATTCAGTACTGTGAGAGTCCAGGTCGAGAGCACTGCTTBAAGCCAGAGTTCA	61		
Db	131562	CCTGTAATTCAGTACTGTGAGAGTCCAGGTCGAGAGCACTGCTTBAAGCCAGAGTTTG	131503		
Oy	62	AGAGAGAGCTGGACAACAAGAGGAGACCTGTCCTACTACAAGAATAAATTAATTCAGCAG	121		
Db	131502	AGAGAGAGCTGGACAACAATAGAGAACTCATCTCTACAAAAAATAACAAAATTAGCTAAG	131443		
Oy	122	CTTAGTGGCTATCCCTGTGTTTCCAGCTACTAGGAGGACAGAAGTAGGA---CTGCTT	177		
Db	131442	CGTGTGGCACTATGCTGTAGTCCAGCTACTAGGAGGACTGAGTGGAGAGATGGCTTG	131383		
Oy	178	GTCCAGAGGCTGACAGACTGCAGTAGCTGAGACCCAGACACCTGCTTCAAGCTGGGC	237		
Db	131382	AGCCCAAGAGCTGAGAGATGCAAGTAGAGCCGAGATTGGACACA-CTGCAGCTCAAGCTGGGT	131322		
Oy	238	AACAAAAAGAGACCTGTCTCAAAAAATAAGTTAAATAAATAAATAAATAAGTTTA	297		
Db	131323	GACAAAGCAAGACCTGTCTCAAAAAATAAATAAATAAATAAATAAATAAATAAAGCAG	131264		
Oy	298	AACCTTAAC	307		
Db	131263	ATCCTTAGAC	131254		
RESULT 12					
AC138897/c					
LOCUS					
AC138897					
175785 bp					
DNA					
linear					
HTG 21-JAN-2003					

DEFINITION Homo sapiens chromosome 16 clone RP11-482B16, WORKING DRAFT
SEQUENCE, 3 unordered pieces.
ACCESSION AC138897
VERSION AC138897.1 GI:27805309
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 175785)
DOE Joint Genome Institute.
AUTHORS Sequencing of Human Chromosome 16
TITLE Unpublished
JOURNAL 2 (bases 1 to 175785)
REFERENCE DOE Joint Genome Institute.
AUTHORS Direct Submission
TITLE Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 591493
Center clone name: RP11_482B16

Summary Statistics
Consensus quality: 175156 bases at least Q40
Consensus quality: 175239 bases at least Q30
Consensus quality: 175390 bases at least Q20
Estimated insert size: 180000; agarose-fp estimation
Estimated insert size: 175585; sum-of-contigs estimation
Quality coverage: 16.07 in Q20 bases; agarose-fp estimation
Quality coverage: 16.47 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 47298: contig of 47298 bp in length
* 47299 47398: gap of unknown length
* 47399 106534: contig of 59136 bp in length
* 106535 106634: gap of unknown length
* 106635 175785: contig of 69151 bp in length.
Location/Qualifiers
1.175785
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-482B16"
/clone_1lb="RP11 human BAC library 11"
47299..47398
/estimated_length=unknown
106535..106634
/estimated_length=unknown
ORIGIN
Query Match 34.2%; Score 158.4; DB 12; Length 175785;
Best Local Similarity 73.9%; Pred. No. 3.6e-32;
Matches 229; Conservative 0; Mismatches 76; Indels 5; Gaps 2;
2 CCTGTAATTCAGACTGTGAGAGTCCAGAGTCAAGAGCTTGTGAGGACAGGTTCA 61
Db 108733 CCTGTATTCACACACTTTGAGAGCCAGGAGGTGATTTGAGCCAGAGTTTG 108674
Gy AGAGCAGCTTGACACAGGAGGAGCTGTCACTACCAAGATTAATTAATTAAGCAGG 121
|||||

Db 108673 AGACCAAGCTGGGACATGAGAGACTATCTTACAAAAAATCAAAAATTAAGTACG 108614
Gy 122 CTTAGTGGCTCATCCCTGTGTGTCCTAGCTAGAGAGGAGAGTAGA-----CTGCTT 177
Db 108613 CTTGTGTGACATGCTGTGTAGTCCAGCTACTAGAGAGGCTGAGTGGAGGATGCTTG 108554
Gy 178 GTCCAGAGGTCAAGACTGAGTACAGTACCCAGCCACTGCTGATTCAGCTTGCGC 237
Db 108553 AGCCCAAGAGGTGAGAGATGACAGTGAAGCCAGATTGACCA-CTGCACTCCAGCTGCGT 108495
Gy 238 AACAAAAGAGACCCCTCTCAAAAAAATAGTTAATTAATTAATTAATTAATTAATGTTA 297
Db 108494 GACAGACCAAGACCTGTCTCAAAAAAATTAATTAATTAATTAATTAATTAATGTTA 108435
Gy 298 AACCTTAAC 307
Db 108434 ATCCCTTAGC 108425
RESULT 13
AC136434
LOCUS
DEFINITION Homo sapiens chromosome 16 clone RP11-261B14, WORKING DRAFT
SEQUENCE, 4 unordered pieces.
ACCESSION AC136434
VERSION AC136434.1 GI:24462324
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 189911)
DOE Joint Genome Institute.
AUTHORS Sequencing of Human Chromosome 16
TITLE Unpublished
JOURNAL 2 (bases 1 to 189911)
REFERENCE DOE Joint Genome Institute.
AUTHORS Direct Submission
TITLE Submitted (01-NOV-2002) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 506699
Center clone name: RP11_261B14

Summary Statistics
Consensus quality: 187721 bases at least Q40
Consensus quality: 188330 bases at least Q30
Consensus quality: 188586 bases at least Q20
Estimated insert size: 160000; agarose-fp estimation
Estimated insert size: 189611; sum-of-contigs estimation
Quality coverage: 9.23 in Q20 bases; agarose-fp estimation
Quality coverage: 7.79 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1304: contig of 1304 bp in length
* 1305 1404: gap of unknown length
* 1405 3583: contig of 2179 bp in length
* 3584 3684: gap of unknown length
* 3684 51653: contig of 47970 bp in length
* 51654 51754: gap of unknown length
* 51754 189911: contig of 138158 bp in length.

COMMENT

-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1611829
Center clone name: RPCI-11_826F21

Summary Statistics

Consensus quality: 233805 bases at least Q40
Consensus quality: 234198 bases at least Q30
Consensus quality: 234471 bases at least Q20
Estimated insert size: 175000; agarose-fp estimation
Estimated insert size: 234930; sum-of-configs estimation
Quality coverage: 13.22 in Q20 bases; agarose-fp estimation
Quality coverage: 9.85 in Q20 bases; sum-of-configs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 20830: contig of 20830 bp in length
* 20831 20930: gap of unknown length
* 20931 42777: contig of 21847 bp in length
* 42778 42877: gap of unknown length
* 42878 78821: contig of 35944 bp in length
* 78822 78921: gap of unknown length
* 78922 131770: contig of 52849 bp in length
* 131771 131870: gap of unknown length
* 131871 235330: contig of 103460 bp in length.

FEATURES

source

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42778. .42877
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78822. .78921
/estimated_length=unknown
131771. .131870
/estimated_length=unknown

ORIGIN

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Best Local Similarity 73.9%; Pred. No. 3.4e-32;
Matches 229; Conservative 0; Mismatches 76; Indels 5; Gaps 2;

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DB 2105 CCTGTAAATTCACCTAGTGTGAGAGTCCGAGGTGAGAGCACTGCTGAGAGCCAGAGTTG 2046
QY 62 AGAGCAGCCTGAGACACAGAGGAGCCTGTCACTACAAAGAATTAATAATTAGCCAGG 121
DB 2045 AGACCAAGCCTGGGACACATAGAGAGCTCATCTACAAAATAATTAATTAAGCTAGG 1986
QY 122 CTTAGTGGCTATCCCTGTGTGCTCCAGCTACTAGGAGGAGCAAGTAGA----CTGCTT 177
DB 1985 CTTAGTGGCTATCCCTGTGTGCTCCAGCTACTAGGAGGAGCTGAGTGGGAGATGGCTTG 1926
QY 178 GTGCCAGGAGGTGAAGCTGAGCTGAGAGCCAGCACTGCACTTCAGCTGAGG 237
DB 1925 AGCCCAAGAGGTGAGAGTGAAGTGAAGCCAGAGTGCACA-CTGCACTTCAGCTGAGGT 1867
QY 238 AACAAAAAGAGCCCTGTCTCAAAAAATAAGTTAAATAATAATAATAATAATAAGTTTA 297

DB 1866 GACAGAGCAAGACCTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAGCAG 1807
QY 298 AACCTTAAC 307
DB 1806 ATCCCTAGAC 1797

Search completed: June 5, 2006, 22:27:29
Job time : 3138.62 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:15:11 ; Search time 402.823 Seconds
(without alignments)
8013.826 Million cell updates/sec

Title: US-09-869-098a-1_COPY_255_717

Perfect score: 463
Sequence: 1 acctgcatccagctactgt.....atcttcctctgttgacag 463

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: N_Geneseq_8:*
2: geneseqn1980s:*
3: geneseqn1990s:*
4: geneseqn2000s:*
5: geneseqn2001as:*
6: geneseqn2001bs:*
7: geneseqn2002as:*
8: geneseqn2002bs:*
9: geneseqn2003as:*
10: geneseqn2003bs:*
11: geneseqn2003cs:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	463	100.0	3505	3	AAA62932
2	152	32.8	135005	12	AD019501
3	150.4	32.5	23579	10	AD687112
4	149.4	32.3	186510	10	AD624797
5	148.8	32.1	151909	14	ABE96535
6	147.4	31.8	81099	11	ACN45018
7	147.2	31.8	110000	14	ABE61124_0
8	147	31.7	110000	10	AD670447_0
9	147	31.7	110000	10	AB279565_0
10	146.8	31.7	7739	4	AA136824
11	146.8	31.7	7739	8	ABX59812
12	146.8	31.7	7739	12	ADJ30562
13	146.8	31.7	226475	9	AA582279
14	146.4	31.6	41150	10	AD113819
15	146.4	31.6	41150	14	AD118343
16	146.4	31.6	44348	12	ADN48556
17	145.4	31.4	31749	4	AAK72959
18	145.4	31.4	78925	3	AA089888

19	145.4	31.4	143947	15	AEF38790	AEF38790 Human fib
20	145.4	31.4	143947	15	AEF38751	AEF38751 Human fib
21	145.4	31.4	143947	15	AEF35247	AEF35247 Human fib
22	145.4	31.4	143947	15	AEF64068	AEF64068 Human fib
23	145.4	31.4	143947	15	AEF63985	AEF63985 Human fib
24	144.8	31.3	53122	11	ACN43998_6	Continuation (7 of
25	144.8	31.3	110000	11	ACN43998_5	Continuation (6 of
26	144.6	31.2	2096	8	ACCT2436	AccT2436 Human sec
27	144.6	31.2	93500	13	ADT77142	Adt77142 Type II d
28	144.4	31.2	32169	5	ABAI4358	Abai4358 Human ner
29	144	31.1	109906	6	ABK94411	ABK94411 DNA encod
30	144	31.1	109906	12	ADL08112	Adl08112 Human gen
31	144	31.1	158417	13	ADS36461	Ads36461 Human aut
32	143.8	31.1	11006	14	AEA61101	Aea61101 Human GUC
33	143.6	31.0	58822	9	ADA02540	Ada02540 Human TCO
34	143.6	31.0	58822	10	AD872278	Adb72278 Human TCO
35	143.6	31.0	58822	10	AD855788	Ades5788 Human TCO
36	143.6	31.0	110000	12	ADN06353_0	Adn06353 Human FLA
37	143.6	31.0	110000	13	ADS94372_0	Ads94372 Human 5-1
38	143.6	31.0	145616	14	AED17971	Aed17971 Fibrotic
39	143.6	31.0	174472	14	ADZ13139	Adz13139 Human can
40	143.6	31.0	174703	11	ACN44738	Acn44738 Human gen
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44	143.4	31.0	22428	4	AA541759	AA541759 Genomic s
45	143.4	31.0	22428	8	AB274201	Ab274201 Secreted

ALIGNMENTS

RESULT 1	AAA62932 standard; DNA; 3505 BP.
ID	AAA62932
AC	AAA62932;
DT	02-NOV-2000 (first entry)
DE	DNA containing human uncoupling protein-2 (UCP-2) promoter region.
KW	Promoter; human; uncoupling protein-2; UCP-2; obesity; diabetes;
KW	hypotension; hyperlipidaemia; anti-pyretic; db.
OS	Homo sapiens.
XX	WO200039315-A1.
XX	06-JUL-2000.
XX	22-DEC-1999; 99WO-JP007198.
XX	24-DEC-1998; 98JP-00366719.
XX	(TAKE) TAKEDA CHEM IND LTD.
PI	Toyoda Y, Kobayashi M, Igaki S;
DR	WPI; 2000-452407/39.
XX	DNA with promoter region containing regulator sequence of uncoupling protein-2 (UCP-2), applicable in screening anti-obesity, anti-diabetic, hypotensive, anti-hyperlipidemic and anti-pyretic drugs for use in therapy.
PT	Claim 4; Fig 1-6; 43pb; Japanese.
XX	This invention relates to DNA comprising a promoter region containing the regulatory sequences of human uncoupling protein-2 (UCP-2). Included in the invention are a recombinant vector containing the DNA sequence, cells transformed by the vector, and a method for screening for compounds or salts that can promote or inhibit the UCP-2 promoter activity using the


```
XX Suwa M, Asai K, Akiyama Y, Aburatani H;
XX WPI; 2003-335783/31.
DR P-PSDB; ADC87113.
XX
PT New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanosine triphosphate-binding protein coupled receptor.
XX
PS Claim 1; SEQ ID NO 1565; 28pp; English.
XX
CC The invention relates to a novel polynucleotide encoding a guanosine
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The
CC polynucleotide sequences shown in ADC85948-ADC87616 encode GPCR's of the
CC invention.
XX
SQ Sequence 23579 BP; 6524 A; 5062 C; 5419 G; 6574 T; 0 U; 0 Other;
XX
Query Match 32.5%; Score 150.4; DB 10; Length 23579;
Best Local Similarity 72.4%; Pred. No. 6.6e-29;
Matches 223; Conservative 0; Mismatches 81; Indels 4; Gaps 2;
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DB 14855 CCTATAAGCCCGACACTTTGGGAGCTGAGGTGGCTCATCATCTTGAGGCCAGAGATTGG 14914
QY 62 AGAGCAGCCTGGAACAACAAGGAGCCTGTCTACTAACAAGATTAATTATGACAGG 121
DB 14915 AGACACGACATGCGCAACATGGTGAAACCGTCTACTATAAATAAATAATTAAGCCAGG 14974
QY 122 CTTAGTGGCTCATCCCTGTGGTCCACGCTACTAGAGAGGC---AGAACTAGGACTGCTTG 178
DB 14975 CTTGTGTGTGCATCCCTATATATCCAGCTACTTGGAGGCTGAGAGAAATCGGCTTG 15034
QY 179 TCCAGAGAGGTCAAGACTGCACTGAGAGCTGAGACCCAGCCACTGCTCAGCTGGGCA 238
DB 15035 AACCGGAGGCGGAGGTGGCAGTGAATGTGCCA--TTGCACCTCCGGCTGGGCA 15093
QY 239 ACAAAGAAGAGACCTGTCTCAAAAATAAGTTAATAATAATAATAATAATAGTTAA 298
DB 15094 ACGAGCAAGACTGTCTCTAAAAATAATAATAATAATAATAATAATAATAAT 15153
QY 299 ACCCTAAA 306
DB 15154 AAAATAAA 15161
XX
RESULT 4
ADE24797/c
ID ADE24797 standard; DNA; 186510 BP.
XX
AC ADE24797;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human endothelin-1, EDN1, gene.
XX
XX de; gene; human; vascular disease; endothelin-1; EDN1;
XX coronary artery disease; myocardial infarction.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT replace(157790,C)
XX FT /*tag= a
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XX FT replace(159908,T)
XX FT /*tag= b
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FT /standard_name= "Single nucleotide polymorphism"
XX US2003143544-A1.
XX
XX 31-JUL-2003.
XX
XX 09-JAN-2002; 2002US-00043715.
XX
XX 09-JAN-2002; 2002US-00043715.
XX
XX 09-JAN-2002; 2002US-00043715.
XX
XX (VITL-) VITVITY INC.
XX
XX McCarthy J;
XX
XX WPI; 2003-874790/81.
XX
XX P-PSDB; ADE24798, ADE24801.
XX
XX Identifying a subject as a candidate for a particular therapy to treat a
XX vascular disease or disorder, particularly coronary artery disease or
XX myocardial infarction, comprises detecting polymorphisms of the
XX endothelin-1 gene.
XX
XX Claim 58; SEQ ID NO 1; 177pp; English.
XX
XX The invention relates to a method of identifying a subject as a candidate
XX for a particular therapy to treat a vascular disease or disorder
XX comprising determining the presence of nucleotides at polymorphic regions
XX of an endothelin-1 (EDN1) gene. The invention is used to determine risk
XX of developing a vascular disease or disorder, particularly coronary
XX artery disease or myocardial infarction. The present sequence represents
XX the human endothelin-1 gene.
XX
SQ Sequence 186510 BP; 56192 A; 36427 C; 37117 G; 56774 T; 0 U; 0 Other;
XX
Query Match 32.3%; Score 149.4; DB 10; Length 186510;
Best Local Similarity 74.1%; Pred. No. 2.5e-28;
Matches 217; Conservative 0; Mismatches 71; Indels 5; Gaps 2;
QY 1 ACCGTGAATTCGACTGTGAGAGTCCGAGGTGAGAGGACTGCTTGAGGCCAGAGTTC 60
DB 175801 ACCGTGAATTCGAGCACTTTGGAGATGAGGCAAGAAATTAATTGAGGACAGATT 175742
QY 61 AAGAGCAGCCTGGAACAACAAGGAGACCTGTCTACTAACAAGATTAATAATTAGCCAG 120
DB 175741 GAGACCGCCTGGGTAAACAAGTAGAGCGCATCTCTCAAAAAATAATAATTAAGCTG 175682
QY 121 GCTTAGTGTCTCATCCCTGTGTGCTCCAGCTACTAGGAGGAGAGTAGA---CTGCT 176
DB 175681 GCATGTGTGTGTGCACTGTAGTCCAGCTACTCAGAGGCTGAGGTGGAGATCGCTT 175622
QY 177 TGTCCGAGAGGTCAACAAGCTGCACTGAGCTGAGACCCAGCACTGATTCAGACTGGG 236
DB 175621 GAGCCAAAGAGGTGAGACCTGTGTGTGCTGTCTATGCA-CTGCACTCAGCACTGGG 175563
QY 237 CAACAAAAAAGAGACCTGTCTCAAAAATAAGTTAATAATAATAATAATAATAA 289
DB 175562 CAACAGAGAGACCTGTCTCAAAAATAAGTTAATAATAATAATAATAATAA 175510
XX
RESULT 5
AEB96535/c
ID AEB96535 standard; DNA; 151909 BP.
XX
XX AEB96535;
XX
XX 06-OCT-2005 (first entry)
XX
XX Human CABIN1 gene, SEQ ID 19.
XX
XX
XX hepatitis C virus infection; antiinflammatory; hepatotropic; virucide;
XX liver cirrhosis; fibrosis; hepatoma; SNP detection; CABIN1; ds.
XX
XX Homo sapiens.
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32.1%; Score 148.8; DB 14; Length 151909;					
72.8%; Pred. No. 3.3e-28;					

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Qy	62	AGAGCAGGCTTGAGCAACACAGGAGAGC-CTGTCACTACAAGAATATAATTAATTAGCCAG	120
Db	60437	AAACCAAGCTTGGGCAACAAAGTAGACTCTGTCTTACAAAAATTTAAATTAACCCAG	60378
Qy	121	GCTTAGTGGCTCATCCCTGTGGTCCACAGTACTAGAGGAGCAGAAGTAGGACTGCTTGT-	179
Db	60377	GCAATGATGGTSCAACCTGTAGTCCAGCTTACGTGGGAGGCTTAAGGAGGAAACACTGCTTC	60318
Qy	180	---CCAGAGAGTCAAGATGTGACTGAGTGAAGCCAGCCACTTGCAITTCAGCCTGGG	236
Db	60317	GAGCCAGGAGAGTCCAGGCTGCAGTGAGCTGTGATCGTACCACTGCACCTTTAGCAATGGG	60258
Qy	237	CAACAAAAAGAGACCCCTGTCTCAAAAAATAAGTTAAATTAATTAATTAATAATAGTTT	296
Db	60257	CAACAGAGTGGAGACCTGTCTCAAAAAATAATTAATTAATTAATTAATAAGAGAGATTAATTC	60198
Qy	297	AA 298	
Db	60197	AA 60196	

ACN45018/C
ID ACN45018 standard; DNA; 81099 BP.
XX
XX ACN45018;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human genomic sequence hCG17395.
XX
XX
XX Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX
XX Homo sapiens.
XX
XX WO2003073826-A2.
XX
XX 12-SEP-2003.
XX
XX 28-FEB-2003; 2003WO-US006235.
XX
XX 01-MAR-2002; 2002US-00087192.
XX
XX (SAGR-) SAGRES DISCOVERY.
XX
XX Morris DW;
XX
XX WPI; 2003-328604/31.
XX
XX
XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT comprises a nucleotide sequence.
PS
PS Claim 1; SEQ ID NO 1756; 0pp; English.
XX
XX The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a blocking;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (Ca) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published
XX
XX Sequence 81099 BP; 20015 A; 18716 C; 19786 G; 22439 T; 0 U; 143 Other;

Query Match 31.8%; Score 147.4; DB 11; Length 81099;
Best Local Similarity 72.9%; Pred. No. 6,2e-28;
Matches 218; Conservative 0; Mismatches 76; Indels 5; Gaps 2;

QY 2 CCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAAGSCCAGAGTTCA 61
DB 18811 CCTGAATATCCAGACACTTTGGGAGGCCMAAGCGAGAGAGACTGTGTCGTCAGCCAGAGTTCC 1875
QY 62 AGAGCAGCGTGGACAACACAGGAGGAGCCTGTCACTCAAAAGAAATTAATTAATTAAGCCAG 121
DB 18751 AGACACAGCTTGGGCAACATGAAAGACCTCATCTCTACAAAAATTAATAATTAATTAAGCCAG 18691
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DB 18691 CGTGTGTCTCACCCCTGTGATGCCACACTACTAGGAGGCGTGAAGTGGGAGACTCTCTTG 18631
QY 180 --CCAGAGGTCGAAGCTGAGAGTGAAGTGAAGCCAGCACTGCACTTCACAGCTGGG 237
DB 18611 AGCTTGGAGTTCAAGGCTACAGTAGGCCCTGTATCGAGCCA -CTGCACTCCAGTCTGGGT 18571
QY 238 AACAAAAAGAGACCTGTCTCAAAAAATTAAGTTAATTAATTAATTAATTAATTAAGTTT 296
DB 18572 GACACAGAGGAGACCTGTCTCAAAAAACAAACAAACAAAAATCAATTAAGAAAGTGTTTT 18514

MP	Sequence split into 4 fragments	LOCUS	AA61124	Accession	AA61124
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MP	Fragment Name	Begin	End		
WP	AA61124_0	1	11000		
WP	AA61124_1	100001	210000		
WP	AA61124_2	200001	310000		
WP	AA61124_3	300001	383432		
ID	AA61124 standard; DNA; 383432 BP.				
XX	AA61124;				
AC					
DT	25-AUG-2005 (first entry)				
DE	Human SLC4A4 gene genomic sequence SEQ ID NO:34.				
XX					
KM	DNA methylation; biomarker; cancer; gene; ds; SLC4A4.				
XX					
OS	Homo sapiens.				
PN	US2005130172-A1.				
XX					
PD	16-JUN-2005.				
XX					
PF	27-JAN-2004; 2004US-00765790.				
XX					
PR	16-DEC-2003; 2003US-00737082.				
XX					
PA	(FARB) BAYER CORP.				
XX					
PI	Beard C, Burgess C, Gannon A, Harvey J, Lechner JF, Li Z;				
XX					
DR	WPI: 2005-456891/46.				
XX					
DR	GENBANK; AF011390, NM_003759.				
XX					
PT	Identifying nucleic acid sequences as biomarker for disease, by				
PT	identifying nucleic acid sequences comprising methylated CpG site and				
PT	down-regulated in diseased cells and comprising its expression level with				
PT	demethylated nucleic acid.				
XX					
XX					
XX	Claim 11; SEQ ID NO 34; 27pp; English.				
XX					
XX	The invention relates to a method (M1) for identifying one or more				
XX	nucleic acid sequences useful as a biomarker for a disease to be				
XX	detected. (M1) involves identifying nucleic acid sequences comprising				
XX	methylated CpG site in promoter-first exon region and that are down-				
XX	regulated in diseased cells, comparing expression level of nucleic acid				
XX	sequences with that of demethylated nucleic acid sequences and				
XX	identifying nucleic acid sequences exhibiting increase in expression				
XX	after demethylation. Also described: (1) detecting (M2) the presence or				
XX	stage of a disease in a subject, which involves determining the degree of				
XX	methylation of one or more CpG sites on nucleic acid sequences in a				
XX	biological sample obtained from the subject, and determining the presence				
XX	of, predisposition to, or stage of the disease in the subject based on				
XX	the degree of methylation; (2) monitoring the onset, progression, or				
XX	regression of a disease in a subject; (3) determining the efficacy of a				
XX	test compound for inhibiting a disease in a subject; and (4) a kit (I)				
XX	useful for diagnosis, prognosis, staging, monitoring, and therapeutic				
XX	treatment of a disease. (M1) is useful for identifying one or more				
XX	nucleic acid sequences useful as a biomarker for a disease to be				
XX	detected, where the nucleic acid sequences are useful for detecting, the				
XX	presence or stage of a disease such as cancer e.g. colorectal cancer in a				
XX	subject. The present sequence represents a specifically claimed human				
XX	genomic sequence for use in the method of the invention. Note - The				
XX	sequence data for this patent is not represented in the printed web				
XX	specification but was obtained in electronic format from the USPTO web				
XX	site.				
XX					
XX	Sequence 383432 BP; 113010 A; 69169 C; 74959 G; 126294 T; 0 U; 0 Other;				
XX					
XX	Query Match	31.8%;	Score 147.2;	DB 14;	Length 110000;
XX	Best Local Similarity	74.0%;	Pred No. 7; 8e-28;		

	Matches	213;	Conservative	0;	Mismatches	73;	Indels	2;	Gaps	2;
QY	2	CCCTGTAATTC	CACTACTG	GAGAGT	CCGAGAGT	CAGAGAG	CTGCTT	TAGGCC	CAGAGT	CA 61
Db	90502	CTGTGATCTCC	ACACACTTT	TGAGAGT	GTGAGAGT	TAGTGTGAT	CCCTT	TAGGCC	CAGAGT	CTTG 90566
QY	62	AGAGCAGCCT	TGACAA	CA	CAGGAGAC	-TGT	CATCTAC	CAAGAT	TAAATTAAT	TAGCCAG 120
Db	90562	AGACACAGCCT	TGGCAAT	TATGG	CAAAACCT	TGTCTCT	TACAAAAA	GACAA	GAATTAAT	TAACCAG 90621
QY	121	GCTTAGTGTCT	ATCCCTGT	GTGTGCC	AGCTACT	ATAGGAG	GAGCA	AAATTA	AGACCT	GTGAC 180
Db	90622	GTTGTGTGTG	CAACACT	CTGTGTGCC	AGCTACT	TGTGAG	GCTTAG	TGGAG	CTTAG	TGGAC 90681
QY	181	CCAGSAGGT	CAAACT	GCACTGA	GTAGAG	CCAGC	CACTGT	CCAGC	CTGTGG	CAAC 240
Db	90682	CCAGSAGGT	CGAATCT	GTGTAGT	GTAGCC	MAAGT	TGTGCA	-CTG	CATCTC	CAAGCCTGTGGTAA 90740
QY	241	AAAAAGAG	ACCCTGTCT	CAAAAAA	TATAGT	TAAATTAAT	TAAATTAAT	TAA		288
Db	90741	AGAATGAG	ACCCTGTCT	CAAA	CAAAAA	CAAAAA	CAAAAA	CAAA	CAAA	CA 90788

XX	ADSG70447 0/c	LOCUS	ADSG70447	Accession	Adg70447
ADSG70447 0/c	Sequence split into 5 fragments				
WP	Fragment Name	Begin	End		
WP	ADSG70447_0	1	110000		
WP	ADSG70447_1	100001	210000		
WP	ADSG70447_2	200001	310000		
WP	ADSG70447_3	300001	410000		
WP	ADSG70447_4	400001	410846		
ID	ADSG70447 standard; DNA;				410846 BP.
XX	ADSG70447;				
AC					
XX	11-MAR-2004 (first entry)				
DT					
XX	Human ANGE-CLD8-CLD7 hybrid gene.				
DE					
XX	ANGE, CLD8, CLD7, ANGE-CLD8; ANGE-CLD7; CLD7-CLD8;				
KW	ANGE-CLD8-CLD7; anti-allergic; antiasthmatic; dermatological;				
KW	antipyretic; antiinflammatory; gene therapy; IGE-mediated disease;				
KW	ANGE 1; single nucleotide polymorphism; ds.				
XX					
OS	Chimeric.				
OS	Homo sapiens.				
XX					
PH	Key	Location/Qualifiers			
FT	variation	replace(186655,g)			
FT		/*tag= a			
FT	variation	/standard_name= "Single nucleotide polymorphism"			
FT		replace(338770,g)			
FT		/*tag= b			
FT	variation	/standard_name= "Single nucleotide polymorphism"			
FT		replace(350186,g)			
FT		/*tag= c			
FT		/standard_name= "Single nucleotide polymorphism"			
XX					
PN	MO2003000727-A2.				
XX					
PD	03-JAN-2003.				
XX					
PF	21-JUN-2002; 2002MO-GB002859.				
XX					
PR	21-JUN-2001; 2001GB-00015211.				
PR	21-JUN-2001; 2001GB-00015212.				
XX	21-JUN-2001; 2001GB-00015213.				
XX					
PA	(ISIS-) ISIS INNOVATIONS LTD.				
XX					
PI	Zhang Y, Mofatt M, Cookson W, Tinsley J;				
XX					

DR WP1; 2003-201405/19.

XX New nucleic acid sequence comprising an ANGE, CLD8 or CLD7 mRNA, or
PT their hybrid, useful for screening agents for treating Ige-mediated
PT diseases, e.g. asthma, atopy, hay fever, eczema, atopical dermatitis, or
XX allergic rhinitis.

PS Claim 12; Fig 5; 423pp; English.

XX The invention relates to a novel isolated or recombinant nucleic acid
CC sequence comprising an ANGE, CLD8 or CLD7 mRNA, or ANGE-CLD8, ANGE-
CC CLD7, CLD7-CLD8, or ANGE-CLD8-CLD7 hybrid mRNA sequence, its
CC complement, homologue or fragment. The novel nucleic acid sequences have
CC the following activities: antiallergic, antiasthmatic, dermatological,
CC antipruritic, and antiinflammatory. The nucleic acids of the invention may
CC be used in gene therapy to treat disorders. The nucleic acid sequences
CC are useful for screening agents that inhibit or enhance activity of an
CC ANGE, CLD8 or CLD7 gene. The agent or antibody is useful for treating
CC Ige-mediated diseases such as asthma, atopy, hay fever, eczema, atopical
CC dermatitis, allergic rhinitis or non-atopic asthma. The antibody is
CC useful in an assay detecting or measuring the polypeptide in the sample.
CC The host cell is useful for producing, regulating and analyzing the
CC polypeptide. The splice variant of ANGE, CLD8, or CLD7 is useful for
CC diagnosing an Ige-mediated disease, atopy, a form of atopic disease or
CC non-atopic asthma, or predicting the severity, or predisposition to a
CC disease. This polynucleotide sequence represents the human ANGE-CLD8-
CC CLD7 hybrid gene of the invention.

XX Sequence 410846 BP; 125178 A; 83171 C; 81704 G; 120793 T; 0 U; 0 Other;
SQ

Query Match 31.7%; Score 147; DB 10; Length 110000;
Best Local Similarity 68.8%; Pred. No. 8.8e-28;
Matches 232; Conservative 0; Mismatches 100; Indels 5; Gaps 2;

OY 2 CCTGTAATTCACAGACTGTGAGAGTCCGAGGTCAAGAGCATCTTGAGGCCAGGAATTCA 61
Db 98790 CCTGTAATTCACAGACTTTGGAGAGCGAGGCGGCAGATCCTAGCTCAGGAATTGG 98731

OY 62 AGAGCACCTTGACAAACAAGAGAGA-CCTGTCACTAACAAGATTAATAATTAGCCAG 120
Db 98730 AGAGCACCTCGGACAAACATGGCCAAACCCTGTCTAATAATAATCAAAAATTAGCCAG 98671

OY 121 GCTTAGTGCTCATCTCCGTGTGCCAGTACTAGAGGAGCAGAAATAGAGA---CTGCT 176
Db 98670 GCGTGATGCGCGGCGCTGTAAATCCAGCTAATCGGGGGGCTGAGACAGAAATCATCTT 98611

OY 177 TGTTCCAGAGAGTCAAAGCTGCAGTAGTGCAGAACCCAGCACCTGCATTCAGCCTGGG 236
Db 98610 GAACCCAGAGGCGGAGTGTGCAGTAGGCCGAATGACGACATGGCACCTCCAGCCTAGG 98551

OY 237 CAACAAAAAGAGACCTGTCTCAAAAATAAAGTTAATAATAATAATAATAATAATAGTTT 296
Db 98550 CAACAGAGAGAGACTGTCTCTCAAAATAATAATAATAATAATAATAATAATAATAATA 98491

OY 297 AAACCTPAAACACATCTTTTTTCAAAAGAGACTTC 333
Db 98490 TAATAATTTGTTGAACCTTTAAAGAGGTGGGAATC 98454

RESULT 9
ABZ79565_0/c
WP Sequence split into 5 fragments LOCUS ABZ79565 Accession Abz79565
WP Fragment Name Begin End
WP ABZ79565_0 1 110000
WP ABZ79565_1 100001 210000
WP ABZ79565_2 200001 310000
WP ABZ79565_3 300001 410000
WP ABZ79565_4 400001 410846
ID ABZ79565 standard; DNA; 410846 BP.
XX
AC ABZ79565;
XX 01-JUL-2003 (first entry)

XX	CLD8 and NY-REN-34 encoding DNA.
DE	
XX	Cytostatic; gene therapy; B-cell chronic lymphocytic leukemia; BCL;
KW	CLD8; NY-REN-34; gene; ds.
XX	
OS	Unidentified.
XX	
FH	Key
FT	Location/Qualifiers
FT	CDS
FT	294727..309803
FT	/+tag= a
FT	/product= "CLD8"
FT	313649..346509
FT	/+tag= b
FT	/product= "NY-REN-34"
PN	WO2003000296-A2.
PD	
XX	03-JAN-2003.
XX	
PF	21-JUN-2002; 2002MO-GB002857.
PR	
PR	21-JUN-2001; 2001GB-00015211.
PA	(ISIS-) ISIS INNOVATIONS LTD.
PI	Zhang Y, Mofafat M, Cookson W;
DR	WPI; 2003-221370/21.
PT	Treating B-cell chronic lymphocytic leukemia in an individual by
PT	modulating the expression of the CLD8 and/or the NY-REN-34 gene.
PS	Disclosure; Fig 1; 154bp; English.
XX	
CC	The invention relates to a method for treating B-cell chronic lymphocytic
CC	leukemia (BCLL), comprising modulating the expression of the CLD8
CC	and/or the NY-REN-34 gene. The polynucleotide sequence or gene product of
CC	the CLD8 and/or NY-REN-34 gene or agent is useful for the manufacture of
CC	a diagnosis and treatment of BCLL. The current sequence represents CLD8
CC	and NY-REN-34 encoding DNA
XX	
SQ	Sequence 410846 BP; 125177 A; 83172 C; 81704 G; 120793 T; 0 U; 0 Other;
	Query Match 31.7%; Score 147; DB 10; Length 110000;
	Best Local Similarity 68.8%; Pred. No. 8.8e-28;
	Matches 232; Conservative 0; Mismatches 100; Indels 5; Gaps 2;
OY	2 CCTGTAAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGTCTTAGGCCCGAGACTTCA 61
DB	98790 CTTGTATATCCACGACTTTTGAGAGCGAGGCGGGCGGATCAGCTGAGCTCAGGAATTGG 98731
OY	62 AGAGCAGCCTTGAGACAACACAGGAGA-CCTGTCACTAACAAATAAATAATTAGCCAG 120
DB	98730 AGACACACCAGCAACATGCGCAAAACCCGCTCTTAATAAATAAATAATTAGCCAG 98677
OY	121 GCTTAGGAGCTCATCCCTGTGTCTCCAGACTACTAGGAGGAGCAAGATAGGA----CTGCT 176
DB	98670 GCGTGTGTGCGCGCGCTGTAAATCCAGCTACTCTGGGGGGGCTGAGACAGAAATCACTT 98611
OY	177 TGTCCTCAGAGGTCAAGACTGCAGTAGAGTGAAGCCAGCCACTGTCATTCCAGCCTGGG 236
DB	98610 GAACCCGAGAGCGGAGGTGTGACGTAGCGAGATGAGCCACTGCGACTCCAGCCTAGG 98551
OY	237 CAACAAAAAAGAACCTGTCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 296
DB	98550 CAACAGAGAAAGACTGTCTCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 98491
OY	297 AAACCCTAACACATCTCTTTTTCAAAGGAGACTTC 333
DB	98490 TAATAATTTGTGAACCTCTTTTAAAAAGGTGGCAATC 98454

RESULT 10
AAL36824/c
ID AAL36824 standard; DNA; 7739 BP.
XX
XX AAL36824;
AC
XX 08-JAN-2002 (first entry)
DT
XX
XX Human musculoskeletal system related polynucleotide SEQ ID NO 3189.
DE
XX
XX Cytostatic; immunosuppressive; nocrotropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; anticancer;
KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; ds.
XX musculoskeletal system; ds.
XX
XX Homo sapiens.
XX
XX WO200155367-A1.
XX
XX 02-AUG-2001.
PD
XX
XX 17-JUN-2001; 2001WO-US001338.
PF
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
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PR 30-JUN-2000; 2000US-0215135P.
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PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
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PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
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PR 18-AUG-2000; 2000US-0226279P.
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PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
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PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
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PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.

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PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
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PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234977P.
PR 25-SEP-2000; 2000US-0234988P.
PR 26-SEP-2000; 2000US-0234984P.
PR 27-SEP-2000; 2000US-0235634P.
PR 27-SEP-2000; 2000US-0235636P.
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PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
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PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
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PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
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PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
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PR 17-NOV-2000; 2000US-0249245P.
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PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.

PR 02-OCT-2000; 2000US-0237037P.
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PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
XX
XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
XX Rosen CA, Ruben SM, Barash SC;
PI
PI WPI; 2003-128199/12.
XX
XX
PT Isolated nucleic acid molecules encoding musculoskeletal system
PT associated polypeptides, useful for detecting disorders, e.g. cancer.
XX
XX
PS Disclosure; SEQ ID NO 3189; 321pp; English.
CC The invention describes an isolated nucleic acid molecule comprising a
CC sequence encoding musculoskeletal system associated polypeptides useful
CC for detecting disorders, e.g., cancer or cancer metastases, in animals or
CC humans. The nucleic acid stimulates re-vascularisation of ischaemic
CC tissues associated with conditions such as thrombosis, arteriosclerosis,
CC and other cardiovascular conditions; treats wounds due to injuries,
CC burns, post-operative tissue repair; and ulcers; stimulates angiogenesis
CC and limb regeneration; stimulates neuronal growth; can treat and prevent
CC neuronal damage occurring in certain disorders or neurodegenerative
CC conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-
CC related complex; stimulates chondrocyte growth, thus they can be used to
CC enhance bone and periodontal regeneration and aid in tissue transports or
CC bone grafts; prevents skin aging due to sunburn by stimulating
CC keratinocyte growth; prevents hair loss, since RGF family members
CC activate hair-forming cells and promotes melanocyte growth; stimulates
CC growth and differentiation of hematopoietic cells and bone marrow cells
CC when used in combination with other cytokines; maintains organs before
CC transplantation or for supporting cell culture of primary tissues;
CC induces tissue of mesodermal origin to differentiate in early embryos;
CC increases or decreases the differentiation or proliferation of embryonic
CC stem cells, besides, hematopoietic lineage; modulates mammalian
CC characteristics, such as, body height, weight, hair colour, eye colour,
CC skin, percentage of adipose tissue, pigmentation, size, and shape (e.g.,
CC cosmetic surgery); modulates mammalian metabolism; changes mammal's metal
CC state or physical state by influencing biohythm, circadian rhythms,
CC depression, tendency for violence, tolerance for pain, reproductive
CC capabilities, hormonal or endocrine levels, appetite, libido, memory, or
CC stress; increases or decreases storage capabilities, fat content, lipid,
CC protein, carbohydrate, vitamins, minerals, cofactors or other nutritional
CC components. This sequence encodes a novel human musculoskeletal system
CC antigen. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID=20020147140
XX
XX Sequence 7739 BP; 1963 A; 1731 C; 1890 G; 2155 T; 0 U; 0 Other;
SQ
Query Match 31.7%; Score 146.8; DB 8; Length 7739;
Best Local Similarity 77.5%; Pred. No. 4e-28;
Matches 217; Conservative 0; Mismatches 57; Indels 6; Gaps 3;
OY 2 CCTGTAATTCGAGTGTGAGTCCGAGTCCAGAGTCTTGAGCCAGAGTTCA 61
DB 5631 CCTATATATCCCAACACTTTGGAGGCCGAGGTGGAGAGATGCTTGAGTCCAGTAGTTCA 5572
OY 62 AGAGCAGCTTGAGACACAGAGGAGA-CCTGTCACTACAAAGATTAATTAGCCAG 120

DB 5571 AGAGCAGCTTGAGACACATAGGAGAGCCTTGACTTACAAATTAATTTAAATTCCTGG 5512
OY 121 GCTTAGTGCTCATCCCTGTGTGCTCCAGCTACTAGAGGAGCAAGATAGGA----CTGCT 176
DB 5511 GTGTATGTCACATACCTGTGTGCTCCAGCTAGTATGTTGGAGGCGAGCAGAGATGCTT 5452
OY 177 TGTCCAGAGGTCAAGACTGCAGTAGTGAAGCCAGCCACTTCATTCAGCTGGG 236
DB 5451 GAGCCAGAGGTCAAGGCTGCAATGAGCTGCATCTTGCCA-CTGCACCTCCAGCCTGGG 5393
OY 237 CAACAAAAAGAACCTGTCTCAAAAAATTAATTAATA 276
DB 5392 CAACAGACTGAGACCTGTCTCAAAAAACAAAAA 5353
RESULT 12
ADJ30562/C
ID ADJ30562 standard; DNA; 7739 BP.
XX
XX AC ADJ30562;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3189.
XX
XX KM musculoskeletal system; cytosolic; osteopathic; cancer; osteoporosis;
XX gene therapy; vaccine; human; de.
XX
XX OS Homo sapiens.
XX
XX PN US2004009488-A1.
XX
XX PD 15-JAN-2004.
XX
XX PF 13-SEP-2002; 2002US-00242515.
XX
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764877.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX PA Rosen CA, Ruben SM, Barash SC;
XX PI WPI, 2004-090458/09.
XX XX
XX XX New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g., cancer of
PT musculoskeletal tissues or osteoporosis.
XX XX
XX PS Disclosure; SEQ ID NO 3189; 289pp; English.
XX XX
XX CC The invention relates to a novel isolated musculoskeletal system-
XX CC associated nucleic acid molecule. The nucleic acid of the invention
XX CC demonstrates cytostatic and osteopathic activities and may be useful for
XX CC preparing a medicament for preventing, treating or ameliorating a medical
XX CC condition such as cancer of the musculoskeletal tissues or osteoporosis,
XX CC possibly via gene therapy or vaccine production. The current sequence is
XX CC that of the human musculoskeletal system-associated genomic DNA of the
XX CC invention. The current sequence is not shown within the specification per
XX CC se but is available on the USPTO web-site
XX CC http://seqdata.uspto.gov/sequence.html?docID=20040009488.
XX XX
XX XX Sequence 7739 BP; 1963 A; 1731 C; 1890 G; 2155 T; 0 U; 0 Other;
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Db 5631 CCTATATATCCCAACACTTGTGGAGGCCGAGGTGGAGGATGCTGTGATCCAGTATTC 5572
QY 62 AGAGCAGCCTGAGCAACACAGGAGGA-CCGTCACTACAAAGATAAATTAATTCAGCAG 120
Db 5571 AGACCAAGCTGGGCAACATATGGAGAGACCTGACTCTTCAAAATTAATTTAAATTCGCTGG 5512
QY 121 GCTTAGTGCTATCCCTGTGTGTCACAGCTACTAGGAGGACAGAACTAGGA---CTGCT 176
Db 5511 GTGTAGTGACATACACTGTGTGTCCAGCTAGTTGGAGGCGCAGGACAGAGATCGCTT 5452
QY 177 TGTCCAGAGAGTCAAGACTGCAAGTGAAGTGAACACCAAGCACTGATTCAGCCCTGGG 236
Db 5451 GAGCCAGAGGTCAAGGCTGCAATGAGCTGCAATCTTGCCA-CTGCACTTCAGCCTGGG 5393

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:39:00 ; Search time 3206.07 Seconds
(without alignments)
8075.514 Million cell updates/sec

Title: US-09-869-098a-1_COPY_255_717

Perfect score: 463
Sequence: 1 accgtcaatccagctactgtc.....attctccctgttgcacag 463

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	150.8	32.6	836	13	CZ458737 MCF746k19
2	146.8	31.7	1033	3	BM556801 AGNCOURT
3	146.4	31.6	315	1	AI961957 w40904.x
4	146.4	31.6	592	4	EX486310 DKFZP586B
5	145.2	31.4	554	11	AQ784105 HS_350_A
6	143.8	31.1	675	11	AQ313572 RPI11-10
7	143.6	31.0	444	11	AQ088791 HS_3002_A
8	143.6	31.0	721	8	CR773238 DKFZP470D
9	143.4	31.0	417	11	AQ215619 HS_3217_B
10	143.4	31.0	454	9	DB322788 DB322788
11	143.4	31.0	551	4	EX487140 DKFZP586G
12	142.8	30.8	2821	6	BC029972 Homo sapi
13	142.6	30.7	916	14	AG014790 Homo sapi
14	142.6	30.7	916	8	CR980253 CR980253
15	141.8	30.6	644	3	BE349022 ht48a11.x
16	141.8	30.6	641	3	BM555373 AGNCOURT
17	141.8	30.6	809	12	BZ603262 WHAAR45TF
18	141.8	30.6	1792	6	CR602256 full-1eng
19	141.8	30.6	1941	6	CR616604 full-1eng

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C 22	141.2	30.5	558	11	AQ480483	RPCI-11-2
23	141	30.5	408	7	BE138484	xr75h02.x
24	141	30.5	749	14	AG014791	Homo sapi
25	141	30.5	1295	2	BG432839	602496047
26	140.8	30.4	374	4	BX954311	DKFZP781A
27	140.8	30.4	561	9	DB358919	DB358919
C 28	140.6	30.4	4833	6	CR936701	CR936701
C 29	140.6	30.4	400	11	AQ007744	CIT-HSP-2
30	140.2	30.3	589	9	DB382632	DB382632
C 31	140.2	30.3	647	7	BB883545	BB883545
C 32	140.2	30.3	750	14	AG015272	Homo sapi
C 33	140.2	30.3	2149	6	CR936757	CR936757
C 34	139.8	30.2	470	4	CD102612	AGNCOURT
C 35	139.8	30.2	606	13	CZ458897	MCF75111
C 36	139.8	30.2	705	14	AG013375	Homo sapi
C 37	139.8	30.2	723	14	DX360777	MGOQ_CH25
C 38	139.6	30.2	547	9	DA315473	DA315473
C 39	139.6	30.2	821	13	CZ449889	MCF730G23
C 40	139.4	30.1	721	9	DA571947	DA571947
C 41	139.2	30.1	500	1	AL712995	AL712995
C 42	139.2	30.1	530	7	AW949355	AW949355
C 43	139.2	30.1	556	3	BU664577	BU664577
44	139.2	30.1	564	7	BE300855	ba77h08.x
C 45	139.2	30.1	624	7	AW945152	EST361345

ALIGNMENTS

RESULT 1
CZ458737 836 bp DNA linear GSS 20-OCT-2005
LOCUS MCF746k19TF Human MCF7 breast cancer cell line library (MCF7_1)
DEFINITION Homo sapiens genomic clone MCF7_46k19, genomic survey sequence.
ACCESSION CZ458737
VERSION CZ458737.1 GI:77936089
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 836)
Volik,S.V., Raphael,B.J., Huang,G.-Q., Murnane,J., Brehner,J.H., Bajsarowicz,K., Parls,P., Tao,Q., Kowbel,D., Lapuk,A.V., Xuo,W.-L., Shagin,D.A., Shagina,I.A., Magrane,G., Gray,J.W., Jan,F.-C., de Jong,P., Pezner,P., and Collins,C.
Decoding the genomic architecture and high throughput detection of fusion transcripts in breast cancer cell lines: implications for a tumor genome project
Unpublished (2005)
Contact: Volik SV
Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7066
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
http://www.genomex.com
Class: BAC ends.
FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="MCF7_46k19"
/sex="female"
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/note="Vector: pECBAC1, site_1: HindIII, This library was

ORIGIN

constructed from MCF7 breast cancer cell line by Amplicon Express (<http://www.genomex.com>) using their standard procedure."

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Best Local Similarity 73.7%; Pred. No. 1.7e-18;
Matches 233; Conservative 0; Mismatches 77; Indels 6; Gaps 3;

QY 1 ACCTGTAATTCGAGTCTGTGAGAGTCCGAGTCAGAGGACCTGTGAGGCCAGGAGTTC 60
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QY 61 AAGAGACGCTGGAACAACAAGAGGAGA-CCTGTCACTACAAAGATAATTAATTAGCCA 119
DB 218 GAAACAGAGCTGTGCAACATAGGAGAGACCTGTCTCAGAGTAATTTAAATTTAGCTG 277
QY 120 GAGCTTAGTGCTATCCCTGTGTGCTCCAGCTTACAGGAGGACAGAGTAGA---CTGC 175
DB 278 GGCCTGATGTGCAACCTGTGTGCTCCAGCTACTTGGAGAGGCTGAAGCAGAGATCACT 337
QY 176 TTGTCCAGAGAGTCAAGTCAAGTGAAGTGAAGCCAGCCTGCAATTCAGAGCTGG 235
DB 338 TGAACCAAGAGGTGAGGCTGAGAGCCGAGATTGCCCA-CTACACTCCAGAGCTGG 396
QY 236 GCAACAAAAGAGACCTGTCTCAAAAATTAATTAATTAATTAATTAATTAATTAAT 295
DB 397 GTGACAGAGTGAACCTGTCTCAAAAATTAATTAATTAATTAATTAATTAATTAAT 456
QY 296 TAAACCTTAAACACAT 311
DB 457 CAACCTCTTAATTCAT 472

RESULT 2
BM556801/c 1033 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT 6540722 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737964
DEFINITION 5', mRNA sequence.

ACCESSION BM556801 GI:18798321
VERSION BM556801
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1033)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LLM12748 row: 0 column: 21
High quality sequence stop: 606.

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/clone_id="NIH_MGC_88"
/note="Organ: small intestine; Vector: pCMV-SPORT5;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;"

ORIGIN

oligo-dt primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."

Query Match 31.7%; Score 146.8; DB 3; Length 1033;
Best Local Similarity 77.5%; Pred. No. 9.1e-18;
Matches 217; Conservative 0; Mismatches 57; Indels 6; Gaps 3;

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DB 316 CCAATTAATCCCAACACTTTGGAGAGCCGAGTGGAGATGCTTAAGTCCAGTATTTCA 257
QY 62 AAGACGCTGGAACAACAAGAGGAGA-CCTGTCACTACAAAGATAATTAATTAGCCAG 120
DB 256 AAGACAGCTGGGCAACATAGGAGAGCCCTGACTTACAAATTAATTAATTTCCCTGG 197
QY 121 GCTTAGTGCTATCCCTGTGTGCTCCAGCTTACAGGAGGACAGAAATAGA---CTGC 176
DB 196 GTGTAGTGGCACTACCTGTGTGCTCCAGCTAGTTGGAGAGCCAGAGAGAGTGCCTT 137
QY 177 TTGTCCAGAGAGTCAAGTCAAGTGAAGTGAAGCCAGCCTGCAATTCAGAGCTGG 236
DB 136 GAGCCAGAGAGTCAAGCTGCAATAGCTGCAATTTGCCA-CTGCACCTCCAGAGCTGG 78
QY 237 CAACAAAAGAGACCTGTCTCAAAAATTAATTAATTAATTAATTAATTAATTAAT 276
DB 77 CAACAGACGAGACCTGTCTCAAAAATTAATTAATTAATTAATTAATTAATTAAT 38

RESULT 3
AI961957/c 315 bp mRNA linear EST 09-MAR-2000
LOCUS WC40604.X1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:2509974 3'
DEFINITION similar to contains Alu repetitive element;; mRNA sequence.

ACCESSION AI961957 GI:5754659
VERSION AI961957.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 315)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bdrp/image/image.html
Insert length: 1397 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 314.

FEATURES
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/issue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_id="NCI-CGAP_Panl"
/note="Organ: pancreas; Vector: pCMV-SPORT5; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN

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	Matches 212	Conservative 0	Mismatches 66	Indels 6	Gaps 2
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Db	284	CCTGTAATCCCATCATCTTTGGAGGCCAGGCGAAGAAGATTGCTTGAATCCAGAGATTG	225		
Qy	62	AGAGCAGCCTGGAACAACAAGGAGACC--TGTCATTACAAGAATTAATTAATTAACC	118		
Db	224	AGACTAGCCTGGGCAACATAGTAGAACCCTCATCTCTACAAAAAATGAACAAATTAAGCC	165		
Qy	119	AGGCTTAATGGCTATCCCTGTGTGCTCCAGTACTTAGGAGGACGAAAGT---AGAGCTGC	175		
Db	164	GGGCTCTGTGTGTGCATGTGCTTAGTCCAGGACTACGGGAAAGCTGAAGGTGGAGGATTGC	105		
Qy	176	TTGTGCCAGGAGGTCGAAGCTGACGTAGAGCCGAGCAGCTGAGTTCGAGCCCTGG	235		
Db	104	TGACCTCGAGGTGTAAAGCTGCACTGAGTCAATGCGCAACTGCACTCCAGCCTAA	45		
Qy	236	GCAACAAAAAAGAGCCCTGTCTCAAAAAAATTAAGTTAATAATAATA	279		
Db	44	GCGACAGCAAGAACCTGTCTCAAAAAAATTAAGTTAATAATAATA	1		

RESULT 4	LOCUS	DEFINITION
BX486310/c	592 bp	mRNA linear EST 04-SEP-2003
DKFZp666B08251_r1	686 (synonym: h1cc3)	Homo sapiens CDNA clone
DKFZp666B08251_5'		mRNA sequence.

ACCESSION	BX486310	GI:31949871
VERSION	BX486310.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
Amorós, W., Krieger, S., Regieri, T., Rittmüller, C., Schwager, B.,
Homínidae, Homo
1 (baes 1 to 582)
Euryota, Metazoa; Chordata; Crinacea; Vertebrates; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
1 (baes 1 to 582)

TITLE
JOURNAL
COMMENT

MIPS
 Ingolstaedter Landstr.1, D-85764 Neuburg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysts, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 Heidelberg/Germany (European Molecular Biology Laboratories,
 German Genome Project).
 No sl sequence available.
 This clone (DKFZp66B08251) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Neuburg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES	Location/Qualifiers
source	1. .592

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/dev_stage="adult"
/lab_host="DH10B"
/clone_id="666 (synonym: hicc3)"
/notes="Vector: pTIPlex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

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			Indels 2
			Gaps 2

QY	1	ACCTGTAATTCACAGACTGTAGAGATCCGAGATCGAGAGCATGCTTGAGGCCAGAGATTC	60
Db	287	ACCTGTAATTCACAGACTGTGAGAGCTGAGAGCAGTGGATTCATTGAGTCCAGAGATTC	228
QY	61	AAGAGCAGCTTGAGCAACACAGGGAGACTT-GTCACTACAAAGATAAATAATTAATGCA	119
Db	227	GAGACACAGCCCTGGGCAACATAGTACACCTCATCTTACAAAATAATCAAAATTAAGCA	168
QY	120	GGCTTAGTGGCTATCCCTGTGTGCCAGTACTAGGAGGACAGAAATGAGGACTGCTGT	179
Db	167	GCTGTGTGTGGGCACTGCTGTAGTTCTTAGCTACTACGGAGACTCAGTGTGATCACTTGAG	108
QY	180	CCCAGAGAGTCAAGACTGCACTGAGCTTGAGACCCAGCCACTTGCTTCAGCTGGGCA	239
Db	107	CCCGGAGAGAGAGAGTTACAGTGTGAGCTGAGATCTGACCA-CTGCACTCCAGCTGGGCA	49
QY	240	CAAAAGAGACCTGTCTCAAAAATAATAGTTAAATAATAATA	283
Db	48	CAGATGAGACCTGTCTCAAAAGAAAAAATAAAAAATCA	5

LOCUS	DEFINITION	554 bp	DNA	linear	GSS 03-AUG-1996
AQ784105	HS 3250 A2 H10 T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3250 Col=20 Row=O, genomic survey sequence.				

ACCESSION	AQ/84105	GI:5691729
VERSION	AQ784105.1	
KEYWORDS	GSS.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	

REFERENCE
1 (bases 1 to 554)
Mahaitas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
AUTHORS
Mammalia: Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
Eucaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

TITLE
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9733-9744 (1999)
Hood, L., Kellier, A., Shaker, R., Furlong, J. J., Young, J., Zhao, S., Adams, M. D. and

PUBLISHED
 10/4/97/64
 COMMENT
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 3250 row: 0 column: 20
 Seq primer: T7
 Class: BAC ends
 High quality sequence: stop: 554.

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FEATURES
    source
        Location/Qualifiers
            1..554
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                /clone="Plate=3250 Col=20 Row=0"
                /sex="male"
                /clone_lib="CIT Approved Human Genomic Sperm Library D"
                /note="Organ: Sperm; Vector: pBelobAC11; BAC Clones in
                    E-Coli DH10B"

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ORIGIN			
Query Match	31.4%	Score 145.2	DB 11
Best Local Similarity	74.3%	Pred. No. 2.1e-17	Length 554
Matches 211	Conservative	0	Mismatches 68
			Indels 5
			Gaps 2

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGGCCAGAGTTCA 61
DB 140 CCTATATATCTGACACTTTGGAGGCGCGAGTGGCGGATTAATTAGGTCAAGAGTTCA 199
QY 62 AAGAGCAGCTTGACAAACAGAGGAGACTGTCTACATAAAGATTAATAATTAGCCAG 121
DB 200 AAGACGAGCTGGGCAATATGATGTAACCTGTCTCTCTAATAAATACAAAAATCAGACAG 259
QY 122 CTATAGTGGTCAATCCCTGTGGTCCCACTACTAGGAGGAGCAAGTAGACTGCTGT-- 179
DB 260 TGTGTGTGACATGCTCTGTATCTCCAGCTACTCAGAGAGGCTGAGGAGGAATTTGTTG 319
QY 180 --CCGAGAGGTCAAGACTGCACTGAGCTGAGACCCAGCCACTGCAATTCAGCTGGGC 237
DB 320 AACCCAGAGATTGAGAGGCTGCAATGAGCTGAGATTGGCA-CTGCACTCCAGCTGGGT 378
QY 238 AACAAAAAGAGACCTGTCTCAAAAAATTAATTAATAATAA 281
DB 379 GATTAAGCGAGACCTGTCTCAAAAAATTAATAATAATAA 422

RESULT 6
AQ313572/c 675 bp DNA linear GSS 04-MAY-1999
LOCUS RPCI11-101F17.TV RPCI-11 Homo sapiens genomic clone RPCI-11-101F17,
DEFINITION genomic survey sequence.
ACCESSION AQ313572
VERSION AQ313572.1 GI:4045035
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 675)
Adams,M.D., Rounsley,S.D., Zhao,S., Baas,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
Other GSSs: RPCI11-101F17.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@edj.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/human/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.

FEATURES
source location/Qualifiers
1..675
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7538536"
/db_xref="taxon:9606"
/clone="RPCI-11-101F17"
/sex="Male"
/cell_type="lymphocytes"
/clone_id="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"

ORIGIN

Query Match 31.1%; Score 143.8; DB 11; Length 675;
Best Local Similarity 69.8%; Pred. No. 3.7e-17;
Matches 238; Conservative 0; Mismatches 97; Indels 6; Gaps 3;

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGGCCAGAGTTTC 60
DB 444 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGGCCAGAGTTTC 385
QY 61 AAGAGCAGCTTGACAAACAGAGGAGACTGTCTACATAAAGATTAATAATTAGCCCA 119
DB 384 AAGATAGAGCTGGGCAACATGATGTAACCTGTCTCTCTAATAAATTAATAATTAGCCA 325
QY 120 GCTTATAGTGGTCAATCCCTGTGGTCCCACTACTAGGAGGAGCAAGTAGA----CTGC 175
DB 324 GCGATGTGTGCAATGTGCTGTATATCCAGCTACTTGGAGGTGAGGAGCAAGAAATCACCC 265
QY 176 TGTGCCAGAGAGTCAAGACTGCACTGAGCTGAGACCCAGCCACTGCAATTCAGCTGG 235
DB 264 TGAATTCAGAGAGCGGAGGTTGCACTGAGACCAAGATCGTGCA-CTGCACTCCAGCTGG 206
QY 236 GCAACAAAAAGAGACCTGTCTCAAAAAATTAATTAATAATAATAATAATAGTT 295
DB 205 GTGACAAAGTGAATTTCTGTCTCAAAAAATTAATTAATAATAATAATAAACCACTGTT 146
QY 296 TAAACCTTAACACATCTTTTTCAGAGAGACTTCTTA 336
DB 145 CTATACCTTTCTTCACTTACTTGAGATGATCCATATTA 105

RESULT 7
AQ088791/c 444 bp DNA linear GSS 26-AUG-1998
LOCUS HS_3002_A1.P05.MP CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone plate=3002 Col=9 Row=K, genomic survey
sequence.
ACCESSION AQ088791
VERSION AQ088791.1 GI:3457702
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 444)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,T., Young,T., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence tagged Connector
Plate: 3002 row: K column: 9
Class: BAC ends
High quality sequence stop: 444.

FEATURES
source location/Qualifiers
1..444
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3002 Col=9 Row=K"
/sex="male"
/clone_id="CIT Approved Human Genomic Sperm Library D"
/note="Organ: Sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"

ORIGIN

Query Match 31.0%; Score 143.6; DB 11; Length 444;
Best Local Similarity 70.3%; Pred. No. 4.3e-17;
Matches 222; Conservative 0; Mismatches 89; Indels 5; Gaps 2;

Oy	3	CTGTAATTCACAGTACTGTGGAAGATCCAGAGTCCAGAGACTCTTTGAGGCGAGAGTTCAA	62
Db	335	CTGTAATTCACAGCACTTTGGAGAGCTGAGGCGGGTGGATCTTCAGACTCAGAGTTCAA	276
Oy	63	GAGCAGCTGTGACAAACAGGAGAGCTGTCACTACAAAGATTAATTAATTGACGAGC	122
Db	275	GACTAGCTGTGCTAACTAGTGAACCTGTCTCTACTAATAATACAAATAATTAGCAGGC	216
Oy	123	TTAGTGGCTATCCCTGTGTGTCCAGCTACTAGGAGGCGAAGTAGA---CTGCTTG	178
Db	215	GTGGTGGCACTATGCTGTAACTCCAGCTCTTTGGAGGCTGAGGAGAAAGATCGCTTGA	156
Oy	179	TCCACGAGAGTTCAAAGACTGCAGTGAGCTGAAGCCAGCCACTGTGATTCAGCTTGAGCA	238
Db	155	GCCTAGGAGGTGAGAGTTGCAAGGAGGTGAGATCGTGCCA-CTGCACTCCAGCTGGGCA	97
Oy	239	ACAAAGAGAGCCCTGTCTCAAAAAATAAGTTAAATAATAATAATAATAAGTTAA	298
Db	96	ACAGGCGCAGACCACTGTTCAAAAAAAAAAAAAAAAAATTAGATTAAAAAAAAAGTTAAAAA	37
Oy	299	ACCCTTAACACACTTT	314
Db	36	GGCTGGAAAAAGTGT	21

RESULT 8	LOCUS	DEFINITION
CR773238	CR773238	721 bp mRNA linear EST 23-SEP-2004
	DKFZp470D2113.r1	470 (synonym: pliv1) Pongo pygmaeus CDNA clone
	DKFZp470D2113-5'	mRNA sequence.

ACCESSION	CR773248	GI:52616511
VERSION	CR773248.1	
KEYWORDS	EST.	
SOURCE	Pongo pygmaeus (orangutan)	
ORGANISM	Pongo pygmaeus	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 721)	Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Schaiipp, A., Mewes, H.W., Weil, B., Amdt, C., Osanger, A., Fobo, G., Han, M., and Wiemann, S.,	Pongo pygmaeus mRNA	Unpublished (2004)	Contact: MIPS
		Deutschenbaur, S., et al.)		

MPIS
Ingolstaedter Landstr. 1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email: s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix
(Martinsried, Germany). Within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp470D2113) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneId=DKFZp470D2113>
Further information about the clone and the sequencing project is
available at <http://mpis.gsf.de/projects/cdna/>.

FEATURES	location/Qualifiers
source	1. .721

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/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp470d213"
/tissue_type="liver"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="470 (synonym: pliv1)"
/note="Vector: pSPORT_Sfi; Site_1: SfiI; Site_2: SfiIb"
ORIGIN

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Query Match 31.0%; Score 143.6; DB 8; Length 721;

[illegible]

LOCUS	DEFINITION	SEQUENCE
AO215619/c	AO215619 HS 3217 B2 A01 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3217 Col=2 Row=B, genomic survey sequence.	417 bp DNA linear GSS 19-SEP-1998

ACCESSION	AQ215619
VERSION	AQ215619.1
KEYWORDS	GI:3630939
SOURCE	GSS.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	PUBLISHED	COMMENT
1 (bases 1 to 417)					
	Mahairas, G.C., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome	Proc. Natl. Acad. Sci. U.S.A.	96 (17), 9739-9744 (1999)	
			10449764		
	Contact: Mahairas CG, Wallace JC, Hood L				

High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 317 row: B column: 2
Class: BAC ends
High quality sequence, stop: 417.

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FEATURES
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        Location/Qualifiers
            1..417
                /organism="Homo sapiens"
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                /sex="male"
                /clone_1lb="CIT Approved Human Genomic Sperm Library D"
                /note="Organ: sperm; Vector: pBeloBac11, BAC clones in E-Coli DH10B"

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ORIGIN

Query Match 31.0%; Score 143.4; DB 11; Length 417;
Best Local Similarity 74.0%; Pred. No. 4,9e-17;
Matches 208; Conservative 0; Mismatches 71; Indels 2; Gaps 2;

QY 2 CCTGTATTCACACTACTGTGAGAGTCCGAGGTGACAGAGACTGTTAGGCCAGAGTTCA 61
DB 413 CCTATATCCCACTACTCTTGATGTGAGGCGGGTGATCCTTGAGGTGACAGAGTTG 354
QY 62 AGAGCAGCCTTGACAAACACAGGAGACT-GTCACTACAAAGAATTAATTAATTAAGCCAG 120
DB 353 AGACCAAGCTTACGTAATGATGTGAACCTCATCTCTACTTAAATTAATTAATTAAGCCAG 294
QY 121 GCTTAGTGCTCATCCCTGTGTCCAGCTACTAGGAGGACAGAGTGAAGTGGCTTGTCT 180
DB 293 GTGTGTGGGACATGCTGTAGTCCGAGCTGTGGGAGAGCTGAGGACAGATGCTTGAA 234
QY 181 CCGAGAGGTCAACACTGACAGTGAAGCCAGGACACTGCACTTCCAGCTGGGAC 240
DB 233 CCGGGGGGCAAAAGGCTGACAGTGAAGTGAAGTGTGCCA-CTGACCTCAGAGCTGGGAC 175
QY 241 AAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 281
DB 174 AGAAGAGAGCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 134

RESULT 10
DB322788/c 454 bp mRNA linear EST 04-DEC-2005
LOCUS DB322788 NT2NE2 Homo sapiens cDNA clone NT2NE2000864 3', mRNA
DEFINITION DB322788 NT2NE2 Homo sapiens cDNA clone NT2NE2000864 3', mRNA
sequence.
VERSION DB322788
KEYWORDS DB322788.1 GI:83261293
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 454)
Kimura, K., Wakamatsu, J., Suzuki, Y., Oca, T., Nishikawa, T.,
Yamashita, R., Yamamoto, J., Sekine, M., Tsutitani, K., Wakaguri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kuehida, N.,
Toneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuna, M.,
Muraikawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isegai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
JOURNAL
PUBMED
COMMENT Contact: Takao Isegai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
Location/Qualifiers
1..454
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2NE2000864"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_id="NT2NE2"
/note="Vector: pME18FLJ3; mRNA from NT2 neuron after the

ORIGIN differentiation of NT2 neuronal precursor cells"

Query Match 31.0%; Score 143.4; DB 9; Length 454;
Best Local Similarity 73.4%; Pred. No. 4,7e-17;
Matches 212; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 2 CCTGTATTCACACTACTGTGAGAGTCCGAGGTGACAGAGACTGTTAGGCCAGAGTTCA 61
DB 293 CCTGTAGTCCACAGACTTTTGGAGGCGGAGTGGGATGCTTGAAGTCAAGAGTTTC 234
QY 62 AGAGCAGCCTTGACAAACACAGGAGAG-CCTGTCACTACAAAGAATTAATTAATTAAGCCAG 120
DB 233 AGAGCAGCCTTGACAAACAGTGAACCCGTGTCTTAAATTAATTAATTAATTAAGCCAG 174
QY 121 GCTTAGTGCTCATCCCTGTGTCCAGCTACTAGGAGGACAGAGTAGA-----CTGC 175
DB 173 GCATGTGGCGCAGCAGCTGTGTTTACGTAACCTGGAAGCTGAAGCAGAGAAATTCCT 114
QY 176 TTGTCCAGAGAGGTCAAGACTGAGTGAAGTGAAGCCAGCCTGACATTCAAGCTTG 235
DB 113 TGAGCCTGGAGAGGTGAAGGCTGAGTGGGCAAGATGTAACCACTGCACTTCAGGCTGG 54
QY 236 GCAACAAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 284
DB 53 GCAACAGAGCAAGACTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 5

RESULT 11
BX487140/c 551 bp mRNA linear EST 04-SEP-2003
LOCUS BX487140
DEFINITION DKFZp686G22255_r1 686 (synonym: hicc3) Homo sapiens cDNA clone
DKFZp686G22255 5', mRNA sequence.
VERSION BX487140
KEYWORDS BX487140.1 GI:31951470
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 551)
Behr, A., Lauber, J., Mewes, H.W., Weill, B., Amid, C., Oanger, A.,
Fobo, G., Han, M. and Wiemann, S.
EST (Behr, A., Lauber, J., Mewes, H.W., Weill, B., et al.)
Unpublished (2003)
Contact: MIPS
MIPS
Ingolstaedter Landstr. 1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Olagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZp686G22255) is available at the RZPD in Berlin.
Please contact the RZPD: Resourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1..551
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686G22255"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hicc3)"
/note="Vector: pT7p18x2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Query Match 31.0%; Score 143.4; DB 4; Length 551;
Best Local Similarity 72.4%; Pred. No. 4,5e-17;

[illegible]

Email: c3apbs-rc@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amgdbcm.tmc.edu
Gunnarstein, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louised, H.,
Kovis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanaavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ULNL at: <http://image.llnl.gov>
Series: IRAC Plate: 42 Row: h Column: 7
This clone has the following problem: no 5' EST match.

FEATURES
SOURCE
1. 2821
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4939961"
/tissue_type="Brain, anaplastic oligodendroglioma with
1p/19q loss"
/clone_id="NCI_GAP_Brn67"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN
Query Match 30.8%; Score 142.8; DB 6; Length 2821;
Best Local Similarity 71.4%; Pred. No. 4.3e-17;
Matches 230; Conservative 0; Mismatches 87; Indels 5; Gaps 3;
QY 2 CCTGTAATTCACGACTGTGAGAGTCCGAGGTCCAGAGACTGCTTGAGGCCAGAGTTCA 61
Db 1686 CCTGTAATTCACGACTGTGAGAGTCCGAGGTCCAGAGACTGCTTGAGGCCAGAGTTTG 1745
QY 62 AGAGCAGCCTTGAGCAACAGAGGAGA-CCTGTCTCTCAAAAGATTAATAATTAATGACGAG 120
Db 1746 AGAGCAGCCTTGAGCAACAGAGGAGAATTCCTCTCTCAAAAGATTAATAATGAGTACG 1805
QY 121 GCTTAATGTCATCCCTGTGTGTCCAGCTTACTAGGAGGAGGAGT--AGAGCTGCTT 177
Db 1806 GTGTGTGTGACACACACTGTGTAGTCCAGCTTAATCAGAGGCTGAGGTGAGGAGATTGCT 1865
QY 178 GTCCAGAGAGGTCAAGACTGAGGTGAGTCCAGCCAGCCACTGCAATTCAGGCTGGGC 237
Db 1866 GAGCCTGTAAGTGAAGGCTGAGGTGAGTGTGATCAGGCCA-CTGACTCCAGCTGGGT 1924
QY 238 AACAAAAAGAGCCCTGTCTCAAAAAATTAAGTTAAATTAATTAATTAATTAATTAAGTTA 297
Db 1925 GACAGAGTGAAGCTCTGTCTTAAAAAATATATATATATTAATTAATTAATTAATTAAGTTA 1984
QY 298 AACCTTAACACATCTTCTTT 319
Db 1985 AAAATCAAAATTAATTAATTT 2006

RESULT 13
LOCUS AG014790 746 bp DNA linear GSS 16-FEB-2005
DEFINITION Homo sapiens genomic DNA, 21q region, clone: 762015N19, genomic
survey sequence.
ACCESSION AG014790 AG006505
VERSION AG014790.1 GI:3650008
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1

AUTHORS Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
REFERENCE 2 (bases 1 to 746)
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (23-SEP-1998) Masahira Hattori, RIKEN Genomic Sciences Center, RIKEN Yokohama Institute, Yokohama Research Promotion Division, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: hattori@gs.c.riken.jp, Tel: 81-45-503-9111, Fax: 81-45-503-9113)
COMMENT On Feb 6, 1999, this sequence version replaced gi:2992383.
AG006505: Submitted (27-Mar-1998).
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Best Local Similarity 73.8%; Pred. No. 6.1e-17;
Matches 220; Conservative 0; Mismatches 72; Indels 6; Gaps 3;
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DB 104 AGACAGCAGCCTGGAACAACATGCAAAACCCACCTCTCAAAAATATCAAAAATTAAGCCAG 163
QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGCTACTAGGAGGAGGAGAGTGAAGTCTGT- 179
DB 164 GCATTAATGGCAATGCTGTGATCTCACTAGGAGGAGGAGTGAAGTGAAGGCTTTCTT 223
QY 180 ---CCGAGAGGAGTCAAGTCAAGTGAAGTGAAGCCAGCCAGCTGATTCAGAGCTGG 236
DB 224 GAGCCAGAGGAGGAGGAGGAGTGAAGTGAAGTGAAGTCAAGCCCA-CTGATCTCCAGCTGG 282
QY 237 CAACAAAAGAGAGCCCTGTCTCAAAAATTAATTAATTAATTAATTAATTAAGT 294
DB 283 TGACAGAGCCAGACCTGTCTCAAAAATTAATTAATTAATTAATTAAGCAGTACAGT 340
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DEFINITION mRNA sequence.
ACCESSION CR980253
VERSION CR980253.1 GI:68218587
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 916)
AUTHORS Heil, O., Ebert, L., Hennig, S., Henze, S., Radelof, U., Schneider, D.
and Korn, B.
TITLE Human T-lymphocytes library
JOURNAL Unpublished (2005)
COMMENT Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD: RZPDp9017H083.
RPDLib: (Human T-lymphocytes) RZPD LIB No. 9017
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9017 Contact:

Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneId=RZPDp9017H083
contact RZPD (product-support@rzpd.de) for further information.
Primer name: q93.4, Primer sequence: CGGATTAACAATTCACACAG.
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/lab_lib="RZPD no. 9017"
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NotI; vector:
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human T-lymphocytes with a NotI-oligo(dT) primer [5'
GACTGATTCAGATCGGAGCGGCCCTTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to SalI adaptor,
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of the pQE80LSN_cloned vector"
ORIGIN
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Best Local Similarity 70.7%; Pred. No. 7.6e-17;
Matches 232; Conservative 0; Mismatches 90; Indels 6; Gaps 3;
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QY 62 AGAGCAGCCTGGAACAACAGGAGAGCCT-GTCACTACAAAGATTAATTAATTAAGCCAG 120
DB 611 AGACAGCAGCCTGGAACAACATGTAACCTCATCTCTAATAAATACAAAATTAAGCCAG 552
QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGCTACTAGGAGGAGGAGTGAAGTGAAGTCTGT 176
DB 551 GCATGTGGGCAATGCTGTGATCCAGCTGTCTGGGAAGCTGAAGTGAAGTACACTT 492
QY 177 TGTCACAGAGTCAAGACCTGAGTGAAGACCAAGCACTGATTCAGAGCTGG 236
DB 491 GAACCCAGAGGAGGAGGAGTGAAGTGAAGTGAAGTCAAGGCCA-CTGCACTCCAGCTGG 433
QY 237 CAACAAAAGAGAGCCCTGTCTCAAAAATTAATTAATTAATTAATTAATTAAGT 296
DB 432 CGACAGAGTGAAGCCCATCTCAAAACAAATTAATTAATTAATTAATTAATTAAGTCTTC 373
QY 297 AAACCTTAACACATCTCTTTTCAAA 324
DB 372 ATACAAACAGAGTCTTCTGCTTAA 345
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ACCESSION BE349022
VERSION BE349022.1 GI:9260875
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE
1 (bases 1 to 444)
AUTHORS
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL, send email to:
info@image.lnl.gov
Seq primer: -400P from Gibco
High quality sequence stop: 414.
Location/Qualifiers
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FEATURES
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Library constructed by Life Technologies."

ORIGIN

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Best Local Similarity 74.6%; Pred. No. 9.5e-17;
Matches 220; Conservative 0; Mismatches 67; Indels 8; Gaps 3;
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DB 129 ACCGTAAATCCAGTACGTGAGAGTCGAGAGCACTGCTTGAGGCCAGAGTTC 188
QY 61 AAGAGCAGCCTGAGCAACACAGGAGA-CCTGTCACTACAAAGAATAATAATTAGCCA 119
DB 189 GAGACCAACCTGGGCAACAGGCGAGATCCATCACTACAAAATTTAGGCCA 248
QY 120 GGCTTAGTGGCTATCCCTGTGTCCAGCTACTAGGAGGCGAGAGTAGA---CTGC 175
DB 249 GGCATGTGTGGTGCACACTTGTAGTCCAGCTACTCAGGAGGCTGAGGTGGAGATTGCT 308
QY 176 TTGTCCAGAGAGTCAAGACGTGAGAGTGAACCAAGCCACTGCAATTCAGCCTGG 235
DB 309 TGGGCCAGAGAAATCAAGGCTAGAGTAGCCGTATC--ACCAAGTCACTTGACCTGG 365
QY 236 GCAACAAAAGAGACCTGTCTCAAAAAAATTAATAATAATAATAATAA 290
DB 366 GCAACAGAGAAAGCCTGTCTCAAAAAAATTAATAATAATAATAATAA 420

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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Title: US-09-869-098A-1_COPY_255_717

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Gapop 10.0, Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461.4	99.7	11808	US-09-949-016-15281	Sequence 15281, A
2	461.4	99.7	11808	US-09-949-016-14689	Sequence 14689, A
3	153.4	33.1	601	US-09-949-016-165996	Sequence 165996, A
4	152.2	32.9	61461	US-09-949-016-16419	Sequence 16419, A
5	149.6	32.3	126237	US-09-949-016-16674	Sequence 16674, A
6	149.6	32.3	126237	US-09-949-016-16675	Sequence 16675, A
7	149.4	32.3	13023	US-09-949-016-16292	Sequence 16292, A
8	149.4	32.3	63783	US-09-949-016-13576	Sequence 13576, A
9	149	32.3	601	US-09-949-016-12883	Sequence 12883, A
10	148.4	32.1	29171	US-09-949-016-13509	Sequence 13509, A
11	148.4	32.1	29171	US-09-949-016-12853	Sequence 12853, A
12	147.2	31.8	601	US-09-949-016-160956	Sequence 160956, A
13	147.2	31.8	601	US-09-949-016-12816	Sequence 12816, A
14	147.2	31.8	99370	US-09-949-016-17561	Sequence 17561, A
15	146.8	31.7	601	US-09-949-016-16780	Sequence 16780, A
16	146.8	31.7	35493	US-09-949-016-14964	Sequence 14964, A
17	146.8	31.7	35493	US-09-949-016-11884	Sequence 11884, A
18	146	31.5	119981	US-09-949-016-13606	Sequence 13606, A
19	146	31.5	119982	US-09-949-016-15096	Sequence 15096, A
20	144.6	31.2	93778	US-09-949-016-13734	Sequence 13734, A
21	144.6	31.2	131254	US-09-949-016-156159	Sequence 156159, A
22	144.6	31.2	601	US-09-949-016-156159	Sequence 156159, A
23	144.4	31.2	601	US-09-949-016-156159	Sequence 156159, A

ALIGNMENTS

24	144.2	31.1	16230	US-09-949-016-14788	Sequence 14788, A
25	144.2	31.1	17607	US-09-949-016-15968	Sequence 15968, A
26	143.8	31.1	601	US-09-949-016-150302	Sequence 150302, A
27	143.8	31.1	39601	US-09-949-016-16045	Sequence 16045, A
28	143.6	31.0	18508	US-09-949-016-13843	Sequence 13843, A
29	143.6	31.0	157032	US-09-949-016-16502	Sequence 16502, A
30	143.2	30.9	601	US-09-949-016-71235	Sequence 71235, A
31	143.2	30.9	601	US-09-949-016-71235	Sequence 71235, A
32	143.2	30.9	40641	US-09-949-016-13376	Sequence 13376, A
33	143.2	30.9	55130	US-09-949-016-11880	Sequence 11880, A
34	143	30.9	30820	US-09-949-016-17145	Sequence 17145, A
35	143	30.9	58821	US-09-949-016-15897	Sequence 15897, A
36	143	30.9	58824	US-09-949-016-12615	Sequence 12615, A
37	142.8	30.8	8133	US-09-949-016-17403	Sequence 17403, A
38	142.8	30.8	17348	US-09-949-016-17403	Sequence 17403, A
39	142.4	30.8	57605	US-09-949-016-13259	Sequence 13259, A
40	142.4	30.8	68702	US-09-949-016-16328	Sequence 16328, A
41	142.4	30.7	93894	US-09-949-016-13629	Sequence 13629, A
42	142.2	30.6	15222	US-09-949-016-11916	Sequence 11916, A
43	141.8	30.6	15223	US-09-949-016-16912	Sequence 16912, A
44	141.8	30.6	44971	US-09-949-016-17049	Sequence 17049, A
45	141.8	30.6	44971	US-09-949-016-17049	Sequence 17049, A

RESULT 1	US-09-949-016-15281	Sequence 15281, Application US/09949016	Patent No. 6812339	GENERAL INFORMATION:
APPLICANT:	VENTNER, J. Craig et al.	TITLE OF INVENTION:	POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF	FILE REFERENCE:
FILE REFERENCE:	CL001307	CURRENT APPLICATION NUMBER:	US/09/949,016	CURRENT FILING DATE:
CURRENT FILING DATE:	2000-04-14	PRIOR APPLICATION NUMBER:	60/241,755	PRIOR FILING DATE:
PRIOR FILING DATE:	2000-10-20	PRIOR APPLICATION NUMBER:	60/237,768	PRIOR FILING DATE:
PRIOR FILING DATE:	2000-10-03	PRIOR APPLICATION NUMBER:	60/231,498	PRIOR FILING DATE:
PRIOR FILING DATE:	2000-09-08	NUMBER OF SEQ ID NOS:	207012	SOFTWARE:
SOFTWARE:	FASTSEQ for Windows Version 4.0	SEQ ID NO 15281	LENGTH: 11808	TYPE: DNA
ORGANISM:	Human	US-09-949-016-15281	Query Match	99.7%; Score 461.4; DB 3; Length 11808;
Best Local Similarity	99.8%; Pred. No. 1.9e-117;	Matches 462; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
QY	1	ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCGAGAGCTGTCGAGGCCGAGATTC	60	
DB	23	ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCGAGGTCGTCGAGGCCGAGATTC	82	
QY	61	AAGAGCAGCTGACACACAGGAGAGCTGTCACTACCAAGAATAAATTAAGCCAG	120	
DB	83	AAGAGCAGCTGACACACAGGAGAGCTGTCACTACCAAGAATAAATTAAGCCAG	142	
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DB	143	GCTTAAGTCTCATCCCTGTGTCCAGCTACTAGGAGGACAGAGTGGCTTGTGTC	202	
QY	181	CCAGAGGTAAACATGACATGAGTGAAGCCAGCACTGATTCACCTGGGGAAAC	240	
DB	203	CCAGAGGTAAACATGACATGAGTGAAGCCAGCACTGATTCACCTGGGGAAAC	262	
QY	241	AAAAAGAGCCCTGTCTCAAAAAATAAATTAATAAATAAATAAATTAATTAAC	300	

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RESULT 2
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14689
; LENGTH: 39754
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)_(39754)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14689

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Db	28298	ATCTCCACTCCCTTTTTCAGCGCTCCACACTTTTAAACAGCTCTTTTGGCAAGATAAATA	28357
QY	421	AGTATATAGTTTCTGGAATCCAAATCTTCCCGTTTGGACAG	463
Db	28358	AGTATATAGTTTCTGGAATCCAAATCTTCCCGTTTGGACAG	28400

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RESULT 3
US-09-949-016-165996/c
: Sequence 165996, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CLO01307
: CURRENT APPLICATION NUMBER: US/09/949,016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 165996
: LENGTH: 601
: TYPE: DNA
: ORGANISM: Human
US-09-949-016-165996

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Query Match 33.1%; Score 153.4; DB 3; Length 601;
Best Local Similarity 68.8%; Pred. No. 8e-33;
Matches 225; Conservative 1; Mismatches 97; Indels 4; Gaps 1;

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Db CCTGTAAATCCAGCACTTTTCAGAGGCCAAGGCAAGTGTGATCACTTGAGGCCAGGATTTGCG 430

Oy 62 AGAGCAGCCTTGGACAACACAGAGGAGACCTGTCACTACAAAGATTAATTAATTAAGCCAGG 121
Db 429 AGAGCAGCCTGCGCGATGTGTGAACCCCGTCTTCAATAAATCAAAAATTAAGCTGGG 370

Oy 122 CTTAGTGGCTCATCCCTGTGGTCCAGGCTACTAGGAGGCAAGATGAGACTGCTTGT-- 179
Db 369 CATGTGTGCACTCTCTTAATCCACGCTACTTGGAGGCTGAGGCAAGAAATTGCTGG 310

Oy 180 --CCGAGAGGTCAAGACTGTGAGTGTGAGACCCAGCCACTGCATTCAGGCTGGGC 237
Db 309 AACCAAGGRTGTGAGGTTGACAGTGTGAGCCAGATCATGCCCTGCACCTCAAGTCTGGGC 250

Oy 238 AACCAAAAAGACCTGTCTCAAAAAATTAAGTTAATTAATTAATTAATTAAGTTA 297
Db 249 AACGAGTGAACCTGTCTCAAAAAACAAAACAAAACAAAAGATGAAAAAGTAATGA 190

Oy 298 AACCTAACAACATCTCTTTTTCAAA 324
Db 189 AAACCTGAAAGTTGTCAAGCTCTTTTGCAA 163

RESULT 4
US-09-949-016-16419
; Sequence 16419, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016

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: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 16419
: LENGTH: 61461
: TYPE: DNA
: ORGANISM: Human
US-03-949-016-16419

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Best Local Similarity	70.6%	Pred. No. 9,4e-32		
Matches 231, Conservative	0	Mismatches 92	Indels 4	Gaps 2

OY	2	CCTGTAATTCACAGTACTGTAGAGTCCGAAGTGCAGAGGACTGGTCAAGGCCACGAGAGTTCA	61
Dd	50081	CGTGTAATCCCAGACATTTCAGAGGCCAAGGCAAGTGATCACTTAGGCCACGAGATTTTG	50140
OY	62	AGAGCAGCCTTGACAACACAGGGAGA CTGTCACTACAAAGATAATTAATTAGCCAG	121
Dd	50141	AGAGCACCTGGCGCATGTGTGA AACC CGTCTCTACTAATAATGCAAAAATTAGCTGGG	50200
OY	122	CTTAGTGGCTCATCCCTGTGGTCCACAGTACTAGGGAGGCAGA -- AGTAGACTGTCTTG	178
Dd	50201	CATGTTGTGTCACTCCCTGTAA TCCCAAGTACTTGGGAGGCTGAGCAGAGAAATTTCTTG	50260
OY	179	TCCCAAGAGG--TCAGACTGTGATGAGTGAAGCCACGACCTGTGATTCAGCTCGGGC	237
Dd	50261	AACCAAGGGGGTTGGAAGTTTCACTGAGCCCAAGATTCATGCCCCGTGCATCAAGTCTGGGC	50320
OY	238	AACAAAAAGAGACCCGTGTCAA AAAAATAAGTTAAATTAATAATATAATAGTTTA	297
Dd	50321	AACGAGTGAAC TCTGTCCA AAAAACAAACAAACAAACAAAGATGA AAAGTAATGA	50380
OY	298	AACCTTAACACATCTCTTTTCAAA	324
Dd	50381	AAACTGGAAGTTGTCA GCTCTTTGCAA	50407

RESULT 5
 US-09-949-016-16674/c
 ; Sequence 16674, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16674
 ; LENGTH: 126237
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-16674

Query Match	32.3%	Score 149.6	DB 3	Length 126237
Best Local Similarity	75.0%	Pred. No. 6.4e-31		
Matches 213	Conservative 0	Mismatches 69	Indels 2	Gaps 2

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Db	21590	ACCTGTAATTCGAGCACTTTGGGAGGCCAAGGAGAGGATCAATGAGCCCGGAGTTT	21531
OY	61	AAGAGCAGCCTGGACAAACAGGGAGA-CCTGTCACTAACAAAGATAAATTAATTAGCCA	119
Db	21530	GAGGCCAGTGTGGGCAACACAGGGAAGCCCACTCTTAAACAAACAAAAAATTAAGCTG	21471
OY	120	GGCTTAATGCGCATCCCTGTGTGCCAGCTACTAGGAGAGGAGAAATGAGACTCTTGT	179
Db	21470	GGCATTAATGATGATGCTGTGTGTCCCAAGTATGTGGGAGGCTGAGGCGAGACTGTTGA	21411
OY	180	CCCAAGAGGTCAAGACTGCAGTGAGCTGAGACCCAGCCA.CTGTGATTCCAGGCTGGGCAA	239
Db	21410	GCCCGAGGTCMAAGACTGCTGTGAGCTGTGACCTGTGCCA-CTGCACTAACAGCCTGGGTGA	21352
OY	240	CAAAAAGAGACCTGTCTCAAAAAAATTAAGTTAAATTAATAATA	283
Db	21351	CAGAGTGAGACCTGTCTTGGAAAAAACAACAAAAACCAAAACA	21308

```

RESULT 6
US-09-949-016-16675/c
; Sequence 16675, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO0107
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16675
; LENGTH: 126237
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16675

```

Query Match	32.3%	Score 149.6	DB 3	Length 126237
Best Local Similarity	75.0%	Pred. 6.4e-11		
Matches 213	Conservative 0	Mismatches 69	Indels 2	Gaps 2
QY	1	ACCTGTAATTCAGACTGTGTGAGAGTCCGAGGTCAGAGGACTGCTTGAGGCCAGAGATTCC	60	
Db	21590	ACCTGTAATCCAGACACTTTGGGAGGCCAAGGCGAGAGATCACTAGACCCGGGAGTTT	215311	
QY	61	AAGAGCAGCCTGACACAACACAGGAGA-CCTGTCACTACAAAAGATTAATTAATTAGCCA	119	
Db	21530	GAGACCAAGCTGTGGCAACACAGGGAACCCACTCTTAACAAACAAAAATTATAGCTG	214711	
QY	120	GGCTTAATGACTATCCCTGTGTGTCCCACTACTAGGAGGCGAAGTAGACTCTTGT	179	
Db	21470	GGCATATGTATGATATCCTGTGTGTCCACTATATGTGGGAGGCTGAGGCGAGACTGTTGA	214111	
QY	180	CCGAGAGGTCAGACCTGCAGTAGCTGAGACCCAGGCCACTTGCAATTCAGAGCTGGGCAA	239	
Db	21410	GCCCGAGAGTCAGACCTGCTGTGAGCTGTGACTGTGCCA-CTGCACCTACAGCGCTGGTGA	213521	
QY	240	CAAAAAGAGCCTGTCTCAAAAAATTAAGTTAATTAATTAATA	283	
Db	21351	CAGAGTGAGACCTGTCTTGGAAAAAACAACAAAAAACCCAAACA	21308	

RESULT 7
US-09-949-016-16292

```
/ Sequence 16292, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 16292
/ LENGTH: 13023
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-16292
```

```
Query Match      32.3%; Score 149.4; DB 3; Length 13023;
Best Local Similarity 73.9%; Pred. No. 3.2e-31;
Matches 218; Conservative 0; Mismatches 71; Indels 6; Gaps 2;
```

```
QY      2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGCTGCTTGAGCCAGAGTTCA 61
DB      4266 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGCTGCTTGAGTCAGAGTTTG 4325

QY      62 AGAGCAGCCTGAGCAACACAGGAGACC--TGTCACTACAAAGATTAATTAATTAAGCC 118
DB      4326 AGACTAGCCTGGGCAACATAGTGAAGCTCATCTCTCAAAAAAATGAACAAATTAATTAAGCC 4385

QY      119 AGGCTTAGTGGCTCATCCCTGTGTGTCCAGCTACTAGGAGGCGAGAAGT--AGAGCTGC 175
DB      4386 GGGCGTGGTGTGATGCTGCTGTATGCTCCAGCTACTGGGGAAGCTGAGGTGGAGGATTCG 4445

QY      176 TTGTCACAGAGGTCAGAGCTGAGTGAAGTCCAGCCACCTGCTATTCAGCCTGG 235
DB      4446 TGACCTCGGTGTCAGAGCTGAGTGAAGTCCAGCTGATGATATGCTCACTCCAGCCTTA 4505

QY      236 GCAACAAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 290
DB      4506 GCACACAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4560
```

```
RESULT 8
US-09-949-016-13576
/ Sequence 13576, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13576
/ LENGTH: 63783
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-13576
```

```
Query Match      32.3%; Score 149.4; DB 3; Length 63783;
Best Local Similarity 68.2%; Pred. No. 5.7e-31;
Matches 238; Conservative 0; Mismatches 106; Indels 5; Gaps 2;
```

```
QY      1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGCTGCTTGAGCCAGAGTTTC 60
DB      35968 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGCTGCTTGAGTCAGAGTTTG 36027

QY      61 AAGAGCAGCCTGAGCAACACAGGAGACCTGTCACTACAAAGATTAATTAATTAATTAATTAAGCCAG 120
DB      36028 AAGCCAGCCTGGCCAAACATGTGAACCCCATCTCTAATAAATTAATTAATTAATTAAGCCAG 36087

QY      121 GCTTAGTGGCTCATCCCTGTGTGTCCAGCTACTAGGAGGAGCAAGATAGGA----CTGCT 176
DB      36088 GCATGTGTACAGGCACTTGTAGTCTTAGCTACTAGGAGGCTGAACAGAGATATCATG 36147

QY      177 TGTCCAGAGAGTCAAGACTGCAAGTGAAGTGAAGCCAGCCTGATTCAGCCTGGG 236
DB      36148 GAACCCAGAGAGAGAGGTTGCAAGTGAAGCTGAGGCGCATGCCA--TTGCACTCCAGCCTGGG 36206

QY      237 CAACAAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAAGTTT 296
DB      36207 CAACAGAGCAAGACTCATCTCAAAAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 36266

QY      297 AAACCTTAACACATCTCTTTTCAAGAGACTTCTTAAGACTTCA 345
DB      36267 TAAACAAATATCTTATTTTACTTATTAAGTATTAATTAATTAATTAATTAATTAATTAATTA 36315
```

```
RESULT 9
US-09-949-016-63328/c
/ Sequence 63328, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 63328
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-63328
```

```
Query Match      32.2%; Score 149; DB 3; Length 601;
Best Local Similarity 67.9%; Pred. No. 1.3e-31;
Matches 237; Conservative 1; Mismatches 106; Indels 5; Gaps 2;
```

```
QY      1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGCTGCTTGAGCCAGAGTTTC 60
DB      439 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGCTGCTTGAGTCACTTGAGTCAAGAGTTTC 380

QY      61 AAGAGCAGCCTGAGCAACACAGGAGACCTGTCACTACAAAGATTAATTAATTAATTAATTAAGCCAG 120
DB      379 AAGGCAAGCCTGGCCAAACATGTGAACCCCATCTCTAATAAATTAATTAATTAATTAAGCCAG 320

QY      121 GCTTAGTGGCTCATCCCTGTGTGTCCAGCTACTAGGAGGAGCAAGATAGGA----CTGCT 176
DB      319 GCATGTGTACAGGCACTTGTAGTCTTAGCTACTCGAGAGGCTGAAGAGATCATCACTG 260

QY      177 TGTCCAGAGAGTCAAGACTGCAAGTGAAGTGAAGCCAGCCTGATTCAGCCTGGG 236
DB      259 GAACCCAGAGAGAGGTTGCAAGTGAAGCTGAAGGCCATGCCA--TTGCACTCCAGCCTGGG 201
```

Oy 237 CACGAAAAAGAGCCCTGCTCAAAAAATAGTTAATATAATATAATATAATGTT 236
 |||||
 Db 200 CACGAGAGAGAGCTCATTCTCAAAAAAAAAAAAAAAAAAAAAATCTCAAAATCATAT 141
 |||||
 Oy 237 AAACCTTAACACATCTTCTTTTCAAGAGAGCTTTAAGAGCTTCA 345
 |||||
 Db 140 TAACAAAAATATCTTATTTACTATATAAGATATTTTAAAGATTACTACA 92
 |||||

RESULT 10
US-09-949-016-12283
; Sequence 12283, Application US/09949016
Patent No. 6813736

```

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12283
; LENGTH: 29171
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(29171)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12283

```

Query Match	32.1%	Score	148.4	DB	3	Length	29171
Best Local Similarity	75.9%	Pred. NO.	8.1e-31				
Matches	223	Conservative	0	Mismatches	66	Indels	5
						Gaps	3

QY	1	ACCGTAATTCACAGTACTGTAGAGATCCGAGGCTCAGAGACCTGCTTGGAGGCCAGGATTC	60
Db	5933	ACCTTAATTCCTAGACCTTTGGGAGGCCAAGGTGATGATGCTTGGAGGCCAGGATTC	5992
QY	61	AAGACGAGCCTTGGACCAACACAGGGAGACC-TGTCACTACAAAGATTAATTAATTAGCCA	119
Db	5993	AAGACGAGCCTTGGACCAACATGGTGTGAACCTTGGCTCTACTTAATAATTAACAAATTAATAC	6052
QY	120	GGCTTAATGTGGCTCATCCCTGTGTGCTCCAGCTACTAGGAGAGCGAGA---AGTAGGACTGCT	176
Db	6053	GCGTAGTGTGTGACGCGCTGTATATCCACGCTGCTTGGAGGCTGAGGCACTAGAAATTCCT	6112
QY	177	TGTCCAGAGAGGTCAAGACTGCAGTGAAGCTGAGACCCAGCCACTGCAATTCAGCGCTGAG	236
Db	6113	TGAACCGGAGGTAAAGGTGACGTGAGCTGAGATTGTGCCA-CGGCACTTCAAGCTGGG	6177
QY	237	CACCAAAAAGAGACCCCTGTCTCAAAAAATTAAGTTAATTAATTAATTAATTAATAA	290
Db	6172	CAATGAGATGACACCTGTCTCAAAAAATTAATTAATTAATTAATTAAGATTA	6225

```

RESULT 11
US-09-949-016-13509
; Sequence 13509, Application US/09949016
; Patent No. 6812339
;
; GENERAL INFORMATION:
;
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307

```

```

?
? CURRENT APPLICATION NUMBER: US/09/949,016
?
? CURRENT FILING DATE: 2000-04-11
?
? PRIOR APPLICATION NUMBER: 60/241,755
?
? PRIOR FILING DATE: 2000-10-20
?
? PRIOR APPLICATION NUMBER: 60/237,768
?
? PRIOR FILING DATE: 2000-10-03
?
? PRIOR APPLICATION NUMBER: 60/231,498
?
? PRIOR FILING DATE: 2000-09-08
?
? NUMBER OF SEQ ID NOS: 207012
?
? SOFTWARE: FASTSQ for Windows Version 4.0.
?
? SEQ ID NO 13509
?
? LENGTH: 29171
?
? TYPE: DNA
?
? ORGANISM: Human
?
? FEATURE:
?
? NAME/KEY: misc feature
?
? LOCATION: (1)...(29171)
?
? OTHER INFORMATION: n = A,T,C or G
?
US-09-949-016-13509

```

Query Match	32.1%	Score 148.4	DB 3	Length 29171
Best Local Similarity	75.9%	Pred. No. 8.1e-31		
Matches 223	0	Mismatches 66	Indels 5	Gaps 3

[illegible]

RESULT 12
US-09-949-016-28523/c
; Sequence 28523, Application US/09949016

```

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1601307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28523
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-28523

```

Query Match	31.8%	Score 147.2	DB 3	Length 601
Best Local Similarity	76.4%	Pred. NO. 4.2e-31		
Matches 220	Conservative 0	Mismatches 63		Indels 5
				Gaps 3

```
QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGATTTC 60
DB 290 ACCTGTAATTCAGTACTGTGAGAGGCCAAGGTGAGATGATTCCTTGAGGCCAGAGATTTC 231
QY 61 AAGAGCAGCTTGACACACAGAGGAGACC-TGTCACTACCAAAATTAATTAATTAGCCCA 119
DB 230 AAGACCAAGCTTGACACACATGATGAAACCTTGCTCTACTTAAATAAATAAATAATTAACTG 171
QY 120 GGGTGTAGTGCATCCCTGTGGTCCAGCTACTAGGAGAGCAGA---AGTAGACTGCT 176
DB 170 GGGGTAGTGTGACAGCCTGTATATCCAGCTGCTTGAGAGGCTGAGAGCACTAATTTGCT 111
QY 177 TGTCCAGAGAGTCAAGACTGACGTGAGAGCCAGCCACTGCATTCAGCCTGGG 236
DB 110 TGAACCGGAGAGTGAAGAGTTGACGTGAGATTTGTGCCA-CGGCACTCTAGCCTGGG 52
QY 237 CAACAAAAGAGACCTGTCTCAAAAATAAGTTAAATTAATTAATA 284
DB 51 CAATAGAGTGAAGACCTGTCTCAAAAATAAATAAATAAATAATA 4
```

RESULT 13

```
US-09-949-016-60956/c
; Sequence 60956, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60956
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-60956
```

```
Query Match 31.8%; Score 147.2; DB 3; Length 601;
Best Local Similarity 76.4%; Pred. No. 4.2e-31;
Matches 220; Conservative 0; Mismatches 63; Indels 5; Gaps 3;
```

```
QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGATTTC 60
DB 290 ACCTGTAATTCAGTACTGTGAGAGGCCAAGGTGAGATGATTCCTTGAGGCCAGAGATTTC 231
QY 61 AAGAGCAGCTTGACACACAGAGGAGACC-TGTCACTACCAAAATTAATTAATTAGCCCA 119
DB 230 AAGACCAAGCTTGACACACATGATGAAACCTTGCTCTACTTAAATAAATAAATAATTAACTG 171
QY 120 GGGTGTAGTGCATCCCTGTGGTCCAGCTACTAGGAGAGCAGA---AGTAGACTGCT 176
DB 170 GGGGTAGTGTGACAGCCTGTATATCCAGCTGCTTGAGAGGCTGAGAGCACTAATTTGCT 111
QY 177 TGTCCAGAGAGTCAAGACTGACGTGAGAGCCAGCCACTGCATTCAGCCTGGG 236
DB 110 TGAACCGGAGAGTGAAGAGTTGACGTGAGATTTGTGCCA-CGGCACTCTAGCCTGGG 52
QY 237 CAACAAAAGAGACCTGTCTCAAAAATAAGTTAAATTAATTAATA 284
DB 51 CAATAGAGTGAAGACCTGTCTCAAAAATAAATAAATAAATAATA 4
```

RESULT 14

```
US-09-949-016-12816
; Sequence 12816, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12816
; LENGTH: 99370
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12816
```

```
Query Match 31.8%; Score 147.2; DB 3; Length 99370;
Best Local Similarity 73.5%; Pred. No. 2.7e-30;
Matches 216; Conservative 0; Mismatches 73; Indels 5; Gaps 2;
```

```
QY 3 CTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGATTCAA 62
DB 66673 CTGTAATTCAGTACTGTGAGAGGCCAAGGTGAGATGATTCCTTGAGGCCAGAGATTCAA 66732
QY 63 GAGCAGCTTGACACACAGAGGAGACC-TGTCACTACCAAAATTAATTAATTAGCCAGG 121
DB 66733 GAGACCTTGACACACATGAGCAAAACCTGTCTCTCAATTAATTAATAAATAATTAGCCAGG 66792
QY 122 CTGAGTGTCTCCTGTGTGCTCCAGCTACTAGGAGGAGAGTGAAGG---CTGCTT 177
DB 66793 CATGTGTGCTTATGCTGTGTGCTCCAGCTACTAGGAGGAGTGAAGGAGTGAAGTCACTTGG 66852
QY 178 GTCCAGAGAGTCAAGACTGAGTGCAGTGCAGCCAGCCACTGCATTCAGCCTGGG 237
DB 66853 AACCCAGAGAGAGAGTGTGAGTGAATGATCATTCGCCACTGCACTTACCTGGG 66912
QY 238 AACAAAAGAGACCTGTCTCAAAAATAAGTTAAATTAATTAATA 291
DB 66913 AACAGAGCAAGACCTGTCTCAAAAATAAATAAATAAATAAATA 66966
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RESULT 15

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US-09-949-016-17540
; Sequence 17540, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17540
; LENGTH: 99370
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17540
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D_b 29892 AACCCAGAGGTGAGGTTACAGGACTGATGAGTTCGACCATCGACCTCGAGCTGGGT 298333
Q_y 238 AACAAAAAGAGACCCCTGTCTCAAAAATAAGTTAAATTAATAATATAAATAACTTTA 297
D_b 29832 GACGAGTGAGACCTCTGTCTCAAAAAAAAAATAAACATGTGAIAAAAAATTAAAAATAAT 297733
Q_y 298 AACCCTAAACACATCTTCTTTTTCAAGAGAGACTCTTAG 338
D_b 29772 ATAGCTAGGAACAACCTTGATGACAAAAATGTGTACTANG 29732

```

RESULT 2
US-10-723-860-2320/c
; Sequence 2320. Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723.860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2320
; LENGTH: 135005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2320

```

```

Query Match      32.8%; Score 152; DB 9; Length 135005;
Best Local Similarity 80.0%; Pred. No. 6.6e-29;
Matches 216; Conservative 0; Mismatches 50; Indels 4; Gaps 3;

QY      1  ACCGTGTAATTCACAGTACTGTGTAGAGTCCGAGGTGACAGAGACTGCTTAGAGCCAGAGATTG 60
DB      84820  ATCTGTAATCTCAGCACTTTGGAGGCGAGAGGTAGAGAGATTGCTTAGAGGCGAGAGATTG 61
QY      61  AAGAGCAGCCTGGACAAACAAGGAGA--CCTGTCACTTACAAAGAAATAATAATTAGGC 118
DB      84760  AAGACTATCTGGGCAACATGATGAGACCCCTGTCTTACAAAAAATGAAAAAATTAGTC 84701
QY      119  AGGCTTAGTGCTCATCTCCCTGTGTGCTCCAGCTACTAGGAGGACAGAGTAGACTGCTTG 178
DB      84700  GGGTATGTTGGACATGCTGTAGTATCCAGCTACTCAAGAGGCTGAGGTAGATTGCTTG 84641
QY      179  -TCCGAGAGAGTCAAGACTGTGAGTGAAGTGAAGCCACCACTGTGATTCAGCCTGGGC 237
DB      84640  AGCTCAGGAGAGTCCAGGCGGAGTGAAGTGAAGACAGTCCA-CTGTACTCCAACTGGGC 84582
QY      238  AACCAAAAGAGACCCCTGTCTCAAAAAATTA 267
DB      84581  AACGAAACAAGACCCCTGTCTCAAAAAAAA 84552

RESULT 3
US-10-756-149-1719/c
/ Sequence 1719, Application US/10756149
/ Publication No. US20050181375A1
/ GENERAL INFORMATION:
/ APPLICANT: Aziz, Natasha
/ APPLICANT: Zlotnik, Albert
/ TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
/ TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
/ FILE REFERENCE: file
/ CURRENT APPLICATION NUMBER: US/10/756,149
/ CURRENT FILING DATE: 2004-01-12
/ NUMBER OF SEQ ID NOS: 5818

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1719
;
; LENGTH: 135005
;
; TYPE: DNA
;
; ORGANISM: Homo Sapiens
US-10-756-149-1719

```

	Query Match	Local Similarity	32.8%;	Score 152;	DB 10;	Length 135005;
	Best Match	Similarity	80.0%;	Pred. 0.6; e-29;		
	Matches	216;	Conservative	0;	Mismatches	50;
					Indels	4;
					Gaps	3;
QY	1	ACTGTTAATTC	CAGTACTGTGAGAGTCCGAGGCTCAAGGAC	CTGTTGAGGCCAGAGTTC	60	
Db	84820	ATCTGTAAATCT	CAGCACTTTGGAGGCAAGAGTGAAGATTTGCTTGAAGGCAAGAGTTC	84761		
QY	61	AAGAGCAGCCT	GTGACACACACAGGAGAA--CTGTCTACTACAAAGAA	TAAATTAATTAGCC	118	
Db	84760	AAGACTATCTCT	GGGCAACATATGATGAGACCCTGTCTCTCAAAAAATTA	GAATAATTAAGTTC	84701	
QY	119	AGGCTTAGTGG	CTTCATCCCTGTGTGTCCTCCAGTCTATCTAGGAGGACAGAAAGTATGAGACTGTG	178		
Db	84700	GGGTATGTGTG	CAACATGCTGTATGTCCCACTACTCAAGAGGGGTGAGGATTTGCTTG	84641		
QY	179	-TCCCAAGAGST	CAAGACTGCTAGTGAAGTGAAGACCAGCACCCTGATTTCAAGCCTGGGC	237		
Db	84640	AGCTCAGAGST	CGAAGCGGCACTGAGCTGAGACAGATGCA-CTGTACTCCAACCTGGGC	84582		
QY	238	AACAAAAAGAG	ACCCTGTCTCAAAAAATTA	267		
Db	84581	AACAGAACAG	ACCCTGTCTCAAAAAATTA	84552		

```

RESULT 4
US-09-925-065A-822292/c
; Sequence 822292, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 036
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252, 147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289, 846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 822292
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-822292

```

	Query Match	32.5%	Score 150.6;	DB 4;	Length 558;
	Best Local Similarity	74.1%;	Pred. No. 1.4e-29;		
	Matches 217;	Conservative 1;	Mismatches 70;	Indels 5;	Gaps 2;
QY	2 CCTGTAATTCAGACTGTGAGAGTCCGAGGTCAGAGGACTCTTGAGGCCAGAGTTCA	61			
Db	345 CCTGTAATCCAGACACTTTGGAGAGGCCAAGGCAGGTGATTACTTGAGGTGAGAGTTCA	286			
QY	62 AGAGAGCCTGGAACAACACAGAGAGACCTGTGCATCACTAAAGAATAATTAATTAGCCAGG	121			
Db	285 AGACCAGCCTTACCGCAACACGAGTAAACCCGCTCTTACTTAATAAATACAAAAATTGCCCAGG	226			

```

Oy      122 CTTAAGAGGCTATACCCCTGGATGATCCAGACTATAGGAGGAGGAAGTAGACTCTGT-- 179
Db      225 TGTGGTGGTCAGAGCCCTGATGTCACGACTATGGAGAGGCTGAGGACGGGGGGTGTGTTG 166
Oy      180 --CCGAGAGGCTCAAGACTGCAAGTAGAGAGACCCAGCCACCTGCATTCACAGCTGGGC 237
Db      165 AACCTGGGAGGATGGAGAGTTGCACTGAGCCAGATCAAGTGA--CTGCCCTCAGGCTGGGG 107
Oy      238 AACAAAAAGAGACCCTGTCTCAAAAATAAAGTTAAATAAATAATAATAATAA 290
Db      106 AACTAAGTAGACTCTGTCTCAAAAAAATAAATAAATAAATAAATAAATAA 54

```

```

RESULT 5
US-09-925-065A-839930
; Sequence 839930, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FASTSeq For Windows Version 4.0
; SEQ ID NO 839930
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-839930

```

Query Match	Similarity	32.5%	Score	150.6	DB 4	length	558
Best Local	Similarity	74.1%	Pred. No.	1,46-29			
Matches	217	Conservative	1	Mismatches	70	Indels	5
						Gaps	2
OY	2	CCTGTAATTCAGTACTGTGAGATGCCAGAGTCAGAGACCTGCTTGAGGCCAGAGATTCA	61				
Db	215	CCTGTAATTCAGAGCCTTTGGGAGGCCAAGGCAGGTGTGATTACTTGAGAGTCAGAGATTCA	274				
OY	62	AGAGAGAGCTGGACAAACAACAGGGAAGCTGTGCATACACAAAGATTAATTAATTACCCAG	121				
Db	275	AGACCAAGCTGGCCAAACACGGGTGAACCCGCTCTTACTTAAATATCAAAAATTAGCCAG	334				
OY	122	CTTAGTGCTCATCCCTGTGGTCCAGCTTACTAGGAGGACAGAAATAGACTGCTTGT--	179				
Db	335	TGTGTGTGTGATGTGCTGTAGTCCACAGCTACTTTGGAGGCTGTAGGACAGGGGGGTGCTTG	394				
OY	180	--CCAGAGAGCTCAAGCTGCAGTGTGAGAACCCAGCCACTTCATCCAGCTGGGC	237				
Db	395	AACCTGGAGAGGTGAGAGCTTGTGACGTAGCCAAATATACGTCACTGCCCTCAGAGCTGGGG	453				
OY	238	AACAAAAAGAGACTCTGTCTCAAAAATTAAGTTAAATTAATTAATTAATAA	290				
Db	454	AACCTAAGAGACTCTGTCTCAAAAATTAATTAATTAATTAATTAATAA	506				

RESULT 6
US-09-925-065A-822292/c
Sequence 822292, Application US/0995065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.

```

; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 822292
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-822292

Query Match      32.5%   Score 150.6;   DB 5;   Length 558;
Beech Local Similarity 74.1%;   Pred. No. 1.4e-29;
Matches 217; Conservative 1; Mismatches 70; Indels 5; Gaps 2

```

QY	2	CTGTAAATTCAGAGTACTGTAGAGTCCGAGGTCAAGAGACTCTTGAGGCCAGAGATTCA	61
Db	345	CTGTAAATCCAGACCTTTGGAGGCCAAGGCAGGTGGATTACTTTGAGGTCAAGAGTTCA	286
QY	62	AGAGCAGCCTTGAGCAACAAGGAGACCTGTCACTCAAAAGATTAATTAATTAGCCAGG	121
Db	285	AGACCAACCTGGCCAAACCGGTGAAACCGCTCTTACTATAAAAAATACAAAAATTGACCCAGG	226
QY	122	CTTAGTGGTCATCCCTGTGGTCCGACGTACTTAGAGAGCGAAGTGGATGCTGTG--	179
Db	225	TGTGTGTGTGCATCCTGTGAGTCCCAAGTACTTGGAGGCTGGAGCAGGGGGGTTGCTTG	166
QY	180	--CCAGAGGTCAAAGCTGCAGTGAAGTGAAGCCAGCCACTGCAATTCAGCCTTGCGC	237
Db	165	AACCTGGAGGTGAGGTTGACAGAGACCAAGATCAGGYCA--CTGCCTCCAGCCTGGGG	107
QY	238	AACAAAAAGAGACCCCTGTCAAATAAATTAATTAAATTAATTAATTAATTAATTAATTA	290
Db	106	AACTAAGTGACCTGTCTTAAAAAAAAAAAAAAAAAGATTAAAAAATTAADA	54

```

RESULT 7
US-09-925-065A-839930
Sequence 839930, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925, 065A
PRIORITY FILING DATE: 2001-08-08
CURRENT APPLICATION NUMBER: US 60/243, 096
PRIORITY FILING DATE: 2000-10-24
PRIORITY APPLICATION NUMBER: US 60/252, 147
PRIORITY FILING DATE: 2000-11-20
PRIORITY APPLICATION NUMBER: US 60/250, 092
PRIORITY FILING DATE: 2000-11-30
PRIORITY APPLICATION NUMBER: US 60/251, 766
PRIORITY FILING DATE: 2001-01-16
PRIORITY APPLICATION NUMBER: US 60/259, 846
PRIORITY FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 839930
LENGTH: 558

```


Oy	179	TCCGAGAGGCTCAGACTGAGTGGTGA	CCGACGACCTGCATTTCCAGCTTGGGA	238
Db	15035	AACCGGAGGGCGGAGTTGCA	GTGAGCTGAGATTGTGCCA	-TTGCACCTCCGGCTTGGGCA 150933
Oy	239	ACAAAGAGAGACCTGCTCTCA	AAAAAATAGTTAAATAAATAAATAAATAAATAGTTTAA	298
Db	15094	ACGGAGCAAGACTGTGTTCTT	AAAAAATAAATAAATAAATAAATAAATAAATAAATAAAT	15155
Oy	299	ACCTTAA	306	
Db	15154	AAATTTAA	15161	

```

RESULT 10
US-10-043-715-1/c
: Sequence 1, Application US/10043715
: Publication No. US20030143544A1
: GENERAL INFORMATION:
: APPLICANT: McCarthy, Jeanette
: TITLE OF INVENTION: DIAGNOSIS AND TREATME
: TITLE OF INVENTION: DISEASE
: FILE REFERENCE: MMI-009
: CURRENT APPLICATION NUMBER: US/10/043, 715
: CURRENT FILING DATE: 2002-01-09
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FASTSQ for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 186510
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-043-715-1

```

Query Match	32.3%	Score	149.4	DB	7	Length	186510
Best Local Similarity	74.1%	Pred	No. 3.8e-28				
Matches	217	Conservative	0	Mismatches	71	Indels	5
						Gaps	2

[illegible]

```

RESULT 11
US-10-741-601-5682/c
; Sequence 5682, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5682
; LENGTH: 561515

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) ..(561515)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
; JS-10-741-601-5682

```

Query Match	32.0%;	Score 148.2;	DB 8;	Length 561515;
Best Local Similarity	70.0%;	Pred. No. 1.3e-27;		
Matches 229;	Conservative	0;	Mismatches 93;	Indels 5; Gaps 2;

[illegible]

```

RESULT 12
US-10-741-600-17730/C
Sequence 17730, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CU001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: PASTESEQ for Windows Version 4.0
SEQ ID NO 17730
LENGTH: 561515
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)_(561515)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-741-600-17730

```

[illegible]

D _b	81588	GTAATGGTGGCATGCACTGTAGTGTCCAGCTACTCAGGAGCGTSAAGCAGAAGATACATT	815229
O _y	177	TGTTCCAGAGAGTCACAACCTGCAGTAGCTGAACCCAGCGACCTTGCAATTCACAGCTTGGG	236
D _b	81528	GAAACCCAGAGCGCAGAGGGTGCGATGAGCTGAATCATGCCA-TTGACCTCCAGGCTTGGG	81470
O _y	237	CACCAAAAAGAACCTGTCTCAAAAAAATAAGTTAAATAATAATAATAATAATAATAGTTT	296
D _b	81469	TGACAGAGTGATCTGTCTCAAAAAAAAAAAAAAAAAAATAAGTAAAAATGCAAT	81410
O _y	297	AAACCTAAACACATCTTCTTTTCAA	323
D _b	81409	AAAAAATGAAGCAACTGATTTAAACAA	81383

```

US-09-925-065A-696683
/ Sequence 696683, Application US/09925065A
/ Publication No. US2004018048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925, 065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243, 096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252, 147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250, 092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261, 766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289, 846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 696683
/ LENGTH: 636
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-696683

```

	Query Match	Similarity	31.8%	Score 147.46	DB 4	Length 636;
	Best Local	Similarity	73.7%	Pred. No. 1e-28;		
Matches	216;	Conservative	0;	Mismatches 71;	Indels 6;	Gaps 2;
Oy	2	CCTGTAATTCACAGTACTGTGAGAGTGCCAGAGTCAGAGGACTGCTTTGAGGCCAGAGTTCA	61			
Db	15	CCTGTAATTCCTAACCTTTGGAGGCTCAGAGGGAGAGATTGCTTGACCCTAGAGATTCA	74			
Oy	62	AGAGAGCCTGGACAACAACAGGAGACCTGTGCATACAAAGAATAAATTAATTAGCCAG	121			
Db	75	AGACAGCGCTGGACAACAATGGCANACCCTGTCTTACAAAAGATACAAAAATTAGCCAGA	134			
Oy	122	CTTAGTGCTCATCCCTGTGTTGTTGCCAGCTACTAGGAGGCCAGAAATAGACTGCT----	176			
Db	135	TGTGTGTGCATACGCGCTGTGTTCTCAGCTACTCAGAGAGCGTAGAGCACAGAGGTTGCTTG	194			
Oy	177	TGTCGCCAGAGGTCAAAGACTGCAGTGAAGCTGAGACCCAGCCACTGCATTCAGCCTGGG	236			
Db	195	AGCCAGAGAGGTTCAGAGTTGCAGTGAAGTGAATTGGCCA-C TGCAACACAGGCTGGG	253			
Oy	237	CACCAAAAAGAGACCTGTCTCAAAAAATAAGTTAAATTAATTAATTAATAA	289			
Db	254	CACAGAGGCACACTTAATCTCAAAAAAAAAAAAAAAAAATAATTAATTAATTAATAA	306			

RESULT 14
US-09-925-065A-696684
; Sequence 696684, Application US/09925065A

```

; Publication No.: US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,036
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 696684
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-696684

```

Query Match	Similarity	31.8%	Score 147.4	DB 4	Length 636
Best Local Match	Similarity	73.7%	Pred. No. 1e-28		
Matches 216	Conservative	0	Mismatches 71	Indels	Gaps 2
Qy	2	CCTGTAAATTCAGTACTGTGTGAGAGTCCGAGGTCAGAGGACTGCTTTGAGGCCAGAGTTCA	61		
Db	15	CCTGTAAATTCCTMAACATTTGGGAGGCTGAGGTGGAGGATTTGAGCTTGAAGCTTCA	74		
Qy	62	AGAGCAGGCTGGAACAACAAGAGAGACCTGTCACTACAAAGATTAATTAATTAGCCAG	121		
Db	75	AGACCAAGCTGGACAAACATGSCAAGCCTGTCTTTACAAAAGATACAAAATTAATGACAGA	134		
Qy	122	CTTAAGTGCTCATCCCTGTGTGCTCCGACTTACTAGGAGGCGAAGTAGAGCTGCT-----	176		
Db	135	TGTGTGTGCATACCCCTGTGTGTTCCAGTACTCAGAGAGGCTGAGGACAGAGGGTTGCTTG	194		
Qy	177	TGTCCCAAGAGGTCAAGACTGACAGTGAAGTGAACCCAGCCACTGACTTCAGGCTTGG	236		
Db	195	AGCCCAAGAGGTGAGAGTTGCAATGAGCTGAATTTGGCCA-CTGCACACCAAGCTGG	253		
Qy	237	CAACAAAAGAGACCTGTCTCAAAAATAAGTTAAATTAAATTAATTAATAA	289		
Db	254	CAACAGAGCCAGACCTTATCTCAAAAATAAGTTAAATTAATTAATTAATAA	306		

```

/ RESULT 15
/ US-09-925-065A-696683
/ Sequence 696683, Application US/09925065A
/ Publication No. US20050228172A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925.065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086

```



```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 696683
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-696683
```

```
Query Match          31.8%; Score 147.4; DB 5; Length 636;
Best Local Similarity 73.7%; Pred. No. 1e-28;
Matches 216; Conservative 0; Mismatches 71; Indels 6; Gaps 2;
```

```
QY      2 CCTGTAATTCAGTACTGTGTGAGAGTCCGAGGTCAGAGACTGCTTGAGGCCAGAGTTCA 61
          |||||
Db      15 CCTGTATCTCTAACACTTTGGAGGCTGAGGTGGAGGATTGCTTGAGCCTAGAGATTCA 74
          |||||
QY      62 AGAGCAGCCTGAGCAACACAGGGGAGACTGTCACTACAAAGATTAATTAATTAGCCAGG 121
          |||||
Db      75 AGACCAAGCCTGAGCAACATGGCAAGCCCTGTCTTTACAAAAGATACAAAATTAAGCCAGA 134
          |||||
QY      122 CTTAGTGGCTCATCCCTGTGGTCCAGCTACTAGGAGGACAGAGTAAGTAAGTGTCT----- 176
          |||||
Db      135 TGTGTGTCCTAACGCTGTGTGTTCCAGCTACTCAGAGGCTGAGGACAGAGGTTGCTTG 194
          |||||
QY      177 TGTCCAGAGAGTCAAGACTGCACTGAGCTGAGACCCAGCCACCTGCATTCCAGCTGGG 236
          |||||
Db      195 AGCCAGAGAGGTGAGGTTGCACTGAGCTGAGATGGGCCA-CTGCACACACAGCTGGG 253
          |||||
QY      237 CAACAAAAGAGACCCCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 289
          |||||
Db      254 CAACAGAGCCAGACTTATCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 306
          |||||
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Job time : 924.76 secs
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 22:44:48 ; Search time 13.4962 Seconds
(without alignments)
4040.340 Million cell updates/sec

Title: US-09-869-098a-1_COPY_255_717
Perfect score: 463
Sequence: 1 acctgtaattccagctactgt.....attctcccttgacag 463

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 246837 seqs, 58886990 residues
Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_New:*
1: /EMC_Celerra_SIDS3/pcodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/pcodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/pcodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/pcodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/pcodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/pcodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/pcodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/pcodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	30.0	2312	US-11-293-697-880	Sequence 880, App
2	136.8	29.5	54550	US-11-318-813-42	Sequence 42, Appl
3	134.6	29.1	2252	US-11-293-697-1292	Sequence 1292, Ap
4	132	28.5	2374	US-11-293-697-441	Sequence 441, App
5	130.2	28.1	3226	US-11-293-697-723	Sequence 723, App
6	129.8	28.0	4156	US-10-511-937-453	Sequence 453, App
7	129.6	28.0	4987	US-10-505-928-433	Sequence 433, App
8	129.6	28.0	4987	US-11-251-465-4	Sequence 4, Appli
9	129.6	28.0	5014	US-11-251-465-5	Sequence 5, Appli
10	129.6	27.9	2682	US-11-293-697-1324	Sequence 1324, Ap
11	128.6	27.8	54550	US-11-318-813-42	Sequence 42, Appl
12	128.2	27.7	3097	US-11-293-697-1206	Sequence 1206, Ap
13	127.8	27.6	2889	US-10-511-937-627	Sequence 627, App
14	127.8	27.6	2889	US-11-293-697-2187	Sequence 2187, Ap
15	127.2	27.5	2140	US-11-293-697-513	Sequence 513, App
16	126.8	27.4	2460	US-11-293-697-595	Sequence 595, App
17	126.8	27.4	2915	US-11-293-697-59	Sequence 59, Appl
18	126.4	27.3	2849	US-11-293-697-404	Sequence 404, App
19	126.2	27.3	1801	US-11-293-697-1829	Sequence 1829, Ap
20	126.2	27.3	2393	US-11-293-697-2395	Sequence 2395, Ap
21	126	27.2	394191	US-10-506-549-3	Sequence 3, Appli
22	125.6	27.1	1237	US-10-511-937-430	Sequence 430, App
23	125.6	27.1	138941	US-10-489-730-10	GENERAL INFORMATI
24	125.4	27.1	1853	US-11-293-697-2266	Sequence 2266, App
25	125.4	27.1	2105	US-11-293-697-122	Sequence 122, App

C 26	125.4	27.1	2949	7	US-11-293-697-426	Sequence 426, App
C 27	125	27.0	4086	7	US-11-301-554-1801	Sequence 1801, Ap
C 28	125	27.0	138941	6	US-10-489-730-10	GENERAL INFORMATI
29	124.6	26.9	2646	7	US-11-293-697-550	Sequence 550, App
30	124	26.8	1601	7	US-11-328-161-25	Sequence 25, Appl
31	124	26.8	1645	7	US-11-328-161-12	Sequence 12, Appl
32	124	26.8	2324	7	US-11-293-697-82	Sequence 82, Appl
33	124	26.8	3766	7	US-11-293-697-647	Sequence 647, App
34	124	26.8	5515	6	US-10-524-021-1	Sequence 1, Appli
35	123.8	26.7	1947	7	US-11-293-697-1980	Sequence 1980, Ap
36	123.8	26.7	2130	7	US-11-293-697-2246	Sequence 2246, Ap
C 37	123.8	26.7	2168	7	US-11-293-697-1286	Sequence 1286, Ap
C 38	123.8	26.7	2648	7	US-11-293-697-807	Sequence 807, App
C 39	123.4	26.7	2308	7	US-11-293-697-1274	Sequence 1274, Ap
40	123.4	26.7	56580	6	US-10-553-298-1	Sequence 1, Appli
41	123.2	26.6	1962	7	US-11-293-697-1638	Sequence 1638, Ap
42	123	26.6	1756	7	US-11-293-697-2159	Sequence 2159, Ap
C 43	123	26.6	2059	7	US-11-293-697-1623	Sequence 1623, Ap
44	122.4	26.4	1629	6	US-10-511-937-444	Sequence 444, App
45	122.4	26.4	2731	7	US-11-293-697-1412	Sequence 1412, Ap

ALIGNMENTS

RESULT 1
US-11-293-697-880
Sequence 880, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length CDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 880
LENGTH: 2312
TYPE: DNA
ORGANISM: Homo sapiens
US-11-293-697-880

Query Match 30.0%; Score 139; DB 7; Length 2312;
Best Local Similarity 76.2%; Pred. No. 7.4e-21;
Matches 211; Conservative 0; Mismatches 60; Indels 6; Gaps 3;

QY	1	ACCTGTAATTCAGTACTGTGAGAGTCGAGAGTCAAGAGACTGCTTGAGCCAGAGTTC	60
DB	1142	ACCTGTAATTCAGTACTGTGAGAGTCAAGAGTCAAGAGTCTGCTTGAGTTCAGAGATTTC	1201
QY	61	AAGAGCAGCTGAGCAACACAGGAGAC-CTGTCACTACAAAGTAATAATTAGCCA	119
DB	1202	AAGAGCAGCTGAGCAACATAGTGAAGCTTGCTTACAAATATATAAATAATTAGCTG	1261
QY	120	GGCTTAATGCTCATCTCTGTGTCCTCACTACTAGAGGACCAAGTAAGA---CTGC	175
DB	1262	GGCATGTGTGCACATGCTGTGTCCTCACTACTAGAGGACCAAGTGAAGTACT	1321
QY	176	TTGTCAGGAGGTCAGATGTCAGTGTGAGTCAAGCCAGCTGATTCAGGCTGG	235
DB	1322	TGAGCCAGGATGTCAGATGTCAGTGTGATTTGATTTGACACA-CTGCACTCCAGCTGG	1380
QY	236	GCAACAAAAGAGACCTGTCTCAAAAAATTAAGTTAA	272
DB	1381	GCAAGCAGAGCAAGACCCGCTTAACAAAGAAAATTA	1417
RESULT 2		US-11-318-813-42	
		Sequence 42, Application US/11318813	

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/ Publication No. US20060105381A1
/ GENERAL INFORMATION:
/ APPLICANT: Ellipsis Biotherapeutics Corporation
/ APPLICANT: Peltekova, Vanya D
/ APPLICANT: Siminovitsh, Katherine A
/ APPLICANT: St George-Hyslop, Peter H
/ APPLICANT: Rubin, Laurence A
/ APPLICANT: Peltekova, Vanya D
/ APPLICANT: Muntle, Richard F
/ TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSOCIATED WITH INFLAMMATORY BOWEL DISORDERS
/ FILE REFERENCE: ELP-020
/ CURRENT APPLICATION NUMBER: US/11/318,813
/ CURRENT FILING DATE: 2005-12-27
/ PRIOR APPLICATION NUMBER: US/10/327,188
/ PRIOR FILING DATE: 2002-12-20
/ PRIOR APPLICATION NUMBER: 60/362,700
/ PRIOR FILING DATE: 2002-03-08
/ PRIOR APPLICATION NUMBER: 60/343,338
/ PRIOR FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 60/427,529
/ PRIOR FILING DATE: 2002-11-19
/ PRIOR APPLICATION NUMBER: 60/362,717
/ PRIOR FILING DATE: 2002-03-08
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 42
/ LENGTH: 54550
/ TYPE: DNA
/ ORGANISM: Homo sapiens
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5 FEATURE:
6 NAME/KEY: misc feature
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8 OTHER INFORMATION: n can be a or t or g or c
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10 NAME/KEY: misc feature
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14 NAME/KEY: misc feature
15 LOCATION: (6668) . (6668)
16 OTHER INFORMATION: n can be a or t or g or c
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18 NAME/KEY: misc feature
19 LOCATION: (7458) . (7458)
20 OTHER INFORMATION: n can be a or t or g or c
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22 NAME/KEY: misc feature
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26 NAME/KEY: misc feature
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28 OTHER INFORMATION: n can be a or t or g or c
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30 NAME/KEY: misc feature
31 LOCATION: (7730) . (7730)
32 OTHER INFORMATION: n can be a or t or g or c
33 FEATURE:
34 NAME/KEY: misc feature
35 LOCATION: (8656) . (8656)
36 OTHER INFORMATION: n can be a or t or g or c
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38 NAME/KEY: misc feature
39 LOCATION: (9403) . (9403)
40 OTHER INFORMATION: n can be a or t or g or c
41 FEATURE:
42 NAME/KEY: misc feature
43 LOCATION: (9598) . (9598)
44 OTHER INFORMATION: n can be a or t or g or c
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47 LOCATION: (10245) . (10245)
48 OTHER INFORMATION: n can be a or t or g or c
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51 LOCATION: (10817) . (10817)
52 OTHER INFORMATION: n can be a or t or g or c
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Query Match	29.5%	Score 136.8	DB 7	Length 54550
Best Local Similarity	69.5%	Pred. No. 3.1e-20		
Matches 228	Conservative 0	Mismatches 94	Indels 6	Gaps 3

QY	2	CCGTGATATTCACATTA	CTGTGATAGAGT	CCGAGGTACAGAGAC	CTGTTGAGGCACGAGATTCA	61
Db	46202	CATGTAAATCCCA	CACACTTTTG	GGAGCCGAAAGT	GTGATCACTGAGGCCAGAGATTCA	46261
QY	62	AGAGCAGCCTTGACA	CAACACAGGGAGA	-CTGTGACTACAAAGATATTAATTTAGCCAG		120
Db	46262	AGACACAGCCTTG	CACAGCATGTGTA	AAACCCGTCTCTACTATTAATAATAATAATAATTAGCCAG		46321
QY	121	GCTTAGTGTGCTCAT	CCCTGTGTGTCC	CAGCTACTAGGAGGACGAAGTAGACCTGTGTG		179
Db	46322	GTGTGCTGTGGAC	GGGCTCTGTAAATCC	CGGCTCACTCTGAAGGCTGAGGTAGAGAAATTGCTT		46381
QY	180	----CCCA	GGAGGTCAAGAC	TCGACGTGACGACCAACCGACCTTGCATTTCCAGCCTGGG		236
Db	46382	GAACCCAGAGGG	CAGAGAGCTGC	CAGTAGATCAAAATTGCACCA-CTGCATCTTCAACCTGGG		46440

OY		237	CACCAAAAAGAGCCCTGTCCTCAAAAAATTAAGTTAAATAAATAAATAAATAAATGT	296
Dd		46441	CACAANAAGCAAACCTCGTCTCAGAAAATTAATAAATAAATAAATAAATAAGAATAA	46500
OY		297	AAACCTTAACACATCTCTTTTTCAAA	324
Dd		46501	ACACACAAATTACATTATATATCTTAA	46528

RESULT 3
US-11-293-697-1292

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Sequence 1292, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDN
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1292
LENGTH: 2252
TYPE: DNA
ORGANISM: Homo sapiens
US-11-293-697-1292

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Query Match	29.1%	Score 134.6	DB 7	Length 2252
Best Local Similarity	72.1%	Pred. No. 5.9e-20		
Matches 204	Conservative 0	Mismatches 74	Indels 5	Gaps 2

Qy	2	CCTGTAAATTCAGATACGTGTAGAGTCCGAGGTCAGAGAACTGTGAGGCGCAGAGTTCA	61
Db	1891	CCTGTAAATCCAGACCTTTGGGATTGGAGAGTGGGCGGATTCACCTTGAGGTGAGAGTTCA	1956
Qy	62	AGAGCAGCCTTGAGCAACACAGGGAGACCTGTCACTACAAAGATTAATTAATTGCCAGG	121
Db	1951	AGACCAACCTGGCCMAATGGTATMAAACCGCTCTCACTAACATTAACAAGATTGACCTGG	2010
Qy	122	CTTAGTGCTCATCCCTGTGGTCCAGACTACTAGGAGGAGAGTAAAGGA-----CTGCTT	177
Db	2011	TGTGTGTGGCAAGGGGCTGTAAATGGCAGGCCCCTTGGAAAGGCCAAGGCAGAGAAATCGCCTC	2070
Qy	178	GTCCCAGAGAGTCAAGACTGCAGTGAAGCTGAGACCCAGCACTTGCAATTCAGGCTTGCGC	237
Db	2071	AACACTGGAGGTGAGGTTGGCAGTGAAGCTGAGATTGGCA-CTGCACCTCAGGCTGGGC	2129
Qy	238	AACAAAAAGAGACCCCTGTCCAAAAATTAAGTTAAATAATTA	280
Db	2130	AATGAGCAAGACCTGTCTCAAAAAATTAATTAATTAATA	2172

RESULT 4

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US-11-293-697--441/C
? Sequence 441, Application US/11293697
? Publication No. US20060105376A1
? GENERAL INFORMATION:
? APPLICANT: HELIX RESEARCH INSTITUTE
? TITLE OF INVENTION: Novel full length cDNA
? FILE REFERENCE: H1-A0106
? CURRENT APPLICATION NUMBER: US/11/293,697
? PRIORITY FILING DATE: 2005-12-05
? PRIOR APPLICATION NUMBER: US/10/108,260
? PRIOR FILING DATE: 2002-03-28
? NUMBER OF SEQ ID NOS: 5458
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 441
? LENGTH: 2374
? TYPE: DNA
? ORGANISM: Homo sapiens

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SOFTWARE: PatentIn 3.2
SEQ ID NO 433
LENGTH: 4987
TYPE: DNA
ORGANISM: Homo sapiens
US-10-505-928-433

Query Match 28.0%; Score 129.6; DB 6; Length 4987;
Best Local Similarity 71.5%; Pred. No. 6.9e-19;
Matches 213; Conservative 0; Mismatches 79; Indels 6; Gaps 3;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTGAGAGAGTCTTGAGGCCAGAGTTCA 61
DB 3805 CCTGTATCTCAGACACTTTGGAGGCTGAGGTGGGCGAGATCACTTGAGTCAAGAGTTT 3746
QY 62 AGAGCAGCCTGGAACAACAGAGGAGA-CCTGTCACTCAAAAGATAAATAATTAGCCAG 120
DB 3745 AGACCAAGCTGGCCCAACATGAGTGAACCTGTCTCTAATAAATAAATAATTAGCCGG 3686
QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGTACTAGAGGAGCAGAAATAGGA---CTGCT 176
DB 3685 GTGTGGTGGACACACCTGTAAATCCAGCTACTTGGGAGGCCAAGGAGAAATATCACTT 3626
QY 177 TGTTCCAGAGGTCAAGACTGCACTGAGTGAAGACCAAGCCACTGATTCAGCCTGG 236
DB 3625 GAACCTGGTAGGTGAAGGTTGCAGTGAGCGAGATTGCACCA-CTGCATCTCAGCCTGG 3567
QY 237 CAACAAAAAGAGACCCCTGTCTCAAAAAATAAGTAATAATAATAATAATACT 294
DB 3566 TGACACAGTAGACTCTATCGCAAAAAAATAATAATAATAATAATAATAAGT 3509

RESULT 8
US-11-251-465-4/C

Sequence 4, Application US/11251465
Publication No. US20060094061A1
GENERAL INFORMATION:
APPLICANT: Brys, Reginald
APPLICANT: Vandeghinste, Nick
APPLICANT: Tomme, Peter
APPLICANT: Klaassen, Hubertus
TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
FILE REFERENCE: P30.172-A USA
CURRENT APPLICATION NUMBER: US/11/251.465
CURRENT FILING DATE: 2005-10-14
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 4987
TYPE: DNA
ORGANISM: Homo sapiens
US-11-251-465-4

Query Match 28.0%; Score 129.6; DB 7; Length 4987;
Best Local Similarity 71.5%; Pred. No. 6.9e-19;
Matches 213; Conservative 0; Mismatches 79; Indels 6; Gaps 3;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTGAGAGAGTCTTGAGGCCAGAGTTCA 61
DB 3805 CCTGTATCTCAGACACTTTGGAGGCTGAGGTGGGCGAGATCACTTGAGTCAAGAGTTT 3746
QY 62 AGAGCAGCCTGGAACAACAGAGGAGA-CCTGTCACTCAAAAGATAAATAATTAGCCAG 120
DB 3745 AGACCAAGCTGGCCCAACATGAGTGAACCTGTCTCTAATAAATAAATAATTAGCCGG 3686
QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGTACTAGAGGAGCAGAAATAGGA---CTGCT 176
DB 3685 GTGTGGTGGACACACCTGTAAATCCAGCTACTTGGGAGGCCAAGGAGAAATATCACTT 3626

QY 177 TGTTCCAGAGGTCAAGACTGCACTGAGTGAAGACCAAGCCACTGATTCAGCCTGG 236
DB 3625 GAACCTGGTAGGTGAAGGTTGCAGTGAGCGAGATTGCACCA-CTGCATCTCAGCCTGG 3567
QY 237 CAACAAAAAGAGACCCCTGTCTCAAAAAATAAGTAATAATAATAATAATACT 294
DB 3566 TGACACAGTAGACTCTATCGCAAAAAAATAATAATAATAATAATAATAAGT 3509

RESULT 9
US-11-251-465-5/C

Sequence 5, Application US/11251465
Publication No. US20060094061A1
GENERAL INFORMATION:
APPLICANT: Brys, Reginald
APPLICANT: Vandeghinste, Nick
APPLICANT: Tomme, Peter
APPLICANT: Klaassen, Hubertus
TITLE OF INVENTION: Molecular Targets And Compounds, And Methods To Identify The
TITLE OF INVENTION: Same, Useful In The Treatment Of Joint Degenerative And
FILE REFERENCE: P30.172-A USA
CURRENT APPLICATION NUMBER: US/11/251.465
CURRENT FILING DATE: 2005-10-14
PRIOR APPLICATION NUMBER: 60/619,384
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 880
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5
LENGTH: 5014
TYPE: DNA
ORGANISM: Homo sapiens
US-11-251-465-5

Query Match 28.0%; Score 129.6; DB 7; Length 5014;
Best Local Similarity 71.5%; Pred. No. 6.9e-19;
Matches 213; Conservative 0; Mismatches 79; Indels 6; Gaps 3;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTGAGAGAGTCTTGAGGCCAGAGTTCA 61
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QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGTACTAGAGGAGCAGAAATAGGA---CTGCT 176
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QY 177 TGTTCCAGAGGTCAAGACTGCACTGAGTGAAGACCAAGCCACTGATTCAGCCTGG 236
DB 3652 GAACCTGGTAGGTGAAGGTTGCAGTGAGCGAGATTGCACCA-CTGCATCTCAGCCTGG 3594
QY 237 CAACAAAAAGAGACCCCTGTCTCAAAAAATAAGTAATAATAATAATAATACT 294
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RESULT 10
US-11-293-697-1324

Sequence 1324, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTYTUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1

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OTHER INFORMATION: n	can be a	or t	or g	or c	
FEATURE:					
NAME/KEY: misc_feature					
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FEATURE:					
NAME/KEY: misc_feature					
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OTHER INFORMATION: n	can be a	or t	or g	or c	
FEATURE:					
NAME/KEY: misc_feature					
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OTHER INFORMATION: n	can be a	or t	or g	or c	
FEATURE:					
NAME/KEY: misc_feature					
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OTHER INFORMATION: n	can be a	or t	or g	or c	
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NAME/KEY: misc_feature					
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NAME/KEY: misc_feature					
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LOCATION: (5207) .. (5207)	n	can be a	or t	or g	or c
OTHER INFORMATION: n	can be a	or t	or g	or c	
FEATURE:					
NAME/KEY: misc_feature					
LOCATION: (6668) .. (6668)	n	can be a	or t	or g	or c
OTHER INFORMATION: n	can be a	or t	or g	or c	
FEATURE:					
NAME/KEY: misc_feature					
LOCATION: (7458) .. (7458)	n	can be a	or t	or g	or c
OTHER INFORMATION: n	can be a	or t	or g	or c	
FEATURE:					
NAME/KEY: misc_feature					
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OTHER INFORMATION: n	can be a	or t	or g	or c	
FEATURE:					
NAME/KEY: misc_feature					
LOCATION: (7687) .. (7687)	n	can be a	or t	or g	or c
OTHER INFORMATION: n	can be a	or t	or g	or c	
FEATURE:					
NAME/KEY: misc_feature					
LOCATION: (7730) .. (7730)	n	can be a	or t	or g	or c
OTHER INFORMATION: n	can be a	or t	or g	or c	
FEATURE:					
NAME/KEY: misc_feature					
LOCATION: (8656) .. (8656)	n	can be a	or t	or g	or c

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1 OTHER INFORMATION: n can be a or t or g or
2 FEATURE:
3 NAME/KEY: misc_feature
4 LOCATION: (9403) .. (9403)
5 OTHER INFORMATION: n can be a or t or g or c
6 FEATURE:
7 NAME/KEY: misc_feature
8 LOCATION: (9598) .. (9598)
9 OTHER INFORMATION: n can be a or t or g or c
10 FEATURE:
11 NAME/KEY: misc_feature
12 LOCATION: (10245) .. (10245)
13 OTHER INFORMATION: n can be a or t or g or c
14 FEATURE:
15 NAME/KEY: misc_feature
16 LOCATION: (10817) .. (10817)
17 OTHER INFORMATION: n can be a or t or g or c
18 FEATURE:

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Query Match	27.8%;	Score 128.6;	DB 7;	Length 54550;
Best Local Similarity	72.5%;	Pred. No. 1.5e-18;		
Matches 208;	Conservative 0;	Mismatches 74;	Indels 5;	Gaps 3;

QY 1 AACTGTATTTCCAGTACTGTGAGAGTCCAGAGTCACAGAGACCTGCTTGAAGGCCAGAGATTTC 50

Db 16700 AACTGTATTTCCAGCACTTTGGGAGGCCGAGGCCGGGTGGTGTCTACCTGTAGAGGTTCAGAGATTTC 16644

QY 61 AAGAGCAGCCTCGACAAACACAGGGAGG - CCGTCACTACAAAGAATAATAATTAGCCA 119
Db 16640 AAGACCAAGCCTCGGTAACTGATGAAACCCCTGTCTTACTTAAATAGCAAAATAATGCTG 16588

QY	120	GGCTTAGTGGCTCATCCCTGTGTGTC	CCAAGTA	CTAAGGAGCAGAACTAGA	---	CTGCT	176
Db	16580	GGACGGTGGACAGTGCCTGTATCCCA	GCCTTA	CTTGGAGACTGAGCAGGAGAGTTGCT			
							16522

QY	177	TCGCCACGAGGTCACAGACTGCATGTAGTGTGACCCAGCCACTGCATTTCCAGCCTTGGG	236
Db	16520	TCAGCCTCGAGGCTGAGGTTGATGAGTAGCTAGATACACCA - CTCGACATTCAGACCTTGGG	16465

QY 237 CAACAAAAGAGACCTGTCTCAAAAAATAAGTTAATAATTAATA 283
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Db 16461 CACAAGAAGTGAAGTTCATCTCAACAACAACAACAACAACAACACTATA 16415

RESULT 12

US-11-293-697-1206/c
Sequence 1206. Application US/11293697

Publication No. US20060105376A1
; Publication No. US20060105376A1
GENERAL INFORMATION.

;; GENERAL INFORMATION:
;; APPLICANT: HELIX RESEARCH INSTITUTE

```

; TITLE OF INVENTION: Novel full length cd
; FILE REFERENCE: H1-A0106

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CURRENT APPLICATION NUMBER: US/11/293,699
CURRENT FILING DATE: 2005-12-05

PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE 2003-03-29

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; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 5458

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1206

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; LENGTH: 3097
; TYPE: DNA

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ORGANISM: Homo sapiens

0027-169-667-11-50

Query Match	27.7%	Score 128.2;	DB 7;	Length 3097;
Best Local Similarity	72.5%;	Pred. No. 1.3e-18;		
Matches 208: Conservative	0;	Mismatches 73;	Indels 6;	Gaps 3;

2 CCTGTATTCCAGTACTGTGAGAGTCCGAGGTGAGAGACTGCTTGAAGCCAGAGTTCA 61

Db 2323 CCGTAATCCAGCATTGGGAGGCCAAGGTGGGACAGATCATTGAGGCCAGGAGTTCA 2264

62 AGAGCAGCCTGSAACAACACAGGAGA - CTTGCTACTACAAGAATAAATTAGCCAG 120

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Db      2263 AGACCGAGCTAGCAACAGTGTAAATCCACTCTACTATAAATCAAAACTTACGTGG 2204
      121 GCTTACTGTGCTACTCCCTGTGCTCCAGCTACTAGGAGGACAAATAGGAGCTTGT- 179
      2203 GCATGTGTGTGACCCCTGTGTAGTCCAGCTACCCAGTAGCTGAGTAGGAGAAATTTGCTT 2144
      180 ---CCGAGAGGTCAAGACTGCAGTAGTGAAGCCAGCCACTGCATTCCAGCTGGG 236
      2143 GAACACGGGAGGAGAGGTTGACGTAGCGGAGATGTGCCA-CTGCATCTCCAGCTAGG 2085
      237 CAACAAAAAGAGACCTGTCTCAAAAAATAGTTAAATTAATTAATTAATTAATTAATTA 283
      2084 TGACAGAGAGAGACTGTCTCTACTATAAATAAATAAATAAATAAATAAATAAATAAATAA 2038

RESULT 13
US-10-511-937-627/c
; Sequence 627, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 627
; LENGTH: 2889
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-627

Query Match      27.6%; Score 127.8; DB 6; Length 2889;
Best Local Similarity 66.9%; Pred. No. 1.5e-18;
Matches 228; Conservative 0; Mismatches 107; Indels 6; Gaps 3;

      QY      2 CCTGTAAATTCGACTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAAGGCCAGAGTTCA 61
      DB      1753 CCTGTGAATCCACACTTTTGAGAGGCCAAGCGCGGAGATCACTTGAGTCAAGAGTTTG 1694
      QY      62 AGAGCAGCCTTGACAACAACAGGAGA-CCTGTCACTCAAAAGATAATTAATTAATTAAGCCAG 120
      DB      1693 AGACGAGCCTTGCGCGGAGATGTGAACCTTATCTCTAATAAATAAATAAATAATTAAGCCAG 1634
      QY      121 GCTTACTGTCTACTCCCTGTGTGCCAGCTACTAGGAGGACGAAGTAGA---CTGCT 176
      DB      1633 GCATGTGTGTGCGCTGTACTATGTCCAGCTACTTGGAGGCTGAGGCAAGAGAAATTCAT 1574
      QY      177 TGTCCTCAGAGGTCAAGACTGCAGTGAAGCCAGCACTGTGATTCGAGCTGGG 236
      DB      1573 GAACCCAGAGGAGGAGGTGACGTGAGTTGCACCA-CTGCATCTCCAGCTGGG 1515
      QY      237 CAACAAAAAGAGACCTGTCTCAAAAAATAGTTAAATTAATTAATTAATTAATTAATTAATTA 296
      DB      1514 CAACAGAGCAAGACTCCGTCTCAAAAAAGAAAAAGAAAAAGAAAAAGAAAAATGCAGAGTCT 1455
      QY      297 AAACCTTAAACATCTTTCTTTTCAAAAGAGACTTCTTAA 337
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Db      1454 TGGGCCCAACCCAGACTATTGAATCAGAGGCTTAAGTTTAA 1414

RESULT 14
US-11-293-697-2187/c
; Sequence 2187, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; PRIOR FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2187
; LENGTH: 2889
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-2187

Query Match      27.6%; Score 127.8; DB 7; Length 2889;
Best Local Similarity 66.9%; Pred. No. 1.5e-18;
Matches 228; Conservative 0; Mismatches 107; Indels 6; Gaps 3;

      QY      2 CCTGTAAATTCGACTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAAGGCCAGAGTTCA 61
      DB      1753 CCTGTGAATCCACACTTTTGAGAGGCCAAGCGCGGAGATCACTTGAGTCAAGAGTTTG 1694
      QY      62 AGAGCAGCCTTGACAACAACAGGAGA-CCTGTCACTCAAAAGATAATTAATTAATTAATTAAGCCAG 120
      DB      1693 AGACGAGCCTTGCGCGGAGATGTGAACCTTATCTCTAATAAATAAATAAATAATTAAGCCAG 1634
      QY      121 GCTTACTGTCTACTCCCTGTGTGCCAGCTACTAGGAGGACGAAGTAGA---CTGCT 176
      DB      1633 GCATGTGTGTGCGCTGTACTATGTCCAGCTACTTGGAGGCTGAGGCAAGAGAAATTCAT 1574
      QY      177 TGTCCTCAGAGGTCAAGACTGCAGTGAAGCCAGCACTGTGATTCGAGCTGGG 236
      DB      1573 GAACCCAGAGGAGGAGGTGACGTGAGTTGCACCA-CTGCATCTCCAGCTGGG 1515
      QY      237 CAACAAAAAGAGACCTGTCTCAAAAAATAGTTAAATTAATTAATTAATTAATTAATTAATTA 296
      DB      1514 CAACAGAGCAAGACTCCGTCTCAAAAAAGAAAAAGAAAAAGAAAAAGAAAAATGCAGAGTCT 1455
      QY      297 AAACCTTAAACATCTTTCTTTTCAAAAGAGACTTCTTAA 337
      DB      1454 TGGGCCCAACCCAGACTATTGAATCAGAGGCTTAAGTTTAA 1414

RESULT 15
US-11-293-697-513/c
; Sequence 513, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; PRIOR FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 513
; LENGTH: 2140
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-513
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Query Match 27.5%; Score 127.2; DB 7; Length 2140;
Best Local Similarity 70.5%; Pred. No. 1.9e-18;
Matches 213; Conservative 0; Mismatches 83; Indels 6; Gaps 3;

QY 2 CCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCAGAGGACTGCTTGAGCCAGAGTTCA 61
|||
Db 1834 CCTGTAAATCCAGCACTTTGGAGGCTGAGGCGGGCGGATTAATGAGGCCAGAGTTGG 1775
62 AGAGCAGCCTGAGACAGACAGGAGAG-CCTGTCACTACAAAGATTAATAATTAGGCAG 120
|||
Db 1774 AGACCAGCCTGGCCAGACATGCTGTAACCTGTCTCTACTAATACATACAAATTTAGTCGG 1715
QY 121 GCTTAGTGGCTCATCCCTGTGTGCCAGCTACTAGGAGGCGAGAGTAGGACTGCTTGT- 179
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Db 1714 GCATGTGGGCAATGCTGTAAATCCAGCTACTTGGGAGGCTGAGGACGAGAAATTGCTT 1655
QY 180 ---CCGAGAGGTCAAGACTGCACTGAGAGCCAGCCACTGCATTCCAGCCTGGG 236
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Db 1654 GAACTCAGAGGTGAGGTTGCACTGAGCCAAAGATCATGCCA-CTACACTCCAGCCTGGG 1596
QY 237 CAACAAAAGAGACCCTGTCTCAAAAATAAGTTAATAATAATAATAATAAGTTT 296
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Db 1595 AGACAGAACGAGACTCCCTCTGAAACAACAAGAAAATCATTAGGAGAGAAAATGGAAT 1536
QY 297 AA 298
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Db 1535 AA 1534

Search completed: June 6, 2006, 00:22:35
Job time : 15.4962 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using bw model

Run on: June 5, 2006, 16:15:46 ; Search time 2823.19 Seconds
(without alignments)
9445.379 Million cell updates/sec

Title: US-09-869-098a-1_COPY_717_1133

Perfect score: 417
Sequence: 1 gccacgggaggaacattcttg.....gctctggctccctcagctgt 417

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_env: *
2: gb_pat: *
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5: gb_pr: *
6: gb_ro: *
7: gb_sts: *
8: gb_un: *
9: gb_vi: *
10: gb_ov: *
11: gb_hcg: *
12: gb_in: *
13: gb_om: *
14: gb_ba: *
15: gb_ba: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	417	100.0	3270	5	AF306570	AF306570 Homo sapi
2	417	100.0	3505	2	ES4511	ES4511 UCP-2 promo
3	417	100.0	12177	5	D0087219	D0087219 Homo sapi
4	417	100.0	155668	12	AC024029	AC024029 Homo sapi
5	417	100.0	156370	5	AP003717	AP003717 Homo sapi
6	417	100.0	199384	5	AP003531	AP003531 Homo sapi
7	405	97.1	3301	5	AF208500	AF208500 Homo sapi
8	400.2	96.0	197031	12	AC019121	AC019121 Homo sapi
9	87	20.9	7218	2	I66494	I66494 Sequence 14
10	76.4	18.3	170579	12	AC020985	AC020985 Homo sapi
11	76.4	18.3	179380	5	AL355501	AL355501 Human DNA
12	75.8	18.2	110000	4	AP008217_231	Continuation (232
13	75.8	18.2	128848	4	AC104844	AC104844 Oryza sat
14	74.4	17.8	154957	5	AC019270	AC019270 Homo sapi
15	74.4	17.8	160556	12	AC013645	AC013645 Homo sapi
16	74.4	17.8	170414	12	AC026019	AC026019 Homo sapi
17	74.4	17.8	197198	12	AC148630	AC148630 Callithrix
18	74.4	17.8	317499	12	AC117407	AC117407 Homo sapi

19	73.8	17.7	184251	12	AC173434	AC173434 Gorilla g
20	73.2	17.6	44515	5	AC114914	AC114914 Homo sapi
21	73.2	17.6	97129	5	HS292H14	AL008710 Human DNA
22	73.2	17.6	114279	12	AC083907	AC083907 Homo sapi
23	73.2	17.6	171941	12	AC026531	AC026531 Homo sapi
24	73.2	17.5	187927	5	AC046142	AC046142 Homo sapi
25	72.6	17.4	858	11	AY522982	AY522982 Colinus v
26	72.6	17.4	130119	12	AC117906	AC117906 Rattus no
27	72.6	17.4	161690	6	AC115697	AC115697 Mus muscu
28	72.6	17.4	211149	6	AC148019	AC148019 Mus muscu
29	72.6	17.4	236159	12	AC130109	AC130109 Rattus no
30	72.6	17.4	241381	6	AC087063	AC087063 Mus muscu
31	72.4	17.4	93767	5	AC136424	AC136424 Homo sapi
32	72.4	17.4	153596	5	AC008640	AC008640 Homo sapi
33	72	17.3	211343	6	AC152953	AC152953 Mus muscu
34	71.8	17.2	623	7	BV394629	BV394629 S243P619P
35	71.8	17.2	148950	5	CT027658	CT027658 Macaca mu
36	71.8	17.2	153726	5	AC120194	AC120194 Homo sapi
37	71.8	17.2	155468	5	AC022730	AC022730 Homo sapi
38	71.6	17.2	182847	12	AC126229	AC126229 Papio anu
39	71.6	17.2	188888	2	AX675240	AX675240 Sequence
40	71.6	17.2	188888	12	AC027142	AC027142 Homo sapi
41	71.6	17.2	193648	5	AC110926	AC110926 Homo sapi
42	71.6	17.2	193953	12	AC149623	AC149623 Papio anu
43	71.4	17.1	186038	6	AC117612	AC117612 Mus muscu
44	71.4	17.1	211604	6	AC113491	AC113491 Mus muscu
45	71	17.0	185608	12	AC149179	AC149179 Papio anu

ALIGNMENTS

RESULT 1
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LOCUS Homo sapiens uncoupling protein 2 gene, promoter region and exon 1;
DEFINITION nuclear gene for mitochondrial product.
ACCESSION AF306570
VERSION AF306570.1 GI:11037742
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 3270)
AUTHORS Schmeitler,C., Oberkofler,H., Baderbauer,H. and Patsch,W.
TITLE UCP2 promoter region and exon 1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3270)
AUTHORS Schmeitler,C., Oberkofler,H., Baderbauer,H. and Patsch,W.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2000) Laboratory Medicine, Landeskranken
Salzburg, Mueller Hauptstr. 48, Salzburg A-5020, Austria
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1..3270
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q13"
1..3117
1318..3241
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/note="UCP2"
3118..3241
/number=1
exon

ORIGIN

Query Match 100.0%; Score 417; DB 5; Length 3270;
Best Local Similarity 100.0%; Pred. No. 5e-103;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGGGGAGCAATTTTGGTCTGCAGAGCCTTTCATCTGTCTGTGCTCAGCAAT 60
DB 1632 GCCAGGGGAGCAATTTTGGTCTGCAGAGCCTTTCATCTGTCTGTGCTCAGCAAT 1691
QY 61 CTCACAGCAAAATTTGGCGAGCCTCTCCGAAATGCACAGCCAGACAGAGCTCAGCGCAAA 120
DB 1692 CTCACAGCAAAATTTGGCGAGCCTCTCCGAAATGCACAGCCAGACAGAGCTCAGCGCAAA 1751
QY 121 GCTAGAGAACTGGCGAGAGGAGACTCAGATGCCACAAAAAACTTTATCTTTCTTT 180
DB 1752 GCTAGAGAACTGGCGAGAGGAGACTCAGATGCCACAAAAAACTTTATCTTTCTTT 1811
QY 181 TTTTTCCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 240
DB 1812 TTTTTCCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1871
QY 241 CTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 300
DB 1872 CTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1931
QY 301 AATTAATCTGCTTGAATTTTCCAGCGCTGCTTCCAGAGACCATGCGTCCGCGT 360
DB 1932 AATTAATCTGCTTGAATTTTCCAGCGCTGCTTCCAGAGACCATGCGTCCGCGT 1991
QY 361 GTTTTCTTTCGCTAATTAATTCAGAGCCCATCCAGCTCTGCTCCCTCAGCTGT 417
DB 1992 GTTTTCTTTCGCTAATTAATTCAGAGCCCATCCAGCTCTGCTCCCTCAGCTGT 2048

RESULT 2
B54511 3505 bp DNA linear PAT 31-JAN-2002
LOCUS B54511
DEFINITION UCP-2 promoter and use thereof.
ACCESSION B54511.1 GI:16629692
VERSION JP 2000236886-A/1.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 3505)
AUTHORS Toyocari, Y., Kobayashi, M. and Igaki, S.
TITLE UCP-2 promoter and use thereof
JOURNAL Patent: JP 2000236886-A 1 05-SEP-2000;
TAKEDA CHEM IND LTD
OS Homo sapiens (human)
PN JP 2000236886-A/1
PD 05-SEP-2000
PF 22-DEC-1999 JP 1999364724
PR

PI YUKIO TOYOCARI, MAKOTO KOBAYASHI, SHIGERU IGAKI
PC C12N15/09, A61K45/00, A61P3/04, A61P9/06, A61P9/10, A61P9/12, PC
A61P9/00, C12N1/21,
PC C12N5/10, C12Q1/02, G01N33/15, G01N33/50, A61K31/711, A61K8/00,
PC A61K48/00,
PC C12N15/09, C12R1:19, (C12N15/09, C12R1:91), (C12N1/21, C12R1:19),
PC (C12N15/10, C12R1:91), (C12N15/00, C12N5/00, A61K37/02, (C12N15/00,
PC C12R1:19),
PC (C12N15/00, C12R1:91), (C12N5/00, C12R1:91)
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CCT
FH
FT
FT

FEATURES
source 1. .3505 Location/Qualifiers
1. .3505 /organism="Homo sapiens (human)".
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 417, DB 2; Length 3505;
Best Local Similarity 100.0%; Pred. No. 5e-103;

Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCCAGGGGAGCAATTTTGGTCTGCAGAGCCTTTCATCTGTCTGTGCTCAGCAAT 60
DB 717 GCCAGGGGAGCAATTTTGGTCTGCAGAGCCTTTCATCTGTCTGTGCTCAGCAAT 776
QY 61 CTCACAGCAAAATTTGGCGAGCCTCTCCGAAATGCACAGCCAGACAGAGCTCAGCGCAAA 120
DB 777 CTCACAGCAAAATTTGGCGAGCCTCTCCGAAATGCACAGCCAGACAGAGCTCAGCGCAAA 836
QY 121 GCTAGAGAACTGGCGAGAGGAGACTCAGATGCCACAAAAAACTTTATCTTTCTTT 180
DB 837 GCTAGAGAACTGGCGAGAGGAGACTCAGATGCCACAAAAAACTTTATCTTTCTTT 886
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QY 241 CTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 300
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QY 301 AATTAATCTGCTTGAATTTTCCAGCGCTGCTTCCAGAGACCATGCGTCCGCGT 360
DB 1017 AATTAATCTGCTTGAATTTTCCAGCGCTGCTTCCAGAGACCATGCGTCCGCGT 1076
QY 361 GTTTTCTTTCGCTAATTAATTCAGAGCCCATCCAGCTCTGCTCCCTCAGCTGT 417
DB 1077 GTTTTCTTTCGCTAATTAATTCAGAGCCCATCCAGCTCTGCTCCCTCAGCTGT 1133

RESULT 3
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LOCUS D0087219
DEFINITION Homo sapiens uncoupling protein 2 (mitochondrial, proton carrier)
ACCESSION D0087219 GI:67515418
VERSION D0087219.1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 12177)
AUTHORS Livingston, R.J., Rieder, M.J., Shaffer, T., Bertucci, C., Baler, C.N.,
Rajkumar, N., Wille, H.T., Daniels, M., Downing, T.K., Stanaway, I.B.,
Nguyen, C.P., Gilderale, H., Cassidy, C.M., Johnson, E.J.,
Swanson, J.E., McFarland, I., Yool, B., Fair, C. and Nickerson, D.A.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-2005) Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA
COMMENT To cite this work please use: NIHIS-SNPs, Environmental Genome
Project, NIHIS B5451478, Department of Genome Sciences, Seattle, WA
(URL: <http://egp.gs.washington.edu>).

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variation
7952

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Best Local Similarity 100.0%; Pred. No.5.4e-103;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CTCACAGCAAAATTTGCCAGCCTCTCCGAAATGACAGCCAGACGCTCAGCGCAAA 120
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QY 121 GCTAGAGAACTTGGCGGAGGAGACTCAGATGCGCAAAAAAATTATCTTTCTTT 180
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QY 241 CTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 300
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DB 755 CTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 814
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QY 301 AAATTAATCTGCTGATCTGCTGCTTTCCAGCGCTGCTGCGAGACCGAGCGCT 360
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DB 815 AAATTAATCTGCTGATCTGCTGCTTTCCAGCGCTGCTGCGAGACCGAGCGCT 874
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RESULT 4
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LOCUS Homo sapiens chromosome 11 clone RP11-167N4, WORKING DRAFT
DEFINITION
SEQUENCE 15 unordered pieces.
AC024029
AC024029.3 GI:7230916
VERSION HTG; HTGS PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Bkaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
            1 (bases 1 to 155668)
REFERENCE 1 (bases 1 to 155668)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 155668)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT On Mar 13, 2000 this sequence version replaced gi:7109555.
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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information -----
Center project name: H.NR0167N04
Summary Statistics -----
Sequencing vector: M13, 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 146450 bases at least Q40
Consensus quality: 149629 bases at least Q40
Consensus quality: 151087 bases at least Q20
Insert size: 154268; agarose-fp
Quality coverage: 3.98 in Q20 bases; agarose-fp
Quality coverage: 4.38 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1807 1906: gap of unknown length
* 1907 4798: contig of 2892 bp in length
* 4799 4898: gap of unknown length
* 4899 7312: contig of 2414 bp in length
* 7313 7412: gap of unknown length
* 7413 11277: contig of 3865 bp in length
* 11278 11377: gap of unknown length
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* 14369 14468: gap of unknown length
* 14469 20130: contig of 5662 bp in length
* 20131 20230: gap of unknown length
* 20231 25513: contig of 5283 bp in length
* 25514 25614: gap of unknown length
* 25614 30765: contig of 5152 bp in length
* 30766 30865: gap of unknown length
* 30866 37337: contig of 6472 bp in length
* 37338 37437: gap of unknown length
* 37438 45571: contig of 8134 bp in length
* 45572 45671: gap of unknown length
* 45672 60199: contig of 14528 bp in length
* 60200 60299: gap of unknown length
* 60300 71424: contig of 11125 bp in length
* 71425 71524: gap of unknown length
* 71525 86218: contig of 14694 bp in length
* 86219 86318: gap of unknown length
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Best Local Similarity 100.0%; Pred. No.6.2e-103;
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DEFINITION
ACCESSION AP003717
VERSION AP003717.3 GI:20334343
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Molecular: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published only in Database (2001)
AUTHORS 2 (bases 1 to 156370)
TITLE 2 (bases 1 to 156370)
JOURNAL Submitted (04-JUN-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
E-mail:hattori@gsc.riken.go.jp; URL:http://hnp.gsc.riken.go.jp/;
Tel:81-45-503-9111; Fax:81-45-503-9170
COMMENT On Apr 26, 2002 this sequence version replaced gi:16904692.
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Best Local Similarity 100.0%; Pred. No.6.2e-103;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 44411 GCCAGGGGGACAATTTTGGTCTGACAGGCTTTGCATCTGTTGCTGCTCAGCAAT 44352
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DB 44291 GCTAGAGAACTGGCGGAGGAGGACCTCAGTGCCACAAAAAACTTATCTTTCTTT 44232
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ACCESSION	AF208500		
VERSION	AF208500.1	GI:6684000	
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	Hominidae; Homo.		
REFERENCE	1 (bases 1 to 3301)		
AUTHORS	Tu,N., Chen,H., Wilmkes,U., Reinert,I., Marmann,G., Pirke,K.M. and Lentes,K.U.		
TITLE	Molecular cloning and functional characterization of the promoter region of the human uncoupling protein-2 gene		
JOURNAL	Biochem. Biophys. Res. Commun. 265 (2), 326-334 (1999)		
PUBMED	10558866		
REFERENCE	2 (bases 1 to 3301)		
AUTHORS	Tu,N., Chen,H., Wilmkes,U., Reinert,I., Pirke,K.M. and Lentes,K.-U.		
TITLE	Functional characterization of the 5'-flanking and promoter regions of the human UCP3 gene		
JOURNAL	Biochem. Biophys. Res. Commun. (2000) In press		
PUBMED	3 (bases 1 to 3301)		
REFERENCE	Lentes,K.-U., Tu,N.O. and Chen,H.		
AUTHORS	Direct Submissions		
TITLE	Submitted (26-NOV-1999) Laboratory of Molecular Neurogenetics,		
JOURNAL	Center for Psychobiological and Psychosomatic Research, University of Trier, Friedrich-Wilhelm-Strasse 23, Trier D-54290, Germany		
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1903	GCTAGAGAACTGGGGGAGGGAGACTCAAGTCCAAAAAATTATCTTTCTTT							
181	TTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
1963	TTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
241	CTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
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361	GTATTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
2143	GTATTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
121	CTGAGAGAACCTGGGGGAGGGGAGATCAACAGGCCAAGAAAAAATTATCTTTCTTT	AC019121	Homo sapiens chromosome 11 clone RP11-535C12, WORKING DRAFT	AC019121	3	GI:8440022	HTG; HTGS_PHASE1; HTGS_DRAFT.	Homo sapiens (human)
1903	GCTAGAGAACTGGGGGAGGGAGACTCAAGTCCAAAAAATTATCTTTCTTT							
181	TTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
1963	TTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
241	CTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
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361	GTATTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
2143	GTATTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
121	CTGAGAGAACCTGGGGGAGGGGAGATCAACAGGCCAAGAAAAAATTATCTTTCTTT	AC019121	Homo sapiens chromosome 11 clone RP11-535C12, WORKING DRAFT	AC019121	3	GI:8440022	HTG; HTGS_PHASE1; HTGS_DRAFT.	Homo sapiens (human)
1903	GCTAGAGAACTGGGGGAGGGAGACTCAAGTCCAAAAAATTATCTTTCTTT							
181	TTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
1963	TTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
241	CTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
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301	AAATATCTGGCTTGAACCTCTGTTTCCACAGCGCTTCCAGAGACATTCCTCAGTGGCT							
2083	AAATATCTGGCTTGAACCTCTGTTTCCACAGCGCTTCCAGAGACATTCCTCAGTGGCT							
361	GTATTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
2143	GTATTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
121	CTGAGAGAACCTGGGGGAGGGGAGATCAACAGGCCAAGAAAAAATTATCTTTCTTT	AC019121	Homo sapiens chromosome 11 clone RP11-535C12, WORKING DRAFT	AC019121	3	GI:8440022	HTG; HTGS_PHASE1; HTGS_DRAFT.	Homo sapiens (human)
1903	GCTAGAGAACTGGGGGAGGGAGACTCAAGTCCAAAAAATTATCTTTCTTT							
181	TTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
1963	TTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
241	CTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
203	CTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
301	AAATATCTGGCTTGAACCTCTGTTTCCACAGCGCTTCCAGAGACATTCCTCAGTGGCT							
2083	AAATATCTGGCTTGAACCTCTGTTTCCACAGCGCTTCCAGAGACATTCCTCAGTGGCT							
361	GTATTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
2143	GTATTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							
121	CTGAGAGAACCTGGGGGAGGGGAGATCAACAGGCCAAGAAAAAATTATCTTTCTTT	AC019121	Homo sapiens chromosome 11 clone RP11-535C12, WORKING DRAFT	AC019121	3	GI:8440022	HTG; HTGS_PHASE1; HTGS_DRAFT.	Homo sapiens (human)
1903	GCTAGAGAACTGGGGGAGGGAGACTCAAGTCCAAAAAATTATCTTTCTTT							
181	TTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT							

	* as soon as it is available and the accession number will
	* be preserved.
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	2971: contig of 2971 bp in length
	2972
	3071: gap of unknown length
	3072
	5764: contig of 2693 bp in length
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	5864: gap of unknown length
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	8568: contig of 2704 bp in length
	8569
	8668: gap of unknown length
	8669
	12865: contig of 4197 bp in length
	12866
	12966: gap of unknown length
	12967
	18581: contig of 5616 bp in length
	18582
	18681: gap of unknown length
	23851: contig of 5170 bp in length
	23852
	23951: gap of unknown length
	23952
	28414: contig of 4463 bp in length
	28415
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	33195: contig of 4681 bp in length
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	33295: gap of unknown length
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	38648: contig of 5353 bp in length
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	38748: gap of unknown length
	38749
	44925: contig of 6177 bp in length
	44926
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	45026
	51784: contig of 6759 bp in length
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	51884: gap of unknown length
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	58955: gap of unknown length
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	77223: gap of unknown length
	87292: contig of 10065 bp in length
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	96029: contig of 8637 bp in length
	96030
	96129: gap of unknown length
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	104791: contig of 8662 bp in length
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	104892
	116512: contig of 12021 bp in length
	116513
	117012: gap of unknown length
	117013
	131368: contig of 14355 bp in length
	131369
	131468: gap of unknown length
	142993: contig of 11525 bp in length
	142994
	143093: gap of unknown length
	143094
	154361: contig of 11266 bp in length
	154362
	154461: gap of unknown length
	154462
	173802: contig of 19341 bp in length
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Matches 413; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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DB 163820 GCCAGGGGAGCAATTTTGGTCGACGAGCCCTTGACATCTGTCGTGTCACCAAT 163879

QY 61 CTCACGCAAAATTTGCCGAGCCCTCTCCGAAATGCAAGCCACAGACCTCAGCGCAAA 120
DB 163880 CTCACGCAAAATTTGCCGAGCCCTCTCCGAAATGCAAGCCACAGACCTCAGCATAA 163939

QY 121 GCTAGGAACCTGGGAGGAGGAGACTCACAGTGCACAAAACCTTATCTTTCTTTT 180
DB 163940 TCTAGGAACCTGGGAGGAGGAGACTCACAGTGCACAAAACCTTATCTTTCTTTT 163999

QY 181 TTTTTCCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 240
DB 164000 TTTTTCCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 164059

QY 241 CTGCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 300
DB 164060 CTGCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 164119

QY 301 AATTAATCGCCCTTGACTTCTGTTTCCAGCTGCTCTGCAAGACATGCGCTCGCGCT 360
DB 164120 AATTAATCGCCCTTGACTTCTGTTTCCAGCTGCTCTGCAAGACATGCGCTCGCG-CT 164178

QY 361 GTTTTCTTTCCGCTAATTAATTAATCAAGCCCATCCAGCTCTGCTCCCTCACTGT 417
DB 164179 GTTTTCTTTCCGCTAATTAATTAATCAAGCCCATCCAGCTCTGCTCCCTCACTGT 164235

RESULT 9
166494 7218 bp DNA linear PAT 28-DEC-1997
LOCUS 166494
DEFINITION Sequence 14 from patent US 5670367.
ACCESSION 166494
VERSION 166494.1 GI:2724471
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 7218)
AUTHORS Dörner, F., Scheiflinger, F. and Falkner, F. Gunter.
TITLE Recombinant fowlpox virus
JOURNAL Patent: US 5670367-A 14 23-SBP-1997;
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ORIGIN

Query Match 20.9%; Score 87; DB 2; Length 7218;
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Matches 12; Conservative 197; Mismatches 72; Indels 0; Gaps 0;

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QY 191 TTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 250
DB 1106 TTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1165

QY 251 TTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 310
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RESULT	LOCUS	DEFINITION
10	AC020985	Homo sapiens chromosome 10 clone RP11-10H9 map 10, WORKING DRAFT SEQUENCE, 12 unordered pieces.
	AC020985	170579 bp DNA linear HTG 24-AUG-2002

ACCESSION	AC020985
VERSION	AC020985.4
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Carnivora; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

1 (bases 1 to 170579)
Barren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 10, clone RP11-10H9
Unpublished
2 (bases 1 to 170579)
Barren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

Andereson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavsky, L., Bouhkgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArrellano, K., Dewar, K., Domino, M., Doyle, M., Feneator, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heatford, A., Horton, I., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczy, J., Levine, R., Lien, C., Liu, G., Locke, K., Macdonald, P., Margulis, N., McEwan, P., McGuirk, A., McKernan, K., MCPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rotlman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teefave, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmerman, A. and Zody, M.

TITLE Direct Submission
JOURNAL Submitted (12-JUN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 170579)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beta, F., Boguslavsky, L., Bouhgalter, B., Brown, A., Burnett, G., Campopiano, A., Castle, A., Chopelet, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Deaellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galegan, J., Gardyna, S., Ginde, S., Goeyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heatford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karztas, A., Klein, J., Larocque, K., Lamazartes, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N., McCarthy, M., McEwan, P., McGarr, A., McKernan, K., McPeeters, R., Meldrum, J., Menus, L., Mihov, T., Miranda, C., Mlenka, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Olivier, T.M., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rotman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tassaye, S., Theodore, J., Tirrell, A., Traversas, M., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J. Young, G., Zahoun, J., Zimmer, A. and Zody, M.

TITLE Direct Submission
JOURNAL Submitted (24-ANG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Apr 8, 2000 this sequence version replaced gi:6850480.

All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) <http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www.gcr.wi.mit.edu>

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Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: I2007

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Center project name: B200
Center clone name: 10_H_9
----- Summary Statistics -----
Sequencing vector: M13: M7

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Chemistry: Pre-terminator Big Dye 1: 100% of reads
Assembly program: Phrap version 960731
Consensus quality: 161810 bases at least Q40
Consensus quality: 16410 bases at least Q30
Consensus quality: 167595 bases at least Q20
Insert size: 186000; agarose-fp
Insert size: 165475; sum-of-contigs
Quality coverage: 4.4 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

*	1	2603	conf:ig of 2602 bp in length
*	2	2702	gap of 100 bp
*	3	2703	4785: conf:ig of 2063 bp in length
*	4	4766	4865: gap of 100 bp
*	5	4866	10221: conf:ig of 5356 bp in length
*	6	10222	10331: gap of 100 bp
*	7	10322	15905: conf:ig of 5584 bp in length
*	8	15906	16005: gap of 100 bp
*	9	16006	21519: conf:ig of 5514 bp in length
*	10	21520	29771: gap of 100 bp
*	11	21620	29721: conf:ig of 8102 bp in length
*	12	29722	29831: gap of 100 bp
*	13	29822	41470: conf:ig of 11649 bp in length
*	14	41471	41570: gap of 100 bp
*	15	41571	58157: conf:ig of 16587 bp in length
*	16	58158	58257: gap of 100 bp
*	17	58258	78134: conf:ig of 19877 bp in length
*	18	78135	78234: gap of 100 bp
*	19	78235	100028: conf:ig of 21794 bp in length
*	20	100029	100128: gap of 100 bp
*	21	100129	121594: conf:ig of 21466 bp in length
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[illegible]

ACCESSION	AL355501
VERSION	AL355501.26
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE	1 (bases 1 to 179380)
AUTHORS	Kay, M.
TITLE	Direct Submission
JOURNAL	Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
COMMENT	Clone request: clonesanger.ac.uk On Aug 31, 2001 this sequence version replaced gi:1432545.

The following abbreviations are used to associate primary access numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMMPP; Information on the WORMMPP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpp This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Ch10> RP11-360P7 is from the library RPc1-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.Chori.org/bacpac/home.htm>

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: vega@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digests, except on the rare occasion of the clone being a YAC.

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	join(complement(89736. .89864), complement(46294. .46461), complement(9879. .9997),

Db 154732 CTTTCC 154727

RESULT 12
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WPCOMMENT

Sequence split into 284 fragments LOCUS AP008217 Accession AP008217

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AP008217_006	600001	710000
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AP008217_008	800001	910000
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AP008217_010	1000001	1110000
AP008217_011	1100001	1210000
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LOCUS	AC104844/c	128848 bp	DNA	linear	PIN 22-JAN-2004
DEFINITION	Oryza sativa (japonica cultivar-group)	chromosome 11	BAC clone		
ACCESSION	AC104844				
VERSION	AC104844.2	GI:11058064			
KEYWORDS	HTG.				
SOURCE	Oryza sativa (japonica cultivar-group)				
ORGANISM	Oryza sativa (japonica cultivar-group)				
REFERENCE	1 (bases 1 to 128848)				
AUTHORS	Khurana, J.P., #Linton, E.W., #Messing, J., *Yu, Y., *Rambo, T., *Currie, J., *Collura, K., *Soderlund, C., *Wing, R., Gaur, A., Raghuvanshi, S., Khurana, P., and Tyagi, A.K.				
JOURNAL	Submitted (21-DEC-2001) Indian Initiative for Rice Genome Sequencing, Department of Plant Molecular Biology, University of Delhi South Campus, New Delhi, Delhi 110021, India				
REMARK	# The Plant Genome Initiative at Rutgers - Waksman Institute, Rutgers University 190 Frelinghuysen Road, Piscataway, NJ 08873, USA				
REFERENCE	2 (bases 1 to 128848)				
AUTHORS	Khurana, J.P., #Linton, E.W., #Messing, J., Mohanty, A., Bharti, A.K., Raghuvanshi, S., Khurana, P., and Tyagi, A.K.				
JOURNAL	Submitted (21-DEC-2001) Indian Initiative for Rice Genome Sequencing, Department of Plant Molecular Biology, University of Delhi South Campus, New Delhi, Delhi 110021, India				
REMARK	# The Plant Genome Initiative at Rutgers - Waksman Institute, Rutgers University 190 Frelinghuysen Road, Piscataway, NJ 08873, USA				
REFERENCE	3 (bases 1 to 128848)				
AUTHORS	Khurana, J.P., #Linton, E.W., #Messing, J., *Yu, Y., *Rambo, T., *Currie, J., *Collura, K., *Soderlund, C., *Wing, R., Gaur, A., Raghuvanshi, S., Khurana, P., and Tyagi, A.K.				
JOURNAL	Submitted (22-JAN-2004) Indian Initiative for Rice Genome Sequencing, Department of Plant Molecular Biology, University of Delhi South Campus, New Delhi, Delhi 110021, India				
COMMENT	On Jan 22, 2004 this sequence version replaced gi:11976554. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. There are Bacterial Transposons at base 4874-8468 and 101808-105050 and from base 104112-104122 there are only transposon reads. The assembly overlaps from base 113102-128848 with OSUNBa0034K24 (accession #AF161269). The overlap is from bases 127311-142852 on OSUNBa0034K24. The nucleotide sequence of this BAC clone was completed to Phase 2 jointly by the Indian Initiative for Rice Genome Sequencing Project and The Plant Genome Initiative at Rutgers, and Finished/Annotated (Phase 3) at the Arizona Genomics Institute under the Indo-USA collaboration.				
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[illegible]

REFERENCE	TITLE	COMMENT
4 (bases 1 to 154957)	Research, 320 Charles Street, Cambridge, MA 02141, USA	
Authors	Biten, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Baerentzen, V., Bloom, T., Boguslavsky, L., Bonkhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choquet, Y., Collange, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearrellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fato, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Glind, S., Gord, S., Goyette, M., Graham, L., Grand-pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kellis, C., Larocque, R., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Marguis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Menais, L., Mihova, T., Mleaga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhthang, P., Pierre, N., Pollara, V., Raymond, C., Retter, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rossetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Straus, K., Subramanian, A., Talamas, J., Teafaye, S., Theodore, J., Tophan, K., Travers, M., Travis, N., Triggillo, J., Vassaliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.	
Genome Center	Submitted (14-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	
Genome Center	On Feb 20, 2002 this sequence version replaced g1:1825020.	
Genome Center	All repeats were identified using RepeatMasker:	
Genome Center	Smit, A.F.A. & Green, P. (1996-1997)	
Genome Center	http://ftp.genome.washington.edu/RM/RepeatMasker.html	
Genome Center	Center: Whitehead Institute/ MIT Center for Genome Research	
Genome Center	Center code: MIBR	
Genome Center	Web site: http://www-seq.wi.mit.edu	
Genome Center	Contact: sequence_submissions@genome.wi.mit.edu	
Genome Center	Project Information	
Genome Center	Center project name: L3046	
Genome Center	Center clone name: 10_C_8	
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DEFINITION	Homo sapiens clone RP11-17H6, WORKING DRAFT SEQUENCE, 11 unordered pieces.
ACCESSION	AC013645
VERSION	AC013645.3
KEYWORDS	GI:7381812
SOURCE	HTG: HTGS PHASE1; HTGS_DRAFT.
ORGANISM	Homo sapiens (human)
	Homo saplens

REFERENCE	1 (bases 1 to 160556)
AUTHORS	Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE	Homo sapiens, clone RP11-17H6
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 160556)
AUTHORS	Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

Cooke, P., DeArrellano, K., Dewar, K., Domino, M., Donealán, L., Doyle, M.,
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Tešlaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W. J., Zimmer, A. and Zody, W.

TITLE Direct Submission
JOURNAL Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Apr 1, 2000 this sequence version replaced gi:6478998.

All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) <http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information -----

Center project name: L3643
Center clone name: 17_H 6

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----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
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Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 156212 bases at least Q40
Consensus quality: 157480 bases at least Q30

Consensus quality: 158348 bases at least Q20
Insert size: 157000; agarose-1p

Insert size: 159556; sum-of-contigs
Quality coverage: 7.7 in Q20 bases; agarose-gel

Quality coverage: 7.5 in Q20 bases; sum-of-contri

* NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces

* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1	1050: contig of 1050 bp in length
* 1051	1150: gap of 100 bp
* 1151	4281: contig of 3131 bp in length
* 4282	4381: gap of 100 bp
* 4382	12996: contig of 8615 bp in length
* 12997	13096: gap of 100 bp
* 13097	23548: contig of 10452 bp in length
* 23549	23648: gap of 100 bp
* 23649	36288: contig of 12640 bp in length
* 36289	36289: gap of 100 bp
* 36289	50226: contig of 13838 bp in length
* 50227	50326: gap of 100 bp
* 50327	63487: contig of 13161 bp in length
* 63488	63587: gap of 100 bp
* 63588	82132: contig of 18545 bp in length
* 82133	82232: gap of 100 bp
* 82233	101188: contig of 18956 bp in length
* 101189	101288: gap of 100 bp
* 101289	128638: contig of 27250 bp in length
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FEATURES

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Search completed: June 5, 2006, 22:27:11
Job time : 2830.19 Secs

Job time : 2830.19 sec

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:15:11 ; Search time 362.801 Seconds
(without alignments)
803.826 Million cell updates/sec

Title: US-09-869-098a-1_COPY_717_1133
Perfect score: 417
Sequence: 1 gccagcgggacacatttcgtg.....gtctcgtccctcagctgt 417

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq.8:*
1: geneeqn1980s:*
2: geneeqn1990s:*
3: geneeqn2000s:*
4: geneeqn2001s:*
5: geneeqn2001bs:*
6: geneeqn2002as:*
7: geneeqn2002bs:*
8: geneeqn2003as:*
9: geneeqn2003bs:*
10: geneeqn2003cs:*
11: geneeqn2003ds:*
12: geneeqn2004as:*
13: geneeqn2004bs:*
14: geneeqn2005s:*
15: geneeqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	417	100.0	3505	3	AAA62932 DNA cont
2	71.6	17.2	188888	6	ABQ75562 Human rel
3	70.4	16.9	1548	6	ABZ43078 Human GPC
4	70	16.8	472	9	ACH29376 Human adu
5	69.2	16.6	23122	10	ADL13693 Osteoarth
6	67.4	16.2	288563	14	AE805135 Cancer-as
7	67.2	16.1	3226	12	ADP28980 Human sec
8	67	16.1	1255	12	ADP28980 Human sec
9	67	16.1	277616	13	ABD32602 Human can
10	66.8	16.0	170834	10	AAD62833 Human BAC
11	66	15.8	180821	10	ADL13761 Osteoarth
12	65.6	15.7	3583	12	ADO23651 Human sof
13	65.4	15.7	849	5	AA89073 DNA enco
14	65.4	15.7	1073	12	AD148332 Maize oil
15	65.4	15.7	11456	4	AAK69400 Human imm
16	65.4	15.7	37590	4	AA512439 DNA enco
17	65.4	15.7	99544	14	AD213273 Human can
18	65.4	15.7	99588	11	ACN45034 Human gen

C	19	65.4	15.7	144392	15	AEF75162 Human pol
	20	65.4	15.7	272022	12	ADQ97126 Human can
	21	65.2	15.6	563	5	ABV50724 Human pro
	22	65.2	15.6	42998	8	ADA14747 Human rib
	23	65.2	15.6	42999	6	AB865032 Invertebr
	24	65.2	15.6	42999	10	AD61411 Human rib
	25	65.2	15.6	42999	13	ADR43949 Human rib
	26	65.2	15.6	42999	14	AB25475 Human rib
	27	65	15.6	432	5	ABV58007 Human pro
	28	64.6	15.5	504	5	ABV58626 Human pro
	29	64.6	15.5	42999	8	ABX11086 Human rib
	30	64.6	15.5	89625	11	ACN45194 Human gen
	31	64.4	15.4	1096	10	AD14268 Human enz
	32	64.4	15.4	5845	6	AB13663 Human enz
	33	64	15.3	73465	6	ABO88161 Human ost
	34	63.8	15.3	248	13	ACN55172 Human car
	35	63.8	15.3	392	5	ABV48356 Human pro
	36	63.6	15.3	712	4	AAE81806 Human sec
	37	63.6	15.3	1121	15	AEF30075 Lead Cere
	38	63.6	15.3	3578	13	ADR07968 Full leng
	39	63.6	15.3	8317	4	AA835779 Human car
	40	63.6	15.3	8317	10	AD646473 Human car
	41	63.6	15.3	8317	13	ADJ07891 Human car
	42	63.6	15.3	330973	11	ACN44846 Human gen
	43	63.4	15.2	540	5	ABV58372 Human pro
	44	63.4	15.2	770	4	AA195041 Human neu
	45	63.4	15.2	1840	10	ADC87550 Human GPC

ALIGNMENTS

RESULT 1	AAA62932	standard; DNA; 3505 BP.
ID	AAA62932	
XX	AAA62932;	
AC	02-NOV-2000	(first entry)
DT	DNA containing human uncoupling protein-2 (UCP-2) promoter region.	
XX	Promoter; human; uncoupling protein-2; UCP-2; obesity; diabetes;	
KW	hypotension; hyperlipidaemia; anti-pyretic; ds.	
KM	Homo sapiens.	
OS	WO200039315-A1.	
XX	06-JUL-2000.	
PD	22-DEC-1999;	99WO-JP007198.
PF	24-DEC-1998;	98JP-00366719.
XX	(TAKE) TAKEDA CHEM IND LTD.	
PA	Toyoda Y, Kobayashi M, Igaki S;	
XX	WPI; 2000-452407/39.	
DR	DNA with promoter region containing regulator sequence of uncoupling	
PT	protein-2 (UCP-2), applicable in screening anti-obesity, anti-diabetic,	
PT	hypotensive, anti-hyperlipidemic and anti-pyretic drugs for use in	
XX	therapy.	
PS	Claim 4; Fig 1-6; 43pp; Japanese.	
XX	This invention relates to DNA comprising a promoter region containing the	
CC	regulatory sequences of human uncoupling protein-2 (UCP-2). Included in	
CC	the invention are a recombinant vector containing the DNA sequence, cells	
CC	transformed by the vector, and a method for screening for compounds or	
CC	salts that can promote or inhibit the UCP-2 promoter activity using the	

CC transformants. The DNA and cells transformed using it can be used to
 CC screen for anti-obesity, anti-diabetic, hypotensive, anti-hyperlipidaemic
 CC and anti-pyretic drugs. The present sequence represents DNA containing
 CC the UCP-2 promoter sequences

XX SQ Sequence 3505 BP; 671 A; 1053 C; 894 G; 887 T; 0 U; 0 Other;

Query Match 100.0%; Score 417; DB 3; Length 3505;
 Best Local Similarity 100.0%; Pred. No. 2.5e-79;

Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAGGCGGACAAATTTGGTCTGACAGGCGCTTGCATCTGTTCTGCTGCTACCAAT 60
 DB 717 GCCAGGCGGACAAATTTGGTCTGACAGGCGCTTGCATCTGTTCTGCTGCTACCAAT 776
 QY 61 CTCACGCAAAATTTGCGAGCCCTCCGAAATGCAAGGCGACAGGCTCAGCGCAAA 120
 DB 777 CTCACGCAAAATTTGCGAGCCCTCCGAAATGCAAGGCGACAGGCTCAGCGCAAA 836
 QY 121 GCTAGAGAACTGGCGAGGAGACTCACAGTCCCAAAAAAATTATCTTTCTTT 180
 DB 837 GCTAGAGAACTGGCGAGGAGACTCACAGTCCCAAAAAAATTATCTTTCTTT 896
 QY 181 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 240
 DB 897 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 956
 QY 241 CTGCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 300
 DB 957 CTGCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 1016

QY 301 AATAATATGCTGCTTGAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 360
 DB 1017 AATAATATGCTGCTTGAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1076

QY 361 GTTTTTCTTTCCGCTAT 417
 DB 1077 GTTTTTCTTTCCGCTAT 1133

RESULT 2
 ABQ75562/c
 ID ABQ75562 standard; DNA; 18888 BP.

AC ABQ75562;

DT 11-NOV-2002 (first entry)

DE Human related CYP 27C1 clone Rp11-30F3 SEQ ID NO:21.

XX Cloning; characterisation; human; cytochrome P450; CYP 27C1; cytostatic;
 KM chryomimetic; antidiabetic; antiprositic; tuberculostatic; osteoparitic;
 KM dermatological; antilipemic; gene therapy; vaccine; vitamin D; diabetes;
 KM vitamin D metabolite deficiency; hyperparathyroidism; hypoparathyroidism;
 KM medullary carcinoma; psoriasis; sarcoidosis; tuberculosis; osteomalacia;
 KM chronic renal disease; vitamin D dependent rickets; anticonvulsant;
 KM fibrogenesis imperfecta ossium; osteitis fibrosa cystica; osteoporosis;
 KM osteoparitis; osteoclastosis; renal osteodystrophy; rickets; steatorrhea;
 KM glucocorticoid antagonism; idiopathic hypercalcaemia; tropical sprue;
 KM malabsorption syndrome; cholesterol steroid; lipid metabolic disorder;
 KM gene; de.

OS Homo sapiens.

PN MO200264765-A2.

XX 22-AUG-2002.

XX 11-FEB-2002; 2002MO-CA000163.

XX 09-FEB-2001; 2001US-0267410P.

XX (CYTO-) CYTOCHROME INC.

XX WIPI; 2002-657595/70.

XX New nucleic acid molecules encoding cytochrome P450 proteins, human CYP
 PT 27C1 and a hybrid homologs from Xenopus laevis, useful for treating
 PT diseases related to vitamin D or vitamin D metabolite deficiency, e.g.
 PT parathyroidism and diabetes.

XX Example 1; Fig 1A; 209pp; English.

XX The present invention describes an isolated nucleic acid molecule (1)
 CC encoding human cytochrome P450, CYP 27C1, and a hybrid homologe from
 CC xenopus laevis. (1) has chryomimetic, antidiabetic, cyostatic,
 CC antiprositic, tuberculostatic, osteoparitic, dermatological and
 CC antilipemic activities, and can be used in gene therapy and in vaccines.
 CC The nucleic acid molecules, proteins and methods from the present
 CC invention are useful for treating diseases related to vitamin D or
 CC vitamin D metabolite deficiency, e.g. hyper- and hypo-parathyroidism,
 CC pseudohypo-parathyroidism, secondary hyperparathyroidism, diabetes,
 CC medullary carcinoma, psoriasis, sarcoidosis, tuberculosis, chronic renal
 CC disease, hypophosphatemic VDR, vitamin D dependent rickets,
 CC anticonvulsant treatment, fibrogenesis imperfecta ossium, osteitis
 CC fibrosa cystica, osteomalacia, osteoporosis, osteoparitis, osteoclastosis,
 CC renal osteodystrophy, rickets, glucocorticoid antagonism, idiopathic
 CC hypercalcaemia, malabsorption syndrome, steatorrhea, and tropical sprue,
 CC or cholesterol, steroid and other lipid metabolic disorders. The present
 CC sequence represents a human related CYP 27C1 clone designated Rp11-30F3,
 CC which is given in an example from the present invention

XX SQ Sequence 18888 BP; 51055 A; 42661 C; 43560 G; 47708 T; 0 U; 3904 Other;

Query Match 17.2%; Score 71.6; DB 6; Length 18888;

Best Local Similarity 78.2%; Pred. No. 2e-05;

Matches 86; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 165 CTTATCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 224
 DB 44890 CTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 44831

QY 225 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 274
 DB 44830 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 44781

AC AB243078;

DT 06-MAR-2003 (first entry)

DE Human GPCR polynucleotide SEQ ID NO 417.

XX Human GPCR polynucleotide SEQ ID NO 417.

XX Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
 KM drug development; gustatory; taste; fragrance; gene; de.

OS Homo sapiens.

PN MO200216548-A2.

XX 28-FEB-2002.

XX 30-JUL-2001; 2001MO-IB001446.

XX 04-AUG-2000; 2000JP-00237818.

XX 13-FEB-2001; 2001JP-00034434.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Haga T, Takeda S, Mitaku S;

PI

XX	WPI: 2002-304118/34.
DR	P-P8DB; ABP95804.
PR	Database global search for G protein-coupled receptors, proteins and
PT	encoded genes for studying in vivo signal transduction mechanism and
PT	identifying targets for drug development.
XX	
XX	Claim 9; SEQ ID NO 417; 97pp + Sequence Listing; Japanese.
PS	
CC	The invention relates to a method for screening G protein-coupled
CC	receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-
CC	ABP95982) by extracting open-reading frames containing 6-8 transmembrane
CC	domains with 250-1000 amino acid residues to give a gene homologous with
CC	a known GPCR gene. The receptor proteins and encoded genes are useful for
CC	studying in vivo signal transduction mechanism and identifying targets
CC	for drug development e.g. based on olfactory and gustatory receptors in
CC	form of agonists and antagonists by screening intrinsic and extrinsic
CC	ligands as bitter taste inhibitors, taste enhancers and fragrance
CC	improvers. Note: The sequence data for this patent did not form part of
CC	the printed specification, but was obtained in electronic format directly
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences
SQ	
Sequence	1548 BP; 577 A; 219 C; 320 G; 332 T; 0 U; 100 Other;
Query Match	16.9%; Score 70.4; DB 6; Length 1548;
Best Local Similarity	78.2%; Pred. No. 1.6e-05;
Matches	97; Conservative 0; Mismatches 26; Indels 1; Gaps 1;
OY	168 TATCTTTCTTTTTTTTTTCTTTCTTTCTTTCTTTCTTTCTTGTCGTTTCGTTCTT 227
Db	1148 TCTCTTTCTTTTAATTATTTTCTTTCTTTCTTTCTTTCTTTCTTC-TCTTTCTTTCTC 10950
OY	228 CCTCTCTCTCTCGTCGTCTTTCTTTCTTTCTTTCTTTCTTTTCCACAGCAAGAT 287
Db	1089 TTCTTTTCTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCCCTCC 1030
OY	288 CTCC 291
Db	1029 CTCCTC 1026
RESULT 4	
ACH29376/C	
ID	ACH29376 standard; cDNA; 472 BP.
XX	
AC	ACH29376;
DT	
XX	
DT	13-OCT-2003 (first entry)
XX	
DE	Human adult spleen cDNA #395.
XX	
KM	Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
XX	genome mapping; biodiversity; genetic disorder.
OS	Homo sapiens.
XX	
PN	US2003073623-A1.
PD	
XX	17-APR-2003.
PF	
XX	30-JUL-2001; 2001US-00918995.
PR	
XX	30-JUL-2001; 2001US-00918995.
PA	(DRAVA/) DRMANAC R T.
PA	(LABA/) LABAT I.
PA	(STAC/) STACHE-CRAIN B.
PA	(DICK/) DICKSON M C.
PA	(JONE/) JONES L W.
PI	Dymanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX	

[illegible]

XX	WIPI; 2003-559141/52.
PT	Determining susceptibility of an individual to joint space narrowing,
PT	osteophyte development and/or joint pain comprises identifying whether
PT	the individual has at least one polymorphism in a polynucleotide encoding
PT	a protein.
PS	Disclosure; SEQ ID NO 225; 297pp; English.
XX	The invention relates to a method of determining susceptibility of an
CC	individual to joint space narrowing and/or osteophyte development and/or
CC	joint pain comprising identifying whether the individual has at least one
CC	polymorphism in a polynucleotide encoding at least one of the protein
CC	listed in the specification. The methods, composition and agent are
CC	useful for modulating the susceptibility of an individual to joint space
CC	narrowing and/or osteophyte development and/or joint pain that is
CC	associated with a disease, preferably osteoarthritis. The cell line and
CC	the non-human animal are useful for screening for an agent for diagnosing
CC	an individual having susceptibility to joint space narrowing and/or
CC	osteophyte development and/or joint pain. This sequence corresponds to
CC	the polynucleotide encoding a protein listed in the specification. (Note:
CC	The sequence data for this patent did not form part of the printed
CC	specification but was obtained in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences).
SQ	Sequence 231222 BP; 64006 A; 52087 C; 53478 G; 61650 T; 0 U; 1 Other;
Query Match	16.6%; Score 69.2; DB 10; Length 231222;
Best Local Similarity	75.4%; Pred. No. 6.8e-05;
Matches	86; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
OY	166 TTATCTTTTCTTTTTTTTCTTTCTTTCTTTCTTTCTTTGTCGTCTCT 225
DB	85899 TCTTCTTTTCTTTCCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 85840
OY	226 TTCGCCTCCTCGCTGCTTCTTCTTCTTCTTCTTCTTCTTTTCCACAT 279
DB	85839 TTTCTTTTCTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 85786
RESULT 6	
AEB05135	
ID	AEB05135 standard; DNA; 288563 BP.
XX	AEB05135;
AC	
XX	
DT	26-JAN-2006 (first entry)
XX	
DE	Cancer-associated gene SEQ ID NO:453.
XX	
KW	ds; cancer; microarray; hybridoma; monoclonal antibody; screening;
KW	RNA interference; diagnosis; cytostatic; neoplasm; gene.
XX	
OS	Mus sp.
XX	
PN	WO2005107396-A2.
XX	
PD	17-NOV-2005.
XX	
PF	02-MAY-2005; 2005WO-US014965.
XX	
PR	30-APR-2004; 2004US-00836956.
XX	
PA	(CHIR) CHIRON CORP.
XX	
FI	Morris DW, Melandro MS, Lai A, Tee C, Fatcaey A;
XX	
DR	WIPI; 2005-769640/78.
XX	
PT	New cancer-associated (CA) polynucleotide comprising at least 10
PT	contiguous nucleotides, useful in preparing a composition for diagnosing
PT	or treating cancer.

XX		Diclosure; SEQ ID NO 453; 148bp; English.
PS		The invention relates to new isolated cancer-associated nucleic acid and
CC		polypeptide sequences. Also included are the following: a host cell
XX		comprising the recombinant nucleic acid or expression vector; an
CC		expressing vector comprising the isolated nucleic acid; a microarray for
CC		detecting a cancer associated (CA) nucleic acid comprising at least one
CC		probe comprising at least 10 contiguous nucleotides of the sequence given
CC		in the specification; an isolated polypeptide encoded within an open
CC		reading frame of a CA sequence; an isolated antibody or its antigen
CC		binding fragment that binds to the polypeptide; a hybridoma that produces
CC		the monoclonal antibody; a kit for detecting cancer cells comprising the
CC		antibody; a kit for diagnosing the presence of cancer in a test sample,
CC		comprising at least one polynucleotide that selectively hybridizes to a
CC		CA polynucleotide sequence; a method for detecting a presence or an
CC		absence of cancer cells in an individual; an electronic library
CC		comprising the polynucleotide or polypeptide or its fragment comprising
CC		the CA polynucleotide or polypeptide sequence, or its complement; a
CC		method of screening for anticancer activity; a method for detecting
CC		cancer associated with expression of a polypeptide in a test cell sample;
CC		a method for screening for a bioactive agent capable of modulating the
CC		activity of a CA protein (CAP), where the CAP is encoded by the nucleic
CC		acid sequence given in the specification; a method for diagnosing cancer;
CC		a method for treating cancer; and a method for inhibiting expression of a
CC		cancer associated (CA) gene in a cell. Inhibiting expression of a cancer
CC		associated (CA) gene in a cell comprises contacting a cell expressing a
CC		CA gene with a double stranded RNA comprising a sequence capable of
CC		hybridizing to a cancer associated (CA) mRNA corresponding to the
CC		polynucleotide sequences given in the specification, in an amount
CC		sufficient to elicit RNA interference and inhibiting expression of the CA
CC		gene in the cell. The double stranded RNA is provided by introducing a
CC		short interfering RNA (siRNA) into the cell by transfection,
CC		electroporation or microinjection. The double stranded RNA is provided by
CC		introducing a short interfering RNA (siRNA) into the cell by an
CC		expression vector. The polynucleotides are useful in preparing a
CC		composition for diagnosing or treating cancer. The present sequence
CC		represents a cancer-associated DNA of the invention. Note: This sequence
CC		is not shown in the specification but was obtained in electronic format
CC		directly from WIPO at
CC		ftp.wipo.int/pub/published_pct_sequences/17.11.2005/.
XX		Sequence 288563 BP; 78385 A; 61331 C; 62963 G; 83030 T; 0 U; 2854 Other;
SQ		
	Query Match	16.2%; Score 67.4; DB 14; Length 288563;
	Best Local Similarity	71.2%; Pred. No. 0.00017;
	Matches 89; Conservative 0; Mismatches 36; Indels 0; Gaps 0;	
OY	166 TTATCTTTCTTTTTTTTTTTCCTTCTTCTTCTGCTCTTGCTGTGCTCT	225
DB	17138 TCTCTCTCTCTTTTCTTTTCTCTTTCATCTCTTCTCTTCTCTTCTTTCTT	17139
OY	226 TTCCTCTCTCTCTGCTCTTCTTCCCTCTTCTTCTTCTTCCACATGGCAG	285
DB	17198 TTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTGAACAAG	1725
OY	286 ATCTC 290	
DB	17258 TTTTC 17262	
RESULT 7		
ADK00688/c		
ID	ADK00688 standard; DNA; 3226 BP.	
XX		
AC	ADK00688;	
XX		
DT	06-MAY-2004 (first entry)	
XX		
DE	HOMO protein encoding sequence #33.	
XX		
KW	cancer; Cytostatic; cancer; ds; HOMO; de.	
XX		


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XX      WPI; 2004-348438/32.
DR
XX      New nucleic acid molecule for diagnosing, preventing or treating diseases
PT      such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT      genetic, bacterial and viral diseases.
XX      Claim 1; SEQ ID NO 978; 428bp; English.
XX
CC      The present invention relates to an isolated nucleic acid molecule
CC      encoding a polypeptide which is believed to be cytostatic,
CC      antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC      composition and methods are useful for diagnosing, preventing and
CC      treating diseases such as proliferative (e.g. cancer), inflammatory,
CC      immune, metabolic, genetic, bacterial and viral diseases. The present
CC      sequence represents a human secreted protein encoding sequence. The
CC      present sequence is available on WIPOWEB and is not in the specification.
XX
SQ      Sequence 1755 BP, 715 A, 325 C, 396 G, 319 T, 0 U, 0 Other;
XX
Query Match          16.1%; Score 67; DB 12; Length 1755;
Best Local Similarity 76.6%; Pred.No.8.9e-05;
Matches    82; Conservative   0; Mismatches   25; Indels   0; Gaps   0
OY      165 CTCTATCTTTCTTCTTTTTTTCTTTCTTTCTTCCTGCTCCTTGCTGTC 224
DB      1450 CTTCCTTTTCTTCTTTCTTTCTTTCTTTCTTTCTTCGTCTTTCTTCT 139
OY      225 TTTCCTCGCTCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTTT 271
DB      1390 CTCCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1344
RESULTS 9
ABD32602
ID ABD32602 standard; DNA; 277616 BP.
AC ABD32602;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated genomic DNA HD7-221.
XX
KM Human; ds; cancer-associated protein; gene; cytosstatic; cancer;
KM Leukaemia; lymphoma; CAP.
OS Homo sapiens.
PN WO2004074320-A2.
PD 02-SEP-2004.
PF 17-FEB-2004; 2004WO-US004730.
PR 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-00388838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-0066431.
PR 15-DEC-2003; 2003US-00737318.
PA (SAGR-) SAGRES DISCOVERY INC.
PI Morris DW, Morris DW, Malandro MS;
DR WPI; 2004-652914/63.
XX
New isolated cancer-associated polynucleotides and polypeptides useful
for diagnosing, preventing or treating cancers, especially lymphoma and
leukemia, or in screening for agents that modulate cancer.
claim 16; seqid 109; 310pp; English.

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CC The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP genomic sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://wipo.int/pub/published_pat_sequences

[illegible]

[illegible][illegible]

CC	The invention relates to a recombinant DNA construct comprising a
CC	promoter functional in plants operably linked to an oil-associated gene.
CC	The construct is useful for transgenic plant seed which has in its genome
CC	the construct, that is functional in the plant to transcribe the oil-
CC	associated gene. The transgenic plant seed grows into a plant having
CC	enhanced seed oil as compared to wild type. The construct is useful for
CC	producing hybrid maize seed. The transgenic plant seed is useful for
CC	producing vegetable oil. The present sequence represents a maize oil-
CC	associated gene.
SQ	Sequence 1073 BP; 358 A; 259 C; 232 G; 224 T; 0 U; 0 Other;
OY	Query Match 15.7%; Score 65.4; DB 12; Length 1073;
Db	Best Local Similarity 65.3%; Pred.No. 0.00018;
	Matches 96; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
Oy	166 TTATCTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTCTTCCTTTCTTGTCGTCT 225
Db	713 TT 654
Oy	226 TTCCTCTCTCTCTGTCGCTTCCTTCCTCTCTTCCTTTTCTTCATGCAG 285
Db	653 TTTGATAAAGAAGAC 594
Oy	286 ATCTCCTCATGGCAGAAATATCTGCC 312
Db	593 TTGTTTATTGTTTAATAAATGAAGATC 567
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DT	06-NOV-2001 (first entry)
XX	
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24212.
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KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX	cytostatic; gene therapy; vaccine; metastasis; ds.
OS	Homo sapiens.
PN	WO200157182-AZ.
PD	
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BD	09-AUG-2001.
PF	
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PR	17-JAN-2001; 2001WO-US001354.
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PR	24-FEB-2000; 2000US-0184664P.
PR	02-MAR-2000; 2000US-0186350P.
PR	16-MAR-2000; 2000US-0186374P.
PR	17-MAR-2000; 2000US-0190076P.
PR	18-APR-2000; 2000US-0198123P.
PR	19-MAY-2000; 2000US-0205515P.
PR	07-JUN-2000; 2000US-0209467P.
PR	28-JUN-2000; 2000US-0214886P.
PR	30-JUN-2000; 2000US-0215135P.
PR	07-JUL-2000; 2000US-0216647P.
PR	07-JUL-2000; 2000US-0216880P.
PR	11-JUL-2000; 2000US-0217487P.
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PR	14-AUG-2000; 2000US-0225213P.
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PR	17-NOV-2000;	2000US-0249300P.
PR	01-DEC-2000;	2000US-0250160P.
PR	01-DEC-2000;	2000US-0250391P.
PR	05-DEC-2000;	2000US-0251030P.
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PR	06-DEC-2000;	2000US-0251479P.
PR	08-DEC-2000;	2000US-0251856P.
PR	08-DEC-2000;	2000US-0251868P.
PR	08-DEC-2000;	2000US-0251869P.
PR	08-DEC-2000;	2000US-0251989P.
PR	11-DEC-2000;	2000US-0251990P.
PR	05-JAN-2001;	2001US-0259678P.
PA	(HUMA-) HUMAN GENOME SCI INC.	
PI	Rosen CA, Barash SC, Ruben SM;	
XX	WPI; 2001-483426/52.	
XX	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	
PT	useful for preventing, diagnosing and/or treating cancers and metastasis.	
XX	Disclosure; SEQ ID NO 24212; 3071pp + Sequence Listing; English.	
XX	AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)	
CC	amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic	
CC	activity, and can be used in gene therapy and vaccine production. (I)	
CC	proteins and polynucleotides may be used in the prevention, diagnosis and	
CC	treatment of diseases associated with inappropriate (I) expression. For	
CC	example, they may be used to treat disorders associated with decreased	
CC	expression by rectifying mutations or deletions in a patient's genome	
CC	that affect the activity of (I) by expressing inactive proteins or to	
CC	supplement the patients own production of (I). Additionally, (I)	
CC	polynucleotides may be used to produce the secreted (I), by inserting the	
CC	nucleic acids into a host cell and culturing the cell to express the	
CC	protein. (I) proteins and polynucleotides may be used to prevent,	
CC	diagnose and treat immune/hematopoietic-related diseases, especially	
CC	cancers and cancer metastases of haematopoietic-derived cells. AAK64703	
CC	to AAK87694 represent human immune/haematopoietic antigen genomic	
CC	sequences from the present invention. AAK54942 to AAK54950 and AAM82169	
CC	represent sequences used in the exemplification of the present invention	
XX	Sequence 11456 BP; 2782 A; 2596 C; 2910 G; 3168 T; 0 U; 0 Other;	
SQ		

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Query Match      15.7% ; Score 65.4 ; DB 4 ; Length 11456 ;
Best Local Similarity 75.7% ; Pred. No. 0.00027 ;
Matches      81 ; Conservative    0 ; Mismatches   26 ; Indels     0 ; Gaps       0 ;

QY      166 TTATACCTTTCCTTTTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTGTCGTCT 225
DB      8489 TCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 8548

QY      226 TTCTCTCTCTCTCTCTCTCTCTTTCTTTCTCTCTTTCTTTCTTTT 272
DB      8549 TTCTCTCTCTCTCTCTTTCTCTCTCTCTCTCTTTCTTTT 8595

Search completed: June 5, 2006, 16:57:54
Job time : 366.801 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:39:00 / Search time 2887.54 Seconds
(without alignments)
8075.514 Million cell updates/sec

Title: US-09-869-098a-1_COPY_717_1133

Perfect score: 417
Sequence: 1 gccacgggggacatttgg.....gctctgtccctcagctgt 417

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	276.4	66.3	941	2	BG720951 602692616
2	227	54.4	314	2	AA903751 OK64C05.8
3	75.8	18.2	574	12	CE084870 tigr-gss-
4	72.8	17.5	831	11	AQ748216 HS_5536_A
5	72.8	17.5	558	10	DT851628 DT851628
6	72.6	17.4	285	1	AA267532 m272h06.x
7	72.6	17.4	477	12	CE462296 CE462296
8	72.4	17.4	712	12	CE389737 tigr-gss-
9	72.4	17.4	659	10	DT850178 DT850178
10	72.2	17.3	997	14	CNS0057E
11	71.8	17.2	1611	14	AG381869 Mus muscu
12	71.6	17.2	610	12	CE430482 tigr-gss-
13	71.6	17.2	468	2	CE616821 tigr-gss-
14	71.4	17.1	819	10	DM258451 tigr-gss-
15	71.2	17.1	480	3	BU950798 tigr-gss-
16	71	17.0	480	3	BU950798 tigr-gss-
17	70.6	16.9	305	10	CE136219 tigr-gss-
18	70.6	16.9	354	12	CE136219 tigr-gss-
19	70.6	16.9	354	12	CE136219 tigr-gss-

C 20	70.4	16.9	355	11	BZ25143
C 21	70.4	16.9	428	11	AQ557186
C 22	70	16.8	401	2	BM354761
C 23	70	16.8	688	8	CV664201
C 24	70	16.8	781	8	CV664201
C 25	70	16.8	1387	12	CL019342
C 26	69.8	16.7	226	12	CE033446
C 27	69.8	16.7	764	12	CE543174
C 28	69.6	16.7	1344	14	AG332055
C 29	69.6	16.7	646	10	DV850851
C 30	69.6	16.7	1210	14	AG340857
C 31	69.6	16.7	1322	12	CL078946
C 32	69.4	16.6	513	12	CE495836
C 33	69.4	16.6	532	12	CE199619
C 34	69.4	16.6	533	12	CE182651
C 35	69.4	16.6	610	10	DT459589
C 36	69.4	16.6	845	7	BF616304
C 37	69.4	16.6	885	3	BU957927
C 38	69.4	16.6	1239	14	AG280281
C 39	69.2	16.6	435	1	A1753542
C 40	69.2	16.6	554	12	CE427799
C 41	69	16.5	344	12	CE790240
C 42	69	16.5	501	12	CE738683
C 43	69	16.5	697	14	AG047727
C 44	68.8	16.5	387	12	CE571324
C 45	68.8	16.5	429	5	CF123422

ALIGNMENTS

RESULT 1
BG720951/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 941)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (MIGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E.B. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E.B. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10737 row: 0 column: 03
High quality sequence stop: 666.
Location/Qualifiers
1. 941
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4825178"
/lab_host="DH10B"
/clone_lib="NIH MGC 97"
/note="Organ: testis; Vector: pBluescript (modified
pBluescript KS+); site_1: BamHI, site_2: SalI-xhoI
(gtagag); Oligo-dT primed using primer
5'-TTTTTTTTTTTNN-3', size-selected for average
insert size 2.2 kb and normalized to R0T 5. This is a

ORIGIN

primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NIHRI, National Institutes of Health). Note: this is a NIH-MGC Library."

Query Match 66.3%; Score 276.4; DB 2; Length 941;
Best Local Similarity 91.8%; Pred. No. 4.5e-49;
Matches 349; Conservative 0; Mismatches 21; Indels 10; Gaps 5;

QY 47 TGTTCCTCAGCATTCACAGCAATTTGGCGAGCCCTCCGGAATGACACAGCCAGAG 106
DB 702 TGTTCCTCAGCATTCACAGC-AAATTTGCCAGCCCTCCGGAATGACACAGCCAGAG 644

QY 107 AGCTCAGCGCAAGTAGAGAACTGGCGAGGAGACACAGTGCACAAATAACT 166
DB 643 AGCTCAGCGCAAGTAGAGAACTGGCGAGGAGACACAGTGCACAAATAACT 584

QY 167 TTAATC---TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 222
DB 583 TTAATCAGTTCCGGTGGTTGTTCTGTTCTTTCTTTCTTTCTTTCTTTCTTTCTG 524

QY 223 TCTTTCT 278
DB 523 TCTTTCT 464

QY 279 TGGCAAGATCTCTCATGAGCAAAATATGCTGACTTCTGTTTCCAGCGTCTCT 338
DB 463 TGGCAAGATCTCTCATGAGCAAAATATGCTGACTTCTGTTTCCAGCGTCTCT 404

QY 339 GCCAGAGACATGCGCTCGCGGTGTTTCTTTCCGCTATAA-TTAATCAGGCCATCCCA 397
DB 403 GCCAGAGACATGCGCTCGCGGTGTTTCTTTCCGCTATAAATATCAGGCCATCCCA 344

QY 398 GCTCTGCT 417
DB 343 GCTCTGCT 324

RESULT 2 314 bp mRNA linear EST 09-JUN-1998
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LOCUS OK6405.g1 NCI CGAP G4 Homo sapiens cDNA clone IMAGE:1518728 3'
DEFINITION similar to gb:X17360_fna1 HOMBOX PROTEIN HOX-D4 (HUMAN); mRNA
sequence.
AA903751
VERSION AA903751.1 GI:3038874
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 314)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bdnp/image/image.html
Insert Length: 521 Std Error: 0.00
Seq primer: -40m13 fwd. R from Amersham
High quality sequence stop: 297.
Location/Qualifiers

FEATURES

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/tissue_type="pooled germ cell tumors"
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/note="Vector: pT73D-Pac1; 1st strand cDNA was prepared
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to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 54.4%; Score 227; DB 1; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-38;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 311 CCTTGACTTCTGTTTCCAGCTGCTTCTGCGAGACATGCGCTCGGCGTCTTCTT 370
DB 121 CCTTGACTTCTGTTTCCAGCTGCTTCTGCGAGACATGCGCTCGGCGTCTTCTT 180

QY 371 CCGCTATTAATTATCCAGGCCCATCCAGCTCTGCTCCCTCAGCTGT 417
DB 181 CCGCTATTAATTATCCAGGCCCATCCAGCTCTGCTCCCTCAGCTGT 227

RESULT 3 574 bp DNA linear GSS 24-SEP-2003
CE084870
LOCUS tigr-gss-dog-1700035898436 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
CE084870
VERSION CE084870.1 GI:35151716
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 574)
AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, D.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org
Class: shotgun
Location/Qualifiers

FEATURES

1. 574
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_id="Dog Library"

Db 310 GCCTGACTTCCTGTTCCACGCTGCTTCGACAGAACATGCGCGTGTTCCTT 369
Qy 342 TTAATGGCTCATGTATGAGAAATGCTTTGGGGGACAAATGGCTTCGGGTGTCAA 283
Db 370 TCCGCTAATATATTCACAGGCCCATCCAGCTCTGTCCTCCCTCAGCTCT 417
Qy 282 TGTAGTGTGACATCTGATTTCTCCCACTTCAGCTCCTCTGCTGT 235

RESULT 6
AA267532/c 285 bp mRNA linear EST 21-MAR-1997
LOCUS m272h06.r1 Soares mouse lymph node NbMUN Mus musculus cDNA clone
DEFINITION IMAGE:719003 5' similar to gb:X75947 M.musculus mCBP mRNA (MOUSE);
AA267532
VERSION AA267532.1 GI:1904267
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Mus.
REFERENCE 1 (bases 1 to 285)
Maire, M., Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Theissenberg, K., Stepec, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:444439
Seq primer: -28m3 rev2 ET from Amersham
High quality sequence stop: 204.
Location/Qualifiers
1..285
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/mol_type="mRNA"
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/clone_lib="IMAGE:719003"
/sex="male"
/issue_type="lymph node"
/dev_stage="4 weeks"
/lab_host="DHI08"
/clone_id="Soares mouse lymph node NbMUN"
/note="Organ: lymph node; Vector: pUT73-PacI; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I
- oligo(dT) primer (5'
TGTTCATATCTGATGAGGAGGAGCGCCGACATCTTTTCTTTTCTTTTCTTTT
3'); double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pUT73 vector. RNA
provided by Dr. Bertrand Jordan. Library constructed and
normalized by Bento Soares and M. Patricia Bonaldo."

ORIGIN
Query Match 17.4%; Score 72.6; DB 1; Length 285;
Best Local Similarity 62.3%; Pred. No. 3.1e-05;
Matches 11; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
Qy 166 TTTATCTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 225
Db 111 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT

Db 279 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 220
Qy 226 TTTCTCTCTCTCTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTAC 285
Db 219 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 160
Qy 286 ATCTCTCATGAGGAGAAATATCTGCTTGAATCTTTCTTTCTTTCTTTCTTT 345
Db 159 TTCCTGACATTCACAGAACTAACTGAATGTATTAATCACTTTACATTTCA 100
Qy 346 CCA 348
Db 99 CAA 97

RESULT 7
CE462296 477 bp DNA linear GSS 27-SEP-2003
LOCUS tigr-gss-dog-17000309531079 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
CE462296
VERSION CE462296.1 GI:36762471
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 477)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, M., Fraser, C.M. and
Venter, J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org
Class: shotgun.
Location/Qualifiers
1..477
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 17.4%; Score 72.6; DB 12; Length 477;
Best Local Similarity 59.4%; Pred. No. 3.2e-05;
Matches 123; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
Qy 165 CTTATCTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 224
Db 230 CTTCTCTCTCTCTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 289
Qy 225 TTTCTCTCTCTCTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 284
Db 290 TTTCTCTCTCTCTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 349
Qy 285 GATCTCTCATGAGGAGAAATATCTGCTTGAATCTTTCTTTCTTTCTTTCTTT 344
Db 350 CTTCTCTCTCTCTCTCTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 409
Qy 345 ACCATGGGCGGGGGTGTTCCTTT 371
Db 410 TCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTT 436


```

, RESULT 4
, US-09-949-016-12591
, Sequence 12591, Application US/099499016
, Patent No. 6812339
, GENERAL INFORMATION:
, APPLICANT: VENTER, J. Craig et al.
, TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
, TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
, FILE REFERENCE: CL001307
, CURRENT APPLICATION NUMBER: US/09/949,016
, CURRENT FILING DATE: 2000-04-14
, PRIOR APPLICATION NUMBER: 60/241,755
, PRIOR FILING DATE: 2000-10-20
, PRIOR APPLICATION NUMBER: 60/237,768
, PRIOR FILING DATE: 2000-10-03
, PRIOR APPLICATION NUMBER: 60/231,498
, PRIOR FILING DATE: 2000-09-08
, NUMBER OF SEQ ID NOS: 207012
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 12591

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OTHER INFORMATION: n = A, T, C or G
US-09-949-016-12591

Query Match	16.9%	Score 70.6	DB 3	Length 65744
Best Local Similarity	78.0%	Pred. No. 2.3e-07		
Matches 85; Conservative	0	Mismatches 24	Indels 0	Gaps 0

[illegible]

RESULT 5
US-09-948-016-15871
; Sequence 15871, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

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: CURRENT APPLICATION NUMBER: US/09/949,016
:
: CURRENT FILING DATE: 2000-04-14
:
: PRIOR APPLICATION NUMBER: 60/241,755
:
: PRIOR FILING DATE: 2000-10-20
:
: PRIOR APPLICATION NUMBER: 60/237,768
:
: PRIOR FILING DATE: 2000-10-03
:
: PRIOR APPLICATION NUMBER: 60/231,498
:
: PRIOR FILING DATE: 2000-09-08
:
: NUMBER OF SEQ ID NOS: 207012
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 15871
:
: LENGTH: 65745
:
: TYPE: DNA
:
: ORGANISM: Human
:
: FEATURE:
:
: NAME/KEY: misc_feature
:
: LOCATION: (1)...(65745)
:
: OTHER INFORMATION: n = A,T,C or G
:
: US-09-949-016-15871

```

Query Match	16.9%	Score 70.6;	DB 3;	length 65745;
Best Local Similarity	78.0%	Pred. No. 2.3e-07;		
Matches 85;	Conservative	0;	Mismatches 24;	Indels 0;
				Gaps 0;

[illegible]

RESULT 6
US-09-949-016-13358
; Sequence 13358, Application US/09949016

```

PATENT NO.: 0612259
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13358
LENGTH: 260247
TYPE: DNA
ORGANISM: Human
US-09-949-016-13358

```

Query Match	67;	16.1%;	DB 3;	length	260247;
Best Local Similarity		76.6%;			
Pred. No. 2-5e-06;					
Matches	82;	Conservative	0;	Mismatches	25;
				Indels	0;
				Gaps	0;

Qy	166	182931	182937
Qy	166	182931	182937
Db	182931	182931	182937
Qy	226	182931	182937
Db	182931	182931	182937

```

RESULT 7
US-09-949-016-12014/c
Sequence 12014, Application US/09949016
Patent No. 681239
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CU001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12014
LENGTH: 39433
TYPE: DNA

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US-09-949-002-678/c
; Sequence 678, Application US/09949002
; Patent No. 690016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 678
; LENGTH: 56399
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(56399)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-678

Query Match 15.6%; Score 65.2; DB 3; Length 56399;
Best Local Similarity 67.9%; Pred. No. 4.6e-06;
Matches 106; Conservative 0; Mismatches 48; Indels 2; Gaps 1;

QY 139 GGGAGACTCAGTCAGCCAAAAAAGCTTATCTTTTCTTTTCTTTTCTTTCTTTCT 198
DB 46588 GAGAAATCTCCAAATACATTAAGAAAGCTTCTTCTTCTTCTTCTTCTTCTCA 46529
QY 199 TTCTCTTCTTCTTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 256
DB 46528 CACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 46469
QY 257 TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 292
DB 46468 TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 46433

RESULT 12
US-09-949-002-839/c
; Sequence 839, Application US/09949002
; Patent No. 690016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 839
; LENGTH: 56399
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(56399)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-839

Query Match 15.6%; Score 65.2; DB 3; Length 56399;
Best Local Similarity 67.9%; Pred. No. 4.6e-06;
Matches 106; Conservative 0; Mismatches 48; Indels 2; Gaps 1;

QY 139 GGGAGACTCAGTCAGCCAAAAAAGCTTATCTTTTCTTTTCTTTTCTTTCTTTCT 198

DB 46588 GAGAAATCTCCAAATACATTAAGAAAGCTTCTTCTTCTTCTTCTTCTTCTCA 46529
QY 199 TTCTCTTCTTCTTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 256
DB 46528 CACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 46469
QY 257 TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 292
DB 46468 TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 46433

RESULT 13
US-09-949-016-12871
; Sequence 12871, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12871
; LENGTH: 100836
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(100836)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12871

Query Match 15.5%; Score 64.8; DB 3; Length 100836;
Best Local Similarity 75.0%; Pred. No. 6.7e-06;
Matches 81; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 166 TTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 225
DB 87889 TTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 87948
QY 226 TTCT 273
DB 87949 TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 87996

RESULT 14
US-09-949-016-17063
; Sequence 17063, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

[illegible]

```

RESULT 2
US-09-925-065A-566754
; Sequence 566754, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 566754
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-566754

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	Query Match	92.0%; Score 217; DB 5; Length 562;
	Best Local Similarity	59.26%; Pred. No. 4, 2e-41;
Matches	228; Conservative	0; Mismatches 0; Indels 1; Gaps 1
OY	189	TTTTCTTTCTTTCCTTTCTTTGTGCTTGCTCTCTCTCTCTCTT
Db	1	TTTTCTTTCTTTCCTTTCTTTGTGCTTGCTCTCTCTCTCTCTT
OY	249	CTTTCCTCTCTTCTTTCTTTTCCATAGGCAGAATCTCCTCATGGCAATAATC
Db	61	CTTTCCTCTCTTCTTTCTTTTCTTAATGGCAAGATCTCTAATGGCAAAATATC
OY	309	TGCTTAGCTTCTGTTTCACAGCTGCTTCTGCCAGAACATGCGCTGCTGTTTTCT
Db	121	TGCTTAGCTTCTGTTTCACAGCTGCTTCTGCCAGAACATGCGCTGCTGTTTTCT
OY	369	TTTCGCAATATATATCAGGCCCATCCAGACTCTGGTCCCCTCACTGT
Db	180	TTTCGCAATATATATCAGGCCCATCCAGACTCTGGTCCCCTCACTGT

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RESULT3
US-10-437-963-95688/C
; Sequence 95688, Application US/10437966/C
; Publication NO. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbasuk, Brad
; APPLICANT: Li, Ping

```

```

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ. ID NOS.: 204966
SEQ ID NO 95688
LENGTH: 1678
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_93858C.1
US-10-437-963-95688

Query Match          17.1%; Score 71.2; DB 8; Length 1678;
Best Local Similarity 66.0%; Pred. No. 1,3e-06;
Matches 103; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy      166 TTTATCTTTCCTTTTTTTTTCTTTCTGTCCTTCCTTCCTTCCTTCCTTCGTCT 225
        ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
Db      1517 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1458

Qy      226 TTCTCTCTCTCTCGTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTACATGGCAAG 285
        ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
Db      1457 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGATGTAAA 1398

Qy      286 ATCTCTCATGGAGAATAATATCTGCCTTGACTTC 321
        ||| |||| | |||| | |||| | |||| | |||| | |||| | ||||
Db      1397 ATGGCAACATTTTAGGTCAAATTGCTTGCCCTTC 1362

```

```

RESULT 4
US-09-925-065A-164899
Sequence 164899, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925, 065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243, 096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289, 846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 164899
LENGTH: 501
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-164899

```

[illegible]


```

; SEQ ID NO 417
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ..(1548)
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (896)..(995)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-343-650A-417

Query Match      16.9%; Score 70.4; DB 8; Length 1548;
Best Local Similarity 78.2%; Pred. No. 2e-06; Mismatches 26; Indels 1; Gaps 1;
Matches          97; Conservative 0;

168 TATCTTTTCTTTTTTTTTTTTTTTTCCTTTGTCGTCTTGTCGTCTTT    227
Db       TCCTCTTTCTTTTAATTCTTTCTTTCTTTCTTTCTTTCTTC-TCCTTTCTTTCC 1090

Oy      228 CCTCTCTCTCTGCTCTTTCTTTCTCTCTTTCTTTTTCCTACAGCAAGAT 287
Db      1089 TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCCTCC 1030

Oy      288 CTCCT 291
         |||||
Db      1029 CTCC 1026


RESULT 9
US-10-741-600-33383/c
; Sequence 33383, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33383
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-33383

Query Match      16.8%; Score 70.2; DB 9; Length 201;
Best Local Similarity 78.5%; Pred. No. 1.2e-06; Mismatches 23; Indels 0; Gaps 0;
Matches          84; Conservative 0;

165 CTTTAACTTTTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTGGCTTCTGC 224
Db      190 CTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTCTC 131

Oy      225 TTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTTTT 271
         |||||
Db      130 TTTCCTCTCTCTCTCTCTCTCTCTTTCTTTCTTTCTCTCTCTCTTTCTTT 84


RESULT 10
US-10-741-600-33385/c
; Sequence 33385, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
```

```

; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33385
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-33385

Query Match      16.8% Score 70.2; DB 9; Length 201;
Best Local Similarity 78.5%; Pred. No. 1.2e-06;
Matches    84; Conservative   0; Mismatches 23; Indels   0; Gaps   0;

OY       165 CTTATCTTTCCTTTTTTTTCCTTTCTTGCTGCTGTGC 224
          ||||| | | | | | | | | | | | | | | | | | 
DB       192 CTCCTTCCTTTCTTTCTCGCTCCTTCCTCCCTTCTTCTTCTCTGC 133
          ||||| | | | | | | | | | | | | | | | | 

QY       225 TTTCCTCTCTCTCTGCTCTTCTTTCCTTCTTCTTTT 271
          ||||| | | | | | | | | | | | | | | | | 
DB       132 TTTCTCTCTCTCTCTTCTTCTTCTTCTTCTT 86
          ||||| | | | | | | | | | | | | | | | 

RESULT 11
US-10-741-600-33386/c
; Sequence 33386, Application US/10741600
; Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33386
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-741-600-33386

Query Match      16.8% Score 70.2; DB 9; Length 201;
Best Local Similarity 78.5%; Pred. No. 1.2e-06;
Matches    84; Conservative   0; Mismatches 23; Indels   0; Gaps   0;

QY       165 CTTAACCTTCTTTTCTTTTCTTCTTCTTCTTCTGCTGCTGTC 224
          ||||| | | | | | | | | | | | | | | | | 
DB       197 CTCCTTCTTTCTTTCTTCTGCTCTTCTCCCTTCTTCTTCTCTC 138
          ||||| | | | | | | | | | | | | | | | | 

QY       225 TTTCCCTCTCTCTGCTGCTTCTTCTTCTTCTTCTTTT 271
          ||||| | | | | | | | | | | | | | | | | 
DB       137 TTCCTCTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTT 91
          ||||| | | | | | | | | | | | | | | | 

RESULT 12
US-10-741-600-33388/c
; Sequence 33388, Application US/10741600
; Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33388
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-741-600-33388

Query Match      16.8% Score 70.2; DB 9; Length 201;

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 22:44:48 ; Search time 12.1553 Seconds
(without alignments)
4040.340 Million cell updates/sec

Title: US-09-869-098a-1_COPY_717_1133

Perfect score: 417
Sequence: 1 gccacgggggacacatttgg.....gtctgtccctcagctgt 417

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA New:
1: /EMC_Celerra_SIDS3/prodata/1/pubpna/US09_NEW_PUB.seq:
2: /EMC_Celerra_SIDS3/prodata/1/pubpna/US06_NEW_PUB.seq:
3: /EMC_Celerra_SIDS3/prodata/1/pubpna/US07_NEW_PUB.seq:
4: /EMC_Celerra_SIDS3/prodata/1/pubpna/US08_NEW_PUB.seq:
5: /EMC_Celerra_SIDS3/prodata/1/pubpna/PCT_NEW_PUB.seq:
6: /EMC_Celerra_SIDS3/prodata/1/pubpna/US10_NEW_PUB.seq:
7: /EMC_Celerra_SIDS3/prodata/1/pubpna/US11_NEW_PUB.seq:
8: /EMC_Celerra_SIDS3/prodata/1/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB	ID	Description
1	65.2	15.6	42999	7	US-11-284-877-17	Sequence 17, Appl
2	63.6	15.3	1292	6	US-10-953-349-10307	Sequence 10307, A
3	63	15.1	2442	6	US-10-953-349-35802	Sequence 35802, A
4	62.2	14.9	1985	6	US-10-196-749-27	Sequence 27, Appl
5	61.4	14.7	1999	6	US-10-505-928-758	Sequence 758, App
6	60.8	14.6	2773	6	US-10-196-749-149	Sequence 149, App
7	60.8	14.6	2773	7	US-11-101-316-33	Sequence 33, Appl
8	60	14.4	4600	7	US-11-301-554-1797	Sequence 1797, Ap
9	59	14.1	4640	6	US-10-196-749-75	Sequence 75, Appl
10	58.8	14.1	2272	6	US-10-953-349-37381	Sequence 37381, A
11	58.6	14.1	2163	6	US-10-953-349-37514	Sequence 37514, A
12	58.2	14.0	1628	6	US-10-953-349-28506	Sequence 28506, A
13	58.2	14.0	2378	7	US-11-293-697-1075	Sequence 1075, Ap
14	58	13.9	1843	6	US-10-511-937-620	Sequence 620, Appl
15	58	13.9	4670	7	US-11-145-307A-29	Sequence 29, Appl
16	57.8	13.9	2861	6	US-10-953-349-7328	Sequence 7328, Ap
17	57.6	13.8	2846	6	US-10-196-749-169	Sequence 169, Appl
18	57.6	13.8	2846	6	US-11-101-316-37	Sequence 37, Appl
19	57.4	13.8	2261	6	US-10-511-937-415	Sequence 415, App
20	57.2	13.7	1734	6	US-10-196-749-201	Sequence 201, Appl
21	57.2	13.7	1734	7	US-11-101-316-51	Sequence 51, Appl
22	56.2	13.5	1771	6	US-10-953-349-37996	Sequence 37996, A
23	56.2	13.5	1771	6	US-10-196-749-17	Sequence 17, Appl
24	56.2	13.5	1771	6	US-11-296-092-36	Sequence 36, Appl
25	56	13.4	2541	7	US-11-293-697-2275	Sequence 2275, Ap

C	26	55.6	13.3	1820	7	US-11-316-907-14	Sequence 14, Appl
	27	55.6	13.3	2111	7	US-11-293-697-379	Sequence 379, App
	28	55.6	13.3	6065	6	US-10-528-659-3	Sequence 3, Appl1
C	29	55.4	13.3	762	6	US-10-953-349-30826	Sequence 30826, A
	30	54.8	13.1	641	6	US-10-488-619-15077	Sequence 15077, Ap
	31	54.6	13.1	1395	6	US-10-953-349-36407	Sequence 36407, A
	32	54.4	13.0	2059	7	US-11-293-697-1623	Sequence 1623, Ap
C	33	54.2	13.0	431	6	US-10-488-619-1226	Sequence 1244, Ap
	34	54	12.9	2059	7	US-11-293-697-1244	Sequence 38337, A
C	35	53.8	12.9	1761	6	US-10-953-349-38337	Sequence 596, App
	36	53.8	12.9	70655	6	US-10-505-928-596	Sequence 1, Appl1
C	37	53.6	12.9	56580	6	US-10-553-298-1	Sequence 164, Appl
	38	53.4	12.8	2278	7	US-11-293-697-164	Sequence 9921, Ap
C	39	53.2	12.8	2205	6	US-10-953-349-9921	Sequence 36144, A
	40	52.8	12.7	807	6	US-10-953-349-36144	Sequence 237, App
C	41	52.8	12.7	1234	6	US-10-196-749-237	Sequence 63, Appl
	42	52.8	12.7	1234	7	US-11-101-316-63	Sequence 483, App
C	43	52.8	12.7	2379	6	US-10-196-749-483	Sequence 30078, A
	44	52.6	12.6	1456	6	US-10-953-349-30078	Sequence 335, App
C	45	52.2	12.5	1570	6	US-10-196-749-335	

ALIGNMENTS

RESULT 1
US-11-284-877-17
; Sequence 17, Application US/11284877
; Publication No. US20060095984A1
; GENERAL INFORMATION:
; APPLICANT: Hadlaczky, Gyula
; TITLE OF INVENTION: Artificial Chromosomes, Uses Thereof and Methods
; FOR PREPARING ARTIFICIAL CHROMOSOMES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson
; STREET: 12390 El Camino Real
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92130
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/284,877
; FILING DATE: 21-Nov-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/808,689
; FILING DATE: 24-MAR-2004
; APPLICATION NUMBER: 10/219,694
; FILING DATE: 14-AUG-2002
; APPLICATION NUMBER: 10/151,081
; FILING DATE: 16-MAY-2002
; APPLICATION NUMBER: 10/151,078
; FILING DATE: 16-MAY-2002
; APPLICATION NUMBER: 10/125,767
; FILING DATE: 17-APR-2002
; APPLICATION NUMBER: 10/287,313
; FILING DATE: 01-NOV-2002
; APPLICATION NUMBER: 09/799,462
; FILING DATE: 05-MAR-2001
; APPLICATION NUMBER: 09/724,872
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 09/724,726
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 09/724,693
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 08/835,682

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1      FILING DATE: 10-APR-1997
2      APPLICATION NUMBER: 08/695,191
3      FILING DATE: 07-AUG-1996
4      APPLICATION NUMBER: 08/682,080
5      FILING DATE: 15-JUL-1996
6      APPLICATION NUMBER: 08/629,822
7      FILING DATE: 10-APR-1996
8
9      ATTORNEY/AGENT INFORMATION:
10     NAME: Seidman, Stephanie L
11     REGISTRATION NUMBER: 33,779
12     REFERENCE/DOCKET NUMBER: 17084-004018/402QC
13
14     TELECOMMUNICATION INFORMATION:
15     TELEPHONE: 858-678-4777
16     TELEFAX: 202-626-7796
17
18     TELEX: <Unknown>
19
20     INFORMATION FOR SEQ ID NO: 17:
21
22     SEQUENCE CHARACTERISTICS:
23
24         LENGTH: 42399 base pairs
25         TYPE: nucleic acid
26         STRANDEDNESS: single
27         TOPOLOGY: linear
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29         MOLECULE TYPE: Genomic DNA
30
31         HYPOTHEetical: NO
32
33         ANTI-SENSE: NO
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35         FRAGMENT TYPE: <Unknown>
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37         ORIGINAL SOURCE:
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39         SEQUENCE DESCRIPTION: SEQ ID NO: 17:
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41     US-11-284-877-17

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Best Local Similarity	74.5%;	Pred. No. 4.4e-05;		
Matches	82;	Conservative	0;	Mismatches 28; Indels 0;

[illegible]

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RESULT 2
US-10-953-349-10307/c
; Sequence 10307, Application US/10953349
; Publication No. US20060107345A1
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GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10307
;
; LENGTH: 1292
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; TYPE: DNA
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; ORGANISM: Arabidopsis thaliana
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; NAME/KEY: misc_feature
; LOCATION: (874)..(875)
; OTHER INFORMATION: n is a, c, g, or t
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FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (877)..(877)
; OTHER INFORMATION: n is a, c, g, or t
;
US-10-953-349-10307

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Query Match	15.3%	Score 63.6;	DB 6;	Length 1292;
Best Local Similarity	62.7%;	Pred. No. 5.4e-05;		
Matches	96;	Conservative	0;	Mismatches 57;
			Indels	0;
			Gaps	0;

[illegible]

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RESULT 3
US-10-953-349-35802/c
; Sequence 35802, Application US/10953349
; Publication NO. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35802
; LENGTH: 2442

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/ ORGANISM: Zea mays subsp. mays
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (539)..(539)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (659)..(660)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (2405)..(2411)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (2432)..(2433)
/ OTHER INFORMATION: n is a, c, g, or t
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US-10-953-349-35802

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[illegible]

RESULT 4
US-10-196-749-27/c
; Sequence 27, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc

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; LENGTH: 1999
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-758

Query Match      14.7%; Score 61.4; DB 6; Length 1999;
Best Local Similarity 62.9%; Pred. No. 0.00016;
Matches 95; Conservative 0; Mismatches 56; Indels 0; Gaps 0

OY    166 TTATACCTTTCTTTTTTTTTTCTTTCTTTCTTTCTTTCTTTCTTTGTCCTTGTCT 225
DB    1961 TTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1902

OY    226 TTCGCCTCCTCGTCGTCGTCCTTTCTTCCCTCCTCTTCTTTCTTTCTCAATGGCAAG 285
DB    1901 TTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCTCCAACC 1844

OY    286 ATCTCCATCGCAGAAATAATCTGCCCTGA 316
DB    1841 ATTTCGTTTATTATATAAAGCTTACTTAA 1811

RESULT 6
US-10-196-749-149/c
; Sequence 149, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deanoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 149
; LENGTH: 2773
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-149

Query Match      14.6%; Score 60.8; DB 6; Length 2773;
Best Local Similarity 62.5%; Pred. No. 0.000224;
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Dd	2756	TT	2697							
Oy	226	TTCCTCTCTCTCTCTCTCTTCTTCTCTCTTCTTCTTCTCAATGGCAG	285							
Dd	2696	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATTTTTCATCCCTCTAACC	2637							
Oy	286	ATTCTCCATGGCAGAAATAATCTGCCTTGAC	317							
Dd	2636	ATTTAATTACGAATTCCTACTCATTTGTCAATGAC	2605							

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1      RESULT 7
2      US-11-101-316-33/c
3      ; Sequence 33, Application US/11101316
4      ; Publication NO. US20060099657A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Goddard, Audrey
7      ; APPLICANT: Godowski, Paul J.
8      ; APPLICANT: Grimaldi, Christopher J.
9      ; APPLICANT: Gurney, Austin L.
10     ; APPLICANT: Wood, William I.
11     ; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
12     ; TITLE OF INVENTION: UNDEREXPRESSED IN MELANOMA
13     ; FILE REFERENCE: P3230R1C17C1
14     ; CURRENT APPLICATION NUMBER: US/11/101.316
15     ; CURRENT FILING DATE: 2005-04-06
16     ; PRIOR APPLICATION NUMBER: 10/063526
17     ; PRIOR FILING DATE: 2002-05-03
18     ; PRIOR APPLICATION NUMBER: 10/006867
19     ; PRIOR FILING DATE: 2001-12-06
20     ; PRIOR APPLICATION NUMBER: PCT/US00/23328
21     ; PRIOR FILING DATE: 2000-08-24
22     ; PRIOR APPLICATION NUMBER: 09/380137
23     ; PRIOR FILING DATE: 1999-08-25
24     ; PRIOR APPLICATION NUMBER: PCT/US99/12252
25     ; PRIOR FILING DATE: 1999-06-02
26     ; PRIOR APPLICATION NUMBER: 60/087759
27     ; PRIOR FILING DATE: 1998-06-02
28     ; NUMBER OF SEQ ID NOS: 170
29     ; SEQ ID NO 33
30     ; LENGTH: 2773
31     ; TYPE: DNA
32     ; ORGANISM: Homo Sapien
33     US-11-101-316-33

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	Query Match	Similarity	Score	DB	Length
	Beet Local	62.5%	Pred.	No. 0.00022	
	Matches	95; Conservative	0;	Mismatches 57;	Indels 0; Gaps 0;
OY	166	TTTATCTTTCCTTTTTTTTTTTCTTCTTCTTCTTCTGCTTCTGTCT	225		
Db	2756	TT	2697		
OY	226	TTCCTCTCTCTCTGCTTCTTCTCTCTTCTTCTTCTTCTTACAGCAAG	285		
Db	2696	TTTAAATTTCATCCTCTAACC	2637		
OY	286	ATCTCCATGGCAGAAATAATCTGCCTTGAC	317		
Db	2636	ATTTAATTCAGCAATTCTCACATTTGATGAC	2605		

RESULT 8
US-11-301-554-1797
; Sequence 1797, Application US/1130155*
; Publication No. US2006008627A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong

```

APPLICANT: Matanabe, Yoshiniro
APPLICANT: Kaios, Michael D.
APPLICANT: Sleath, Paul R.
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Reller, Marc W.
APPLICANT: Durham, Margareta
APPLICANT: Cartier, Derrick
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McInabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C21
CURRENT APPLICATION NUMBER: US/11/301,554
CURRENT FILING DATE: 2005-12-13
PRIOR APPLICATION NUMBER: US 10/283,017
PRIOR FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: US 10/113,872
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 10/017,754
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 09/902,941
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 09/849,626
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US 09/736,457
PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: US 09/702,705
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: US 09/677,419
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 09/671,325
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/658,824
PRIOR FILING DATE: 2000-09-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2157
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1797
LENGTH: 4600
TYPE: DNA
ORGANISM: Homo sapiens
US-11-301-554-1797

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[illegible]

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RESULT 9
US-10-196-749-75/C
Sequence 75, Application US/10196749
Publication No. US2006009464A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.

```

```
; APPLICANT: Pan,James  
; APPLICANT: Smith,Victoria  
; APPLICANT: Watanabe,Colin K.  
; APPLICANT: Wood,William I.  
APPLICANT: Zhang,Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3430R1C340  
CURRENT FILING DATE: US/10/196,749  
CURRENT FILING DATE: 2002-07-16  
PRIOR APPLICATION NUMBER: 10//052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60//059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60//059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60//062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60//063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60//063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60//063486  
PRIOR FILING DATE: 1997-10-21,  
PRIOR APPLICATION NUMBER: 60//063540  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60//063541  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60//063544  
PRIOR FILING DATE: 1997-10-28  
Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 75  
LENGTH: 4640  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-196-749-75
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Beech Local Similarity    69.6%; Pred. No. 0.00053;  
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Db        4639 TTTTATTCTTCTTCTGCTCTCTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCAATG 4580  
  
OY       226 TTCCTCTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTAATG 280  
         ||| | | | | | | | | | | | | | | | | | | | | |  
Db        4579 TTTTATTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTAAACAATG 4525
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RESULT 10  
US-10-953-349-37381/C  
Sequence 37381, Application US/10953349  
Publication No. US20060107345A1  
GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nikolai et al.  
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
TITLE OF INVENTION: ENCODED THEREBY  
FILE REFERENCE: 2750-1579PUS2  
CURRENT FILING DATE: US/10/953,349  
CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 37381  
LENGTH: 2272  
TYPE: DNA  
ORGANISM: Zea mays subsp. mays  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (2086)..(2086)  
OTHER INFORMATION: n is a, c, g, or t  
US-10-953-349-37381
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Query Match Similarity      14.1%; Score 58.8; DB 6; Length 2272;
Best Local Similarity     70.9%; Pred. No. 0.00052;
Matches    78; Conservative   0; Mismatches 32; Indels   0; Gaps   0;

QY          166 TTATCTTTCTTTTTTTCCTTTCTTTCTTTCTTTCTTTCTTTGCTTGCTGT 225
               ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB           2196 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2137

QY          226 TTCGCCTCCTCGCTGCTTTCTTTCCCTCTTCTTTCTT 275
               ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB           2136 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCT 2087


RESULT 11
US-10-953-349-37514/c
; Sequence 37514, Application US/10953349
; Publication NO. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37514
; LENGTH: 2163
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37514
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Query March          14.1%; Score 58.6; DB 6; Length 2163;
Best Local Similarity 67.8%; Pred. No. 0.00057;
Matches      82; Conservative    0; Mismatches   39; Indels     0; Gaps     0;

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QY      226 TTCTCTCTCTCTCTGCTCTTCTTTCCCTCTCTTTCTTTTTCCTACAGGCAG 285
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QY      286 A 286
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DB      1977 A 1977

RESULT 12
US-10-953-349-28506/c
; Sequence 28506, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28506
; LENGTH: 1628
; TYPE: DNA
; ORGANISM: Trilicium aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1422)..(1422)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-28506
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:15:46 ; Search time 1739.95 Seconds
(without alignments)
9445.379 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

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Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
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9:   gb_sy: *
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14:  gb_in: *
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   gb_da: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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1	257	100.0	3505	2	E54511	UCP-2 promo	
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	4	255.4	99.4	3270	5	AF306570	AF306570 Homo sapi
	5	255.4	99.4	12177	5	DQ087219	DQ087219 Homo sapi
c	6	255.4	99.4	156370	5	AP003717	AP003717 Homo sapi
c	7	243.4	94.7	155668	12	AC024029	AC024029 Homo sapi
8	183.2	71.3	3301	5	AF208500	AF208500 Homo sapi	
c	9	41.6	18.2	3306	2	CO841485	CO841485 Sequence
c	10	41.6	16.2	3306	5	AK124524	AK124524 Homo sapi
c	11	41.6	16.2	16256	2	AX647079	AX647079 Sequence
12	41.6	16.2	70975	12	AP000579	AP000579 Homo sapi	
13	41.6	16.2	140356	12	AP000803	AP000803 Homo sapi	
c	14	41.6	16.2	150694	12	AP001459	AP001459 Homo sapi
15	41.6	16.2	211382	5	AP001362	AP001362 Homo sapi	
16	41	16.0	74999	5	AC008960	AC008960 Homo sapi	
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c	18	41	16.0	155025	5	AC034246	AC034246 Homo sapi

19	41	16.0	171274	12	AC026476	AC026476 Homo sapi
20	41	16.0	177797	12	AC016581	AC016581 Homo sapi
C 21	41	16.0	184118	5	AC016580	AC016580 Homo sapi
C 22	41	16.0	191408	12	AC150379	AC150379 Lemur cat
C 23	39.8	15.5	180745	5	AL359183	AL359183 Human DNA
C 24	39.4	15.3	93915	5	DQ201638	DQ201638 Homo sapi
C 25	39.4	15.3	100000	5	AB000499	AB000499 Homo sapi
C 26	39.4	15.3	182224	5	AC093116	AC093116 Homo sapi
27	39.4	15.3	203230	12	AC026346	AC026346 Homo sapi
28	39.4	15.3	205834	5	AP006133	AP006133 Homo sapi
C 29	39.4	15.3	270000	5	AB026898	AB026898 Homo sapi
C 30	38.8	15.1	216287	12	AC165592	AC165592 Bos tauru
C 31	38.4	14.9	131839	5	AC112165	AC112165 Homo sapi
C 32	38.4	14.9	163434	5	AC109460	AC109460 Homo sapi
C 33	38.4	14.9	187788	12	AC138925	AC138925 Homo sapi
C 34	38.4	14.9	219646	12	AC139247	AC139247 Homo sapi
C 35	38.2	14.9	72406	12	AC041027	AC041027 Homo sapi
C 36	38.2	14.9	160135	12	BX649519	BX649519 Homo sapi
C 37	38.2	14.9	200491	5	AC007249	AC007249 Homo sapi
C 38	38	14.8	85864	12	AC015510	AC015510 Homo sapi
C 39	38	14.8	104802	5	AP003026	AP003026 Homo sapi
C 40	38	14.8	137739	5	HS99419	AL0034554 Human DNA
C 41	38	14.8	188635	12	AC011207	AC011207 Homo sapi
C 42	37.8	14.7	111445	6	AL929303	AL929303 Mouse DNA
C 43	37.8	14.7	171290	12	AC182075	AC182075 Bos tauru
C 44	37.6	14.6	139758	12	AC152903	AC152903 Ornithoth
C 45	37.6	14.6	146327	5	AL162253	AL162253 Human DNA

ALIGNMENTS

RESULT 1				
LOCUS	E54511	3505 bp	DNA	linear
DEFINITION	UCP-2 promoter and use thereof.			
ACCESSION	E54511			
VERSION	E54511.1	GI:18629692		
KEYWORDS	JP 2000236886-A/1.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 3505) Toyota,Y., Kobayashi,M. and Igaki,S. UCP-2 promoter and use thereof TAKEDA CHEM IND LTD PN JP 2000236886-A/1 PD 05-SEP-2000 PF 22-DEC-1999 JP 1999364724			
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				
	PR	YUKIO TOYOTA, MAKOTO KOBAYASHI, SHIGERU IGAKI		
	PI	C12N15/09, A61K45/00, A61P3/04, A61P3/10, A61P9/12, PC		
	AG:IP2/00,	C12N1/21.		
	PC	C12N5/10, C12Q1/02, G01N33/15, G01N33/50//A61K31/711, A61K38/00,		
	PC	A61K48/00,		
	PC	(C12N15/09, C12R1:19), (C12N15/09, C12R1:91), (C12N1/21, C12R1:19),		
	PC	(C12N5/10, C12R1:91), C12N15/00, C12N5/00, A61K37/02, (C12N15/00,		
	PC	C12R1:19)',		
	CC	(C12N15/00, C12R1:91), (C12N5/00, C12R1:91)		
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source				
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Query Match 100.0%; Score 257; DB 2; Length 3505;
 Best Local Similarity 100.0%; Pred. No. 3.2e-75;
 Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 ACTGTGTAATATACAGGAAGATGACTGAAGCTTTGGAGACTCCGTTTCTCATTTATA 120
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 Db 1193 AGTGTGTAATATACAGGAAGATGACTGAAGCTTTGGAGACTCCGTTTCTCATTTATA 1252
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 QY 121 ATGAGAGTTAATACAGACCTTCTTACTCTCCCAACGACGTTTGTCCGCGCAGAG 180
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 Db 1253 ATGAGAGTTAATACAGACCTTCTTACTCTCCCAACGACGTTTGTCCGCGCAGAG 1312
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 QY 181 GGCCCAATTGTGCTGCTTACGCGATCAGTTACCCCAAGAGCGGCTCAGCCATTAA 240
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 Db 1313 GGCCCAATTGTGCTGCTTACGCGATCAGTTACCCCAAGAGCGGCTCAGCCATTAA 1372
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 QY 241 GGCGAACCGAGCCCGGT 257
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 Db 1373 GGCGAACCGAGCCCGGT 1389
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RESULT 2 197031 bp DNA 1linear HNG 07-JUL-2000
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 DEFINITION
 AC019121
 AC019121
 AC019121.3 GI:8440022
 HTG: HTGS PHASE1; HTGS_DRAFT.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 197031)
 Waterston,R.H.
 The sequence of Homo sapiens clone
 2 (bases 1 to 197031)
 Waterston,R.H.
 Direct Submision
 Submitted (30-DEC-1999) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Jun 10, 2000 this sequence version replaced gi:7105573.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCES
 AUTHORS
 TITLE
 JOURNAL

COMMENT
 On Jun 10, 2000 this sequence version replaced gi:7105573.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 Project Information -----
 Center project name: H_NH0535C12
 Summary Statistics -----

Sequencing vector: MJ3; 55%
 Sequencing vector: plasmid; 45%
 Chemistry: Dye-Primer ET; 55% of reads
 Chemistry: Dye-terminator Big Dye; 45% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 182418 bases at least Q40
 Consensus quality: 190012 bases at least Q30
 Insert size: 194831; agarose-fp
 Quality coverage: 4.10 in Q20 bases; agarose-fp
 Quality coverage: 4.05 in Q20 bases; sum-of-coverage

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 23 contigs. The true order of the pieces

* is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 2971: contig of 2971 bp in length
 2972 3071: gap of unknown length
 3072 5764: contig of 2693 bp in length
 5765 5865: gap of unknown length
 5866 8668: contig of 2704 bp in length
 8669 12865: contig of 4197 bp in length
 12866 12965: gap of unknown length
 12966 18581: contig of 5616 bp in length
 18582 18681: gap of unknown length
 18682 23951: contig of 5170 bp in length
 23952 28414: contig of 4463 bp in length
 28415 28514: gap of unknown length
 28515 33195: contig of 4681 bp in length
 33196 33295: gap of unknown length
 33296 38648: contig of 5353 bp in length
 38649 38748: gap of unknown length
 38749 44925: contig of 6177 bp in length
 44926 45025: gap of unknown length
 45026 51784: contig of 6759 bp in length
 51785 51884: gap of unknown length
 51885 58855: contig of 6971 bp in length
 58856 58955: gap of unknown length
 58956 68289: contig of 9334 bp in length
 68290 68389: gap of unknown length
 68390 77123: contig of 8734 bp in length
 77124 77223: gap of unknown length
 77224 87392: contig of 10069 bp in length
 87393 87392: gap of unknown length
 87393 96029: contig of 8637 bp in length
 96030 96129: gap of unknown length
 96130 104791: contig of 8662 bp in length
 104792 104891: gap of unknown length
 104892 116912: contig of 12021 bp in length
 116913 117012: gap of unknown length
 117013 131368: contig of 14356 bp in length
 131369 131468: gap of unknown length
 131469 142993: contig of 11525 bp in length
 142994 143093: gap of unknown length
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 154362 154461: gap of unknown length
 154462 173802: contig of 19341 bp in length
 173803 173902: gap of unknown length
 173903 173903: contig of 23129 bp in length.

FEATURES
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="11"
 /clone="RP11-535C12"

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                  104892..116912
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                  116913..117012
misc_feature      /estimated_length=unknown
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ORIGIN
Query Match      100.0%; Score 257; DB 12; Length 197031;
Best Local Similarity 100.0%; Pred. No. 4.5e-75;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTCCTGCGAGTCCCTTCTGCTGGTGAACACATATGCGCGGCTGACAGGGTGA 60
DB      164235 TTCCTGCGAGTCCCTTCTGCTGGTGAACACATATGCGCGGCTGACAGGGTGA 164294

QY      61 AGTGTGTGAATATCAGGAAGATGACGTCTTTGGGACTCCGTTTCTCATTTGTTAA 120
DB      164295 AGTGTGTGAATATCAGGAAGATGACGTGAACTTTGGGACTCCGTTTCTCATTTGTTAA 164354

QY      121 ATGAGGTTAATACAGCCCTTCTTCTACCTCCCAACGACGTTTGTCCCGGCGAG 180
DB      164355 ATGAGGTTAATACAGCCCTTCTTCTACCTCCCAACGACGTTTGTCCCGGCGAG 164414

QY      181 GGCCCAATTGTGTGCTGTTTCAGCATCATTAACCCCGACAGAGGGTCAAGCCATTAAA 240
DB      164415 GGCCCAATTGTGTGCTGTTTCAGCATCATTAACCCCGACAGAGGGTCAAGCCATTAAA 164474

QY      241 GGCGAACCCAGGCCCGGT 257
DB      164475 GGCGAACCCAGGCCCGGT 164491

RESULT 3
AP003531/c      199384 bp      DNA      linear      PRI 27-APR-2002
LOCUS           Homo sapiens genomic DNA, chromosome 11q clone:RP11-535C12,
DEFINITION      complete sequences.
ACCESSION       AP003531
VERSION         AP003531.2 GI:20334341
KEYWORDS        HTG.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE       1
AUTHORS        Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
                Fujiyama,A., Yada,T., Totokl,Y., Watanabe,H. and Sakaki,Y.
TITLE           Published Only in Database (2001)
JOURNAL         2 (bases 1 to 199384)
AUTHORS        Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
                Fujiyama,A., Yada,T., Totokl,Y., Watanabe,H. and Sakaki,Y.
TITLE           Direct Submission
JOURNAL         Submitted (18-APR-2001) Masahira Hattori, The Institute of Physical
                and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
                (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
                Tel:81-45-503-9111, Fax:81-45-503-9170)
                On Apr 26, 2002 this sequence version replaced gi:13699094.
COMMENT         Location/Qualifiers
FEATURES         source
                 1..199384
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ORIGIN
Query Match      100.0%; Score 257; DB 5; Length 199384;
Best Local Similarity 100.0%; Pred. No. 4.5e-75;
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QY	1	TTCCCTGGCAGATCCCTTCTGCTGTGTAAACACATATGTGGCGCCGCTGACACAGGCTGT	60						
Db	181537	TTCCCTGGCAGATCCCTTCTGCTGTGTAAACACATATGTGGCGCCGCTGACACAGGCTGT	181478						
QY	61	AGTGTGTAATATCAAGGAAGATGATCAAGAACGCTTTGGGACCTCGTTTCCATTTGTAAA	120						
Db	181477	AGTGTGTAATATCAAGGAAGATGATCAAGAACGCTTTGGGACCTCGTTTCCATTTGTAAA	181418						
QY	121	ATGAGAGTTAATACACGACCTTCTTCTACTCCCAACGACAGTGTGTTCGCCGACAG	180						
Db	181417	ATGAGAGTTAATACACGACCTTCTTCTACTCCCAACGACAGTGTGTTCGCCGACAG	181358						
QY	181	GGCCCAATTGTTGGCTGTTCACGACATCAATTACCCCAACAGACGGGTACGCCAATTAAA	240						
Db	181357	GGCCCAATTGTTGGCTGTTCACGACATCAATTACCCCAACAGACGGGTACGCCAATTAAA	181298						
QY	241	GGCGAACACGAGCCCGGT 257							
Db	181297	GGCGAACACGAGCCCGGT 181281							
RESULT 4									
LOCUS	AF306570	3270 bp	DNA	linear	PRI 30-OCT-2000				
DEFINITION	AF306570	Homo sapiens uncoupling protein 2 gene, promoter region and exon 1;							
ACCESSION	AF306570	nuclear gene for mitochondrial product.							
VERSION	AF306570.1	GI:11037742							
KEYWORDS									
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;								
	Homidae; Homo.								
REFERENCE	1 (bases 1 to 3270)								
AUTHORS	Schneitler,C., Oberkofler,H., Esterbauer,H. and Patsch,W.								
TITLE	UCP2 promoter region and exon 1								
JOURNAL	Unpublished								
REFERENCE	2 (bases 1 to 3270)								
AUTHORS	Schneitler,C., Oberkofler,H., Esterbauer,H. and Patsch,W.								
TITLE	Direct Sublation								
JOURNAL	Submitted (18-SEP-2000) Laboratory Medicine, Landeslinken								
	Salzburg, Mueller Hauptstr. 48, Salzburg A-5020, Austria								
FEATURES	Location/Qualifiers								
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	1. .3117								
	3118. .3241								
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	/note="UCP2"								
	3118. .3241								
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ORIGIN	exon								
Query Match	99.4%;	Score 255.4;	DB 5;	Length 3270;					
Best Local Similarity	99.6%;	Pred. No. 1.1e-74;							
Matches 256;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;	
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Db	2048	TTCCCTGGCAGATCCCTTCTGCTGTGTAAACACATATGTGGCGCCGCTGACACAGGCTGT	2107						
QY	61	AGTGTGTAATATCAAGGAAGATGATCAAGAACGCTTTGGGACCTCGTTTCCATTTGTAAA	120						
Db	2108	AGTGTGTAATATCAAGGAAGATGATCAAGAACGCT							

QY	Db	181	GGCCCAATTGTTGGCTGTTACGCATCATGTTACCCCAACGAGACGGGTACGCCAATTAAA	240
Db	2228	GGCCCAATTGTTGGCTGTTACGCATCATGTTACCCCAACGAGACGGGTACGCCAATTAAA	2287	
QY	241	GGCGAACCCAGCCCGGT	257	
Db	2288	GGCGAACCCAGCCCGGT	2304	
RESULT 5				
LOCUS	D0087219	12177 bp	DNA	linear PRI 18-JUN-2005
DEFINITION	Homo sapiens uncoupling protein 2 (mitochondrial, proton carrier).			
ACCESSION	D0087219	(UCP2) gene, complete cds; nuclear gene for mitochondrial product.		
VERSION	D0087219.1	GI:67515418		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 12177)			
AUTHORS	Livingston,R.J., Rieder,M.J., Shaffer,T., Bertucci,C., Balcer,C.N., Rajkumar,N., Wills,H.T., Daniels,M., Downing,T.K., Stanaway,I.B., Nguyen,C.P., Gilderleeve,H., Cassidy,C.M., Johnson,B.J., Swenson,D.E., McFarland,I., Yocel,B., Park,C. and Nickerson,D.A.			
TITLE	Direct Submission			
JOURNAL	Submitted (07-JUN-2005) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA			
COMMENT	To cite this work please use: NIH5-SNPs, Environmental Genome Project, NIH5 BS15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).			
FEATURES	Location/Qualifiers			
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	/db_xref="taxon:9606"			
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	/frequency="0.01"			
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repeat_region	989..1075			
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variation	1135			
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	/frequency="0.41"			
	/replace="a"			
variation	1151			
	/frequency="0.04"			
	/replace="a"			
variation	1960			
	/frequency="0.03"			
	/replace="t"			
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	/gene="UCP2"			
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	/gene="UCP2"			
	/product="uncoupling protein 2 (mitochondrial, proton carrier)"			
variation	2052			
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	/frequency="0.04"			
	/replace="t"			
variation	2089			

variation	/gene="UCP2" /frequency="0.06" /replace="g" 2242..2540 /rpt_family="Alu" /rpt_type=dispersed 2469 /gene="UCP2" /frequency="0.48" /replace="c" 2818 /gene="UCP2" /frequency="0.02" /replace="t" 2900 /gene="UCP2" /frequency="0.06" /replace="t" 3310 /gene="UCP2" /frequency="0.05" /replace="t" 3473 /gene="UCP2" /frequency="0.07" /replace="g" 3574..3699 /rpt_family="MIR" /rpt_type=dispersed 3856 /gene="UCP2" /frequency="0.98" /replace="a" 3957 /gene="UCP2" /frequency="0.02" /replace="g" 3999 /gene="UCP2" /frequency="0.02" /replace="a" 4047 /gene="UCP2" /frequency="0.01" /replace="g" 4117 /gene="UCP2" /frequency="0.10" /replace="g" 4180..4254 /rpt_family="MIR" /rpt_type=dispersed 4388..5633 /gene="UCP2" /note="Region not scanned for variation" 5001..5272 /rpt_family="Alu" /rpt_type=dispersed 5273..5581 /rpt_family="Alu" /rpt_type=dispersed 5955 /gene="UCP2" /frequency="0.02" /replace="g" 5972 /gene="UCP2" /frequency="0.01" /replace="a" 6328 /gene="UCP2" /frequency="0.01" /replace="a"	variation	6374 /gene="UCP2" /frequency="0.01" /replace="a" join(6468..6593,6750..6960,7829..8023,8104..8205, 9175..9355,9727..9841) /gene="UCP2" /codon_start=1 /product="uncoupling protein 2 (mitochondrial, proton carrier)" /protein_id="AA568217.1" /db_xref="GI:67515419" /translation="MWGKATDVPPATVKEFLGAGTACIADLITFPLDTAKVRLQIQ GESQGPVATASDAQYGVMTILLVPTBGRSLYNGLVAGLQROMSFASVRIQLYDS VKQFYTGSEHASIGSRLLAGTGAIVAAOPTDVAKYRFOQARAGGRYSQTV NAKTTAREGFRGIMKQTSPNVARNAIVCAELVTVDLKDALKANLMTDDLPCHF TSAFGACFTTVIASPVDVYKTRYNALQYSSAGHCALTMLOKEPRAFYKGFMS FLRLGSNNVMFVTEQLKALMACTSRAPF" 6779 /gene="UCP2" /frequency="0.01" /replace="t" 6787 /gene="UCP2" /frequency="0.46" /replace="t" 6850 /gene="UCP2" /frequency="0.02" /replace="a" 7113..7334 /rpt_family="MIR" /rpt_type=dispersed 7357 /gene="UCP2" /frequency="0.02" /replace="a" 7361..7480 /rpt_family="MIR" /rpt_type=dispersed 7435 /gene="UCP2" /frequency="0.01" /replace="c" 7486..7570 /rpt_family="MIR" /rpt_type=dispersed 7566 /gene="UCP2" /frequency="0.02" /replace="g" 7723 /gene="UCP2" /frequency="0.07" /replace="a" 7747 /gene="UCP2" /frequency="0.02" /replace="a" 7794 /gene="UCP2" /frequency="0.01" /replace="a" 7804 /gene="UCP2" /frequency="0.01" /replace="t" 7952	variation	99.4%; Score 255.4; DB 5; Length 12177; Best Local Similarity 99.6%; Pred. No. 1.2e-74; Matches 256; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 TTCCTGCGAGTCCTCTTCTGCTGTGTAACACATATGCGCGCGCTTACACAGGCTGTA 60
DB 931 TTCCTGCGAGTCCTCTTCTGCTGTGTAACACATATGCGCGCGCTTACACAGGCTGTA 990
QY 61 AGGTGTGAATATACAGAGATGACGTGACGTCTTTGGGACCTCCGTTCTCTCATTTGTAAA 120
DB 991 AGGTGTGAATATACAGAGATGACGTGACGTCTTTGGGACCTCCGTTCTCTCATTTGTAAA 1050
QY 121 ATGAGAGTTAATACAGAGCTTCTTCTACTCTCCCAACAGACGTGTTGTCTCCGCGCAGAG 180
DB 1051 ATGAGAGTTAATACAGAGCTTCTTCTACTCTCCCAACAGACGTGTTGTCTCCGCGCAGAG 1110
QY 181 GGGCCCAATTTGGTGGCTGTTACGCATCATGTTACCCCAACAGAGCGGCTGACCAATTAAA 240
DB 1111 GGGCCCAATTTGGTGGCTGTTACGCATCATGTTACCCCAACAGAGCGGCTGACCAATTAAA 1170
QY 241 GGGGAACACAGCGCCCGGT 257
DB 1171 GGGGAACACAGCGCCCGGT 1187

RESULT 6
AP003717/c 156370 bp DNA linear PRI 27-APR-2002
LOCUS Homo sapiens genomic DNA, chromosome 11q clone:RP11-167N4, complete
DEFINITION sequences.

ACCESSION AP003717
VERSION AP003717.3 GI:20334343
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Torok, Y., Watanabe, H. and Sakaki, Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in Database (2001)
REFERENCE 2 (bases 1 to 156370)
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Torok, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (04-JUN-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suenho-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Apr 26, 2002 this sequence version replaced gi:16904692.

FEATURES
Location/Qualifiers
1..156370
source

ORIGIN
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q"
/clone="RP11-167N4"

Query Match 99.4%; Score 255.4; DB 5; Length 156370;
Best Local Similarity 99.6%; Pred. No. 1.5e-74;
Matches 256; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCCTGCGAGTCCTCTTCTGCTGTGTAACACATATGCGCGCGCTTACACAGGCTGTA 60
DB 43995 TTCCTGCGAGTCCTCTTCTGCTGTGTAACACATATGCGCGCGCTTACACAGGCTGTA 43936
QY 61 AGGTGTGAATATACAGAGATGACGTGACGTCTTTGGGACCTCCGTTCTCTCATTTGTAAA 120
DB 43935 AGGTGTGAATATACAGAGATGACGTGACGTCTTTGGGACCTCCGTTCTCTCATTTGTAAA 43876
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DB 43875 ATGAGAGTTAATACAGAGCTTCTTCTACTCTCCCAACAGACGTGTTGTCTCCGCGCAGAG 43816
QY 181 GGGCCCAATTTGGTGGCTGTTACGCATCATGTTACCCCAACAGAGCGGCTGACCAATTAAA 240
DB 43815 GGGCCCAATTTGGTGGCTGTTACGCATCATGTTACCCCAACAGAGCGGCTGACCAATTAAA 43756
QY 241 GGGGAACACAGCGCCCGGT 257
DB 43755 GGGGAACACAGCGCCCGGT 43739

RESULT 7
AC024029/c 155668 bp DNA linear HTG 07-JUL-2000
LOCUS Homo sapiens chromosome 11 clone RP11-167N4, WORKING DRAFT
DEFINITION SEQUENCE, 15 unordered pieces.

ACCESSION AC024029
VERSION AC024029.3 GI:7230916
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 155668)
AUTHORS Waterston, R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 155668)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Mar 13, 2000 this sequence version replaced gi:7109555.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Project Information -----
Center project name: H NH0167N04
Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 146450 bases at least Q40
Consensus quality: 149629 bases at least Q30
Consensus quality: 151087 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 154268; sum-of-contigs
Quality coverage: 3.98 in Q20 bases; agarose-fp
Quality coverage: 4.38 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1806: contig of 1806 bp in length
* 1807 1906: gap of unknown length
* 1807 1906: gap of unknown length
* 1907 4798: contig of 2892 bp in length
* 4799 4898: gap of unknown length
* 4899 7312: contig of 2414 bp in length
* 7313 7412: gap of unknown length
* 7413 11277: contig of 3865 bp in length
* 11278 11377: gap of unknown length
* 11378 14368: contig of 2991 bp in length

*	14369	14468:	gap of unknown length
*	14469	20130:	contig of 5662 bp in length
*	20131	20230:	gap of unknown length
*	20231	25513:	contig of 5283 bp in length
*	25514	25613:	gap of unknown length
*	25614	30865:	contig of 5152 bp in length
*	30766	30866:	gap of unknown length
*	30866	37333:	contig of 6472 bp in length
*	37338	37433:	gap of unknown length
*	37438	45571:	contig of 8134 bp in length
*	45572	45671:	gap of unknown length
*	45672	60199:	contig of 14528 bp in length
*	60200	60299:	gap of unknown length
*	60300	71424:	contig of 11125 bp in length
*	71425	71524:	gap of unknown length
*	71525	86218:	contig of 14694 bp in length
*	86219	86318:	gap of unknown length
*	86319	104104:	contig of 17786 bp in length
*	104105	104204:	gap of unknown length
*	104205	155666:	contig of 51464 bp in length

FEATURES

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	mol_type="Genomic DNA"
	db_xref="taxon:9606"
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	/clone="RP11-167N4"
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	45672..60139
gap	/note="assembly_name: Contig23
	60200..60299
	/estimated_length=unknown

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misc_feature      60300.  .71424
                   /note="assembly_name:Contig24
gap              71425. .71524
                   /estimated_length=unknown
misc_feature      71525. .86218
                   /note="assembly_name:Contig25
                   clone_end:17
                   vector_side:right"
gap              86219. .86318
                   /estimated_length=unknown
misc_feature      86319. .104104
                   /note="assembly_name:Contig26
gap              104105. .104204
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misc_feature      104205. .15568
                   /note="assembly_name:Contig27
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Query Match	94.7%	Score 243.4	DB 12	Length 155668
Best Local Similarity	99.2%	Pred. No. 1.8e-70		
Matches 255; Conservative	0	Mismatches 1	Indels 1	Gaps 1

QY	1	TTCCCTGGCAGTCCCTTCTGCTGGTGAATAACATATGGCGCGCTACACAGGGTGTAA	60
Db	69281	TTCCCTGGCAGTCCCTTCTGCTGGTGAATAACATATGGCGCGCTACACAGGGTGTAA	69222
QY	61	AGTGTGAATATCAGAGAGATGACTGAACGTCCTTTGGGACTCCGTTTCCTATTGTAA	120
Db	69221	AGTGTGAATATCAGAGAGATGACTGAACGTCCTTTGGGACTCCGTTTCCTATTGTAA	69162
QY	121	ATGAGAGTTAATATCAGCCCTTCCTTTACACCCCAAAAGCAGCGTGTGTGCCGGGCAGAG	180
Db	69161	ATGAGAGTTAATATCAGCCCTTCCTTTACACCCCAAAAGCAGCGTGTGTGCCGGGCAGAG	69102
QY	181	GGCCCAATTGTGTGCTGTTCAAGCATCAGTTACCCCAAGACGGGTGAGCCCAATTAA	240
Db	69101	GG-CCAATTGTGTGCTGTTCAAGCATCAGTTACCCCAAGACGGGTGAGCCCAATTAA	69043
QY	241	GGCGAACCAAGCCCGGT	257
Db	69042	GGCGAACCAAGCCCGGT	69026

RESULT 8	AF208500	3301 bp	DNA	linear	PRI 09-JAN-2000
LOCUS	AF208500				
DEFINITION	Homo sapiens uncoupling protein 2 (UCP2) gene, promoter and exon 1.				
ACCESSION	AF208500				
VERSION	AF208500.1	GI:6684000			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 3301)				
AUTHORS	Tu,N., Chen,H., Winnikes,U., Reinert,I., Marmann,G., Pirke,K.M. and Lentes,K.U.				
TITLE	Molecular cloning and functional characterization of the promoter region of the human uncoupling protein-2 gene				
JOURNAL	Biochem. Biophys. Res. Commun. 265 (2), 326-334 (1999)				
PUBMED	10558866				
REFERENCE	2 (bases 1 to 3301)				
AUTHORS	Tu,N., Chen,H., Winnikes,U., Reinert,I., Pirke,K.M. and Lentes,K.-U.				
TITLE	Functional characterization of the 5'-flanking and promoter regions of the human UCP3 gene				
JOURNAL	Biochem. Biophys. Res. Commun. (2000) In press				
REFERENCE	3 (bases 1 to 3301)				
AUTHORS	Lentes,K.-U., Tu,N. and Chen,H.				
TITLE	Direct Submission				
JOURNAL	Submitted (26-NOV-1999) Laboratory of Molecular Neurogenetics, Center for Psychobiological and Psychosomatic Research, University				

ORIGIN

0-9 **A B C D E F G H I J K L M N O P Q R S T U V W X Y Z**

100

ACCESSION CQ841485

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1

TITLE Full-length human cdna
FORMATTED By 1400001 2 123 00 TTT 2004

source	1. .3506
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ORIGIN	
1	

to Homo sapiens latent transforming growth factor beta binding

SOURCE Homo sapiens (human)

Hominidae; Homo.

Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,

Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
Oshima, A., Sugiura, A., Kawabata, B., Suzuki, Y., Sugano, S.

JOURNAL **Unpublished**

JOURNAL Submitted (15-JUL-2003) Takao Iwogai, Helix Research Institute,

construction: Helix Research Institute (HRI) (supported by Japan

RAB.
Location/Cust: 4402

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/organism="Homo sapiens"  
/mol_type="rRNA"
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/clone="BRACE3003192"  
/className="Cerebo"]""
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ORIGIN

Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

Db 146 TCCCTGTGCTTTTGAAGCCACACAGCATGGGCTTGAACAGGGCTGCTGTG-AC 88
QY 72 ATCAGGAAGATGACTGAACTCTTTGGGAGCTTCCTCATTTGTAAGAGAGTTAA 131
Db 87 CTGGGAGAGTTACTGAACTCTTTGAGGCTCAGCTTCTCATCTGGAACAGAGCTAA 28
QY 132 TACC 135
Db 27 CAAC 24

RESULT 11
AK647079/c 16256 bp DNA linear PAT 04-MAR-2003
LOCUS Sequence 1271 from Patent EP1270724.
DEFINITION AK647079
ACCESSION AK647079 GI:28800062
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1
AUTHORS Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.
TITLE Guanidine triphosphate-binding protein coupled receptors
JOURNAL Patent: EP 1270724-A 1271 02-JAN-2003;
National Institute of Advanced Industrial Science and Technology
(JIP) ; Center for Advanced Science and Technology Incubation, Ltd.
(JIP)

FEATURES
source Location/Qualifiers
1. 16256
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
join(201..306,760..918,1009..1194,1602..1618,1692..1764,
1837..2040,3954..4181,4272..4457,4863..4879,4953..5072,
5184..5294,6999..7197,7651..7809,7900..8085,8493..8586,
8742..8932,14104..14223,14326..14487,14579..14707,
15950..16056)
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD69665.1"
/db_xref="GI:28800063"
translation="MPGVCRHGDCLNPPSGYRCVCPRGHSIGSPRTQCTADKPEKSL
CRLVSPRHQCCPLTLTLRLRLCCSVGKAMARQRCPTDSTAFAKELCPAGKGYH
ILTSHTLTIQGESDPSFLHPDGPPEPQDLPSPOAPPEETEEERGTDSFVSE
ERVQOQSHPTATTPAPRPVLDLSQAGVRAKTEVERASVNIYSDSALPAPLI
SRSPPTMFLPDLPPSRSAVIAITQVAGQRDVNAVQAMPPTMAPADPDE
EKSLCPRLVSPRHQCCPLTLTLRLRLCCSVGKAMARQRCPTDSTAFAKELCPAG
KGYHILTSHTLTIQGESDPSFLHPDGPPEPQDLPSPOAPPEETEEERGTDS
PUSERSVOQSHPTATTPAPRPVLDLSQAGVRAKTEVERASVNIYSDSALPAPLI
SRSPPTMFLPDLPPSRSAVIAITQVAGQRDVNAVQAMPPTMAPADPDE
DKLNNPGRVRCVCPRGHSIGSPRTQCTADKPEKSLCPRLVSPRHQCCPLTLRLRL
LCCSVGKAMARQRCPTDSTAFAKELCPAGKGYHILTSHTLTIQGESDPSFLHPD
DGPPEPQDLPSPOAPPEETEEERGTDSVSMRTQGVNRGQGGADFLIOLP
OAGVGRATTEVERASVNIYSDSALPAPLI SRSPPTMFLPDLPPSRSAVIA
PIQVYRTDECRANQNICGAGECVPPPTDVSCHNCPPTSPAPLIVNCEAPPCPC
RGICMNTGSSYNCHNCRGYRLHVGAGRSVCVGRQGGGLDNECAKPLCGDGGFC
INPFGHYKNCYPGYRLKASRPVCEVQAAVSVDYGTAFQPGQSKPPIQLQNKT
LAG"

ORIGIN
Query Match 16.2%; Score 41.6; DB 2; Length 16256;
Best Local Similarity 63.7%; Freq. No. 0.028;
Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 12 TCCCTGTGCTTTTGAAGCCACACAGCATGGGCTTGAACAGGGCTGCTGTG-AT 71
Db 13196 TCCCTGTGCTTTTGAAGCCACACAGCATGGGCTTGAACAGGGCTGCTGTG-AC 13138
QY 72 ATCAGGAAGATGACTGAACTCTTTGGGAGCTTCCTCATTTGTAAGAGAGTTAA 131

Db 13137 CTGGGAGAGTTACTGAACTCTTTGAGGCTCAGCTTCTCATCTGGAACAGAGCTAA 13078
QY 132 TACC 135
Db 13077 CAAC 13074

RESULT 12
AP000579 70975 bp DNA linear HTG 30-MAY-2000
LOCUS Homo sapiens chromosome 11 clone Xkp1-110a10 map 11q43, WORKING
DEFINITION DRAFT SEQUENCE, 15 unordered pieces.
AP000579
ACCESSION AP000579 GI:8118786
VERSION AP000579.2
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Toroki, Y., Watanabe, H. and Sakaki, Y.
TITLE Homo sapiens 70,975 genomic DNA of 11q43
JOURNAL Published Only in Database (1999)
2 (bases 1 to 70975)
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Toroki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitaato Univ., 1-15-1 Kitaato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL: http://hgp.gsc.riken.go.jp/, Tel: 01-42-778-9923,
Fax: 01-42-778-9924)
On May 31, 2000 this sequence version replaced gi:6997470.

COMMENT
----- Genome Center
Center: RIKEN Genomic Sciences Center (GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDiv11
Center clone name: Xkp1-110a10
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 64047 bases at least Q40
Consensus quality: 6606 bases at least Q30
Consensus quality: 68080 bases at least Q20
Insert size: 69575; sum-of-contigs
Quality coverage: 5.40x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of
15 contigs. The true order of the pieces is not known and their
order in this sequence record is arbitrary. Gaps between the
contigs are represented as runs N, but the exact sizes of the gaps
are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be
preserved

1 24733 24632 contig of 24632 bp in length
24733 34535 contig of 9803 bp in length
34536 40636 contig of 6001 bp in length
40637 45581 contig of 4845 bp in length
45582 49888 contig of 4207 bp in length
49889 53496 contig of 3508 bp in length
53497 56066 contig of 2470 bp in length
56067 58948 contig of 2782 bp in length
58949 60647 contig of 1599 bp in length
60648 62804 contig of 2157 bp in length
62805 64533 contig of 1529 bp in length
64534 66654 contig of 2021 bp in length

66755 68335 contig of 1581 bp in length
 68436 69753 contig of 1318 bp in length
 69854 70975 contig of 1122 bp in length
 Sequence updated (26-May-2000).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 15 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 24632: contig of 24632 bp in length
 * 24732: gap of 100 bp
 * 24733 34535: contig of 9801 bp in length
 * 34536 34635: gap of 100 bp
 * 34636 40636: contig of 6001 bp in length
 * 40637 40736: gap of 100 bp
 * 40737 45581: contig of 4845 bp in length
 * 45582 45681: gap of 100 bp
 * 45682 49888: contig of 4207 bp in length
 * 49889 49988: gap of 100 bp
 * 49989 53496: contig of 3508 bp in length
 * 53497 53596: gap of 100 bp
 * 53597 56066: contig of 2470 bp in length
 * 56067 56166: gap of 100 bp
 * 56167 58948: contig of 2782 bp in length
 * 58949 59048: gap of 100 bp
 * 59049 60647: contig of 1599 bp in length
 * 60648 60747: gap of 100 bp
 * 60748 62904: contig of 2157 bp in length
 * 62905 63004: gap of 100 bp
 * 63005 64533: contig of 1529 bp in length
 * 64534 64633: gap of 100 bp
 * 64634 66554: contig of 2021 bp in length
 * 66555 66754: gap of 100 bp
 * 66755 68335: contig of 1581 bp in length
 * 68336 68435: gap of 100 bp
 * 68436 69753: contig of 1318 bp in length
 * 69754 69853: gap of 100 bp
 * 69854 70975: contig of 1122 bp in length.
 Location/Qualifiers

FEATURES

source

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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="11"
 /map="11q13"
 /clone="XXP1-110A10"
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 /note="assembly_fragment"
 24733. .34535
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 34636. .40636
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 40737. .45581
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 45682. .49888
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 49989. .53496
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 60748. .62904
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 63005. .64533
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 64634. .66554
 /note="assembly_fragment"

misc_feature 66755..68335
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ORIGIN

Query Match 16.2%; Score 41.6; DB 12; Length 70975;
 Best Local Similarity 63.7%; Pred. No. 0.031;
 Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 12 TCCTTCTGCTGATGAAACACATATGCGCGCGCTGACCGAGGTGTAGTGTGAT 71
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 Db 49210 TCCTTGTGCTTTTGAAGCCACACAGCATGGGCTTGAACACGCGCTCAGCTGTG-AC 49268
 QY 72 ATCAGAAATGATGATGAACTGCTTTGGAGCTCGCTTCCATGTAATGAGGTTAA 131
 |||||
 Db 49269 CTGGGCGAGTTACTGAACTCTTGAAGCTCAGCTTCTCATCTGAAACGAGGCTAA 49328
 QY 132 TRAC 135
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 Db 49329 CAAC 49332

RESULT 13

AP000803

LOCUS

Homo sapiens chromosome 11 clone RP11-642F7 map 11q13, WORKING
 DEFINITION
 DRAFT SEQUENCE, 39 unordered pieces.

ACCESSION

AP000803

VERSION

HTG; HTGS PHASE1; HTGS_DRAFT.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

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REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

Submitted (30-NOV-1999) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
 Japan (E-mail:hattori@gsc.riken.go.jp,
 URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
 Fax:81-42-778-9924)
 On May 31, 2000 this sequence version replaced gi:6997640.
 ----- Genome Center
 Center: RIKEN Genomic Sciences Center (GSC)
 Center code: RIKEN
 Web site: http://hgp.gsc.riken.go.jp/
 Contact: hattori@gsc.riken.go.jp
 ----- Project Information
 Center project name: HumDrat11
 Center clone name: RP11-642F7
 ----- Summary Statistics
 Sequencing vector: PCR products; 100% of reads
 Chemistry: Dye-terminator ET-amersham; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 11753 bases at least Q40
 Consensus quality: 128124 bases at least Q30
 Consensus quality: 133785 bases at least Q20
 Insert size: 136556; sum-of-contigs
 Quality coverage: 4.30x in Q20 bases; sum-of-contigs

 NOTE: This is a 'working draft' sequence. It currently consists of

39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs 'N', but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

```
1 13642 contig of 13642 bp in length
13743 21060 contig of 7318 bp in length
21161 30193 contig of 9033 bp in length
30294 38592 contig of 8299 bp in length
38683 45688 contig of 6996 bp in length
45789 53108 contig of 7320 bp in length
53209 58558 contig of 5350 bp in length
58659 63503 contig of 4845 bp in length
63604 69634 contig of 6031 bp in length
69735 75598 contig of 5864 bp in length
69735 75598 contig of 5864 bp in length
13642 contig of 13642 bp in length
13743 21060 contig of 7318 bp in length
21161 30193 contig of 9033 bp in length
30294 38592 contig of 8299 bp in length
38683 45688 contig of 6996 bp in length
45789 53108 contig of 7320 bp in length
53209 58558 contig of 5350 bp in length
58659 63503 contig of 4845 bp in length
63604 69634 contig of 6031 bp in length
69735 75598 contig of 5864 bp in length
69735 75598 contig of 5864 bp in length
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Sequence updated (26-May-2006).

* NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of 'N', but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

FEATURES

source

```
* 75599 75699: gap of 100 bp
* 75699 80624: contig of 4926 bp in length
* 80625 80724: gap of 100 bp
* 80725 84015: contig of 3291 bp in length
* 84016 84115: gap of 100 bp
* 84116 88588: contig of 4473 bp in length
* 88589 88688: gap of 100 bp
* 88689 91909: contig of 3221 bp in length
* 91910 92009: gap of 100 bp
* 92010 95029: contig of 3020 bp in length
* 95030 95129: gap of 100 bp
* 95130 99186: contig of 4057 bp in length
* 99187 99286: gap of 100 bp
* 99287 102612: contig of 3326 bp in length
* 102613 102712: gap of 100 bp
* 102713 104341: contig of 1629 bp in length
* 104342 104441: gap of 100 bp
* 104442 106114: contig of 1673 bp in length
* 106115 106214: gap of 100 bp
* 106215 108067: contig of 1853 bp in length
* 108068 108167: gap of 100 bp
* 108168 111125: contig of 2958 bp in length
* 111126 111225: gap of 100 bp
* 111226 114483: contig of 3258 bp in length
* 114484 114583: gap of 100 bp
* 114584 116815: contig of 2232 bp in length
* 116816 116915: gap of 100 bp
* 116916 119428: contig of 2513 bp in length
* 119429 119528: gap of 100 bp
* 119529 121747: contig of 2219 bp in length
* 121748 121847: gap of 100 bp
* 121848 122878: contig of 1031 bp in length
* 122879 122978: gap of 100 bp
* 122979 124388: contig of 1410 bp in length
* 124389 124488: gap of 100 bp
* 124489 125909: contig of 1421 bp in length
* 125910 126009: gap of 100 bp
* 126010 127923: contig of 1914 bp in length
* 127924 128023: gap of 100 bp
* 128024 129208: contig of 1185 bp in length
* 129209 129308: gap of 100 bp
* 129309 130851: contig of 1543 bp in length
* 130852 130951: gap of 100 bp
* 130952 131540: contig of 589 bp in length
* 131541 131640: gap of 100 bp
* 131641 133056: contig of 1416 bp in length
* 133057 133156: gap of 100 bp
* 133157 134287: contig of 1131 bp in length
* 134288 134387: gap of 100 bp
* 134388 135444: contig of 1057 bp in length
* 135445 135544: gap of 100 bp
* 135545 136744: contig of 1200 bp in length
* 136745 136844: gap of 100 bp
* 136845 137998: contig of 1154 bp in length
* 137999 138098: gap of 100 bp
* 138099 139195: contig of 1097 bp in length
* 139196 139295: gap of 100 bp
* 139296 140356: contig of 1061 bp in length.
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Location/Qualifiers

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/mol_type="genomic DNA"

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/chromosome="11"

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/clone="RP11-642F7"

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21161. 30193

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30294. 38592

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38683. 45688

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45789. 53108

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53209. 58558

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58659. 63503

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63604. 69634

/note="assembly_fragment"

69735. 75598

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75599. 75699

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75699. 80624

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80625. 80724

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80725. 84015

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84016. 84115

/note="assembly_fragment"

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misc_feature 45789..53108
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misc_feature 58659..63503
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Query Match 16.2% Score 41.6; DB 12; Length 140356;
Best Local Similarity 63.7%; Pred. No. 0.033; Indels 1; Gaps 1;
Matches 79; Conservative 0; Mismatches 44;
```

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QY 12 TCCCTTCCTGCTGTAACACATATGCGCCGCGCTGACAGAGGTGTAGTGTGAAT 71
107409 TCCCTTCCTGCTTGAAGCCACACAGGCGATGGCTTGAACAGGCTCAGCTGTGTG-AC 107467
QY 72 ATCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 131
107468 CTGGGCGAGGTTACTGTAACCTCTTGAAGCTTTCATCTGTAACGAGGCTTA 107527
QY 132 TACC 135
DB 107528 CAA 107531
```

```
RESULT 14 AP001459 150694 bp DNA linear HTG 30-MAY-2000
AP001459/c Homo sapiens chromosome 11 clone RP11-856C23 map 11q13, WORKING
LOCUS DEFINITION DRAFT SSEQUENCE, 44 unordered pieces.
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ACCESSION AP001459.2 GI:8117333
VERSION HTG: HTGS PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
```

```
REFERENCE 1 (bases 1 to 150694)
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```
AUTHORS Hattori M., Ishii K., Toyoda A., Taylor T.D., Hong-Seog P.,
```

```
TITLE Fujiyama A., Yada T., Totoki Y., Watanabe H. and Sakaki Y.
```

```
JOURNAL Homo sapiens 150,694 genomic DNA of 11q13
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REFERENCE Published Only in Database (2000)
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```
AUTHORS Hattori M., Ishii K., Toyoda A., Taylor T.D., Hong-Seog P.,
```

```
TITLE Fujiyama A., Yada T., Totoki Y., Watanabe H. and Sakaki Y.
```

```
JOURNAL Direct Submission
```

```
TITLE Submitted (15-MAR-2000) Masahira Hattori, The Institute of Physical
```

```
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
```

```
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
```

```
Japan (E-mail:hattori@gsc.riken.go.jp, Tel:81-42-778-9923,
```

```
URL:http://hgp.gsc.riken.go.jp/, Fax:81-42-778-9924)
```

```
On May 30, 2000 this sequence version replaced gi:7262592.
```

```
COMMENT ----- Genome Center
```

```
Center: RIKEN Genomic Sciences Center (GSC)
```

```
Center code: RIKEN
```

```
Web site: http://hgp.gsc.riken.go.jp/
```

```
Contact: hattori@gsc.riken.go.jp
```

```
----- Project Information
```

```
Center Project name: HumDrat11
```

```
Center Clone name: RP11-856C23
```

```
----- Summary Statistics
```

```
Sequencing vector: PCR products; 100% of reads
```

```
Chemistry: Dye-terminator ET-amersham; 100% of reads
```

```
Assembly program: Phrap; version 0.990329
```

```
Consensus quality: 123414 bases at least Q40
```

```
Consensus quality: 135962 bases at least Q30
```

```
Consensus quality: 142087 bases at least Q20
```

```
Insert size: 146394; sum-of-contigs
```

```
Quality coverage: 4.08x in Q20 bases; sum-of-contigs
```

NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pieces is not known and the order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```
1 11401 contig of 11401 bp in length
11502 23078 contig of 11577 bp in length
23179 32309 contig of 9131 bp in length
32410 38694 contig of 6285 bp in length
38795 45338 contig of 6544 bp in length
45439 53500 contig of 8062 bp in length
53601 57891 contig of 4291 bp in length
57992 62254 contig of 4263 bp in length
62355 68449 contig of 6095 bp in length
68550 74597 contig of 6048 bp in length
74698 79320 contig of 4623 bp in length
79421 84028 contig of 4608 bp in length
84129 89011 contig of 4883 bp in length
89112 92481 contig of 3370 bp in length
92582 96064 contig of 3483 bp in length
96165 99717 contig of 3553 bp in length
99818 102767 contig of 2950 bp in length
102868 104437 contig of 1570 bp in length
104538 107049 contig of 2512 bp in length
107150 109447 contig of 2298 bp in length
109548 112354 contig of 2807 bp in length
112455 114620 contig of 2166 bp in length
114721 118139 contig of 3419 bp in length
118240 120002 contig of 1763 bp in length
120103 122301 contig of 2199 bp in length
122474 124473 contig of 2072 bp in length
124574 126352 contig of 1779 bp in length
126453 128696 contig of 2244 bp in length
128797 130034 contig of 1238 bp in length
130135 130639 contig of 505 bp in length
130740 131925 contig of 1186 bp in length
132026 134015 contig of 1990 bp in length
134116 135860 contig of 1745 bp in length
135961 137276 contig of 1316 bp in length
137377 138486 contig of 1110 bp in length
138587 140068 contig of 1482 bp in length
140169 141262 contig of 1094 bp in length
141363 142808 contig of 1446 bp in length
142909 144345 contig of 1437 bp in length
144446 145547 contig of 1102 bp in length
145548 146594 contig of 1047 bp in length
146795 147949 contig of 1155 bp in length
148050 149156 contig of 1107 bp in length
149257 150694 contig of 1438 bp in length
```

Sequence updated (26-May-2000).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 44 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 11401: contig of 11401 bp in length

* 11402 11501: gap of 100 bp

* 11502 23078: contig of 11577 bp in length

* 23079 23179: gap of 100 bp

* 23179 32309: contig of 9131 bp in length

* 32310 32409: gap of 100 bp

* 32410 38694: contig of 6285 bp in length

* 38695 38794: gap of 100 bp

* 38795 45338: contig of 6544 bp in length

* 45339 45438: gap of 100 bp

* 45439 53500: contig of 8062 bp in length

* 53501 53600: gap of 100 bp

* 53601 57891: contig of 4291 bp in length

```

* 57892 57991: gap of 100 bp
* 57992 62254: contig of 4263 bp in length
* 62255 62354: gap of 100 bp
* 62355 68449: contig of 6095 bp in length
* 68450 68549: gap of 100 bp
* 68550 74597: contig of 6048 bp in length
* 74598 74697: gap of 100 bp
* 74698 79320: contig of 4623 bp in length
* 79321 79421 84028: contig of 4608 bp in length
* 84029 84128: gap of 100 bp
* 84129 89011: contig of 4883 bp in length
* 89012 89111: gap of 100 bp
* 89112 92481: contig of 3370 bp in length
* 92482 92581: gap of 100 bp
* 92582 96064: contig of 3483 bp in length
* 96065 96164: gap of 100 bp
* 96165 99717: contig of 3553 bp in length
* 99718 99817: gap of 100 bp
* 99818 102767: contig of 2950 bp in length
* 102768 102867: gap of 100 bp
* 102868 104437: contig of 1570 bp in length
* 104438 104537: gap of 100 bp
* 104538 107049: contig of 2512 bp in length
* 107050 107149: gap of 100 bp
* 107150 109447: contig of 2298 bp in length
* 109448 109547: gap of 100 bp
* 109548 112354: contig of 2807 bp in length
* 112355 112454: gap of 100 bp
* 112455 114620: contig of 2166 bp in length
* 114621 114720: gap of 100 bp
* 114721 118139: contig of 3419 bp in length
* 118140 118239: gap of 100 bp
* 118240 120002: contig of 1763 bp in length
* 120003 120102: gap of 100 bp
* 120103 122301: contig of 2199 bp in length
* 122302 122401: gap of 100 bp
* 122402 124473: contig of 2072 bp in length
* 124474 124573: gap of 100 bp
* 124574 126452: contig of 1779 bp in length
* 126453 126552: gap of 100 bp
* 126553 128696: contig of 2244 bp in length
* 128697 128796: gap of 100 bp
* 128797 130034: contig of 1238 bp in length
* 130035 130639: gap of 100 bp
* 130640 130739: gap of 100 bp
* 130740 131925: contig of 1186 bp in length
* 131926 132025: gap of 100 bp
* 132026 134015: contig of 1990 bp in length
* 134016 134115: gap of 100 bp
* 134116 135860: contig of 1745 bp in length
* 135861 135960: gap of 100 bp
* 135961 137276: contig of 1316 bp in length
* 137277 137376: gap of 100 bp
* 137377 138486: contig of 1110 bp in length
* 138487 138586: gap of 100 bp
* 138587 140068: contig of 1482 bp in length
* 140069 140168: gap of 100 bp
* 140169 141262: contig of 1094 bp in length
* 141263 141362: gap of 100 bp
* 141363 142808: contig of 1446 bp in length
* 142809 142908: gap of 100 bp
* 142909 144345: contig of 1437 bp in length
* 144346 144445: gap of 100 bp
* 144446 145547: contig of 1102 bp in length
* 145548 145647: gap of 100 bp
* 145649 146694: contig of 1047 bp in length
* 146695 146794: gap of 100 bp
* 146795 147949: contig of 1155 bp in length
* 147950 148049: gap of 100 bp
* 148050 149156: contig of 1107 bp in length
* 149157 149256: gap of 100 bp

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```

* 149257 150694: contig of 1438 bp in length.
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      /mol_type="genomic DNA"
      /db_xref="taxon:9606"
      /chromosome="11"
      /map="11q13"
      /clone="RP11-856C23"
Query Match
  16.2%; Score 41.6; DB 12; Length 150694;
Best Local Similarity 63.7%; Pred. No. 0.033;
Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;
QY 12 TCCCTTCTGCTGTGAACACATATGCGCCGCGCTGACACGAGGTAAAGTGTGAAT 71
  |||||
Db 109272 TCCCTTGTGCTTTTGAAGCCACACAGCATGAGGCTTGAACAGGCTCAGCTGTGTC-AC 109214
  |||||
QY 72 ATCAGGAAGATGACCTGAAACGCTTTGGGACTCCGTTTCTCATTTGTAATGAGGTTAA 131
  |||||
Db 109213 CTGGGGCAGGTTACTGAACTCTTTGAGGCTTTCATCTGTGAAACGAGGCTTAA 109154
  |||||
QY 132 TACC 135
  |||||
Db 109153 CAAC 109150
  |||||
RESULT 15
AP001362 211382 bp DNA linear PRI 07-JUN-2002
LOCUS
DEFINITION
  Homo sapiens genomic DNA, chromosome 11, clone:RP11-856B14,
  complete sequence.
ACCESSION
  AP001362 GI:21327925
VERSION
  AP001362.5
KEYWORDS
  HTG.
SOURCE
  Homo sapiens (human)
  Organism
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homidae; Homo.
REFERENCE
  1 Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,
    Totoki,Y., Watanabe,H. and Sakaki,Y.
    Homo sapiens genomic DNA
    Published Only in Database (2000)
    2 (bases 1 to 211382)
    Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
    Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
    Direct Submission
    Submitted (06-MAR-2000) Masahira Hattori, The Institute of Physical
    and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
    1-7-22 Suenho-chou,Tsuri-ku, Yokohama, Kanagawa 230-0045, Japan
    Tel:81-45-503-9111, Fax:81-45-503-9170
    URL:http://hgp.gsc.riken.go.jp/,
    Tel:81-45-503-9111, Fax:81-45-503-9170
    On Jun 6, 2002 this sequence version replaced gi:20334322.
COMMENT
  Location/Qualifiers
    1..211382
      /organism="Homo sapiens"
      /mol_type="genomic DNA"
      /db_xref="taxon:9606"
      /chromosome="11"
      /map="11q"
      /clone="RP11-856B14"
ORIGIN
  Query Match
    16.2%; Score 41.6; DB 5; Length 211382;
  Best Local Similarity 63.7%; Pred. No. 0.034;
  Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;
  QY 12 TCCCTTCTGCTGTGAACACATATGCGCCGCGCTGACACGAGGTAAAGTGTGAAT 71
    |||||
  Db 29564 TCCCTTGTGCTTTTGAAGCCACACAGCATGAGGCTTGAACAGGCTCAGCTGTGTC-AC 29622
    |||||

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QY 72 ATCAGGAGATGACTGAGCGTCTTTGGGACTCCGTTTCTCATTTGTAATAAGAGGTAA 131
Db 29623 CTGGGGCAGGTTACTGAACTCTTTGAGGCTCAGCTTCTCATCTGAAAAACGAGGCTAA 29682
QY 132 TACC 135
Db 29683 CAACT 29686

Search completed: June 5, 2006, 22:27:17
Job time : 1745.95 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:15:11 ; Search time 223.597 Seconds
(without alignments)
8013.826 Million cell updates/sec

Title: US-09-869-098a-1_COPY_1133_1389

Perfect score: 257
Sequence: 1 ttcctcgagctccctctcg.....aaagcgaccagcccgct 257

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001s:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	257	100.0	3505	3	AAA62932
2	41.6	16.2	3506	12	AD062971
3	41.6	16.2	16256	10	AD068618
4	37.6	14.6	332	4	AAK64094
5	37	14.4	1510	5	AAK84317
6	36.8	14.3	57013	11	ACN45046
7	36.8	14.3	149612	11	ACN45154
8	35.6	13.9	2425	10	ABZ56972
9	35.4	13.8	4673	5	AAS30048
10	35.4	13.8	4673	10	ADB33385
11	35.4	13.8	7220	4	AAK84030
12	35.4	13.8	143306	6	ABK49586
13	35.4	13.8	152037	15	ABF74705
14	35	13.6	100000	14	ADZ04285
15	35	13.6	100001	15	AEF72834
16	34.8	13.5	110000	11	ACN43998_3
17	34.6	13.5	327	14	ACU59982
18	34.6	13.5	612	6	ABN61814

C	19	34.4	13.4	2258	4	AAL05930
C	20	34.4	13.4	2258	4	ABL98494
C	21	34.4	13.4	13286	13	AD889097
C	22	34.4	13.4	113000	9	ABT44365
C	23	34.4	13.4	133955	11	ACN45170
C	24	34.4	13.4	325791	4	AAS43104
C	25	34.4	13.4	337022	12	ADQ59416
C	26	34.4	13.4	338780	14	ADZ13691
C	27	34	13.2	98606	11	ACN43868
C	28	33.8	13.2	13010	4	AAK72395
C	29	33.8	13.2	13012	4	AAK72396
C	30	33.6	13.1	33112	10	ACC85730
C	31	33.6	13.1	39001	12	AD138715
C	32	33.6	13.1	65608	6	ABL62910
C	33	33.6	13.1	65608	6	ABL64414
C	34	33.6	13.1	65608	6	ABL67668
C	35	33.6	13.1	109646	14	ABD18286
C	36	33.4	13.0	5691	4	AAK55423
C	37	33.4	13.0	5691	4	AAK84439
C	38	33.2	12.9	27499	13	ABD32620
C	39	33.2	12.9	36568	6	ABK50980
C	40	33.2	12.9	62118	11	ACN44566
C	41	33.2	12.9	85121	14	ADZ13027
C	42	33.2	12.9	133767	13	ABD33624
C	43	33.2	12.9	147463	15	AEF80127
C	44	32.8	12.7	127145	13	ADQ80254
C	45	32.6	12.7	110000	8	AAD53224_3

ALIGNMENTS

RESULT 1
ID AAA62932 standard; DNA; 3505 BP.
AC AAA62932;
XX
DT 02-NOV-2000 (first entry)
XX
DE DNA containing human uncoupling protein-2 (UCP-2) promoter region.
XX
KW Promoter; human; uncoupling protein-2; UCP-2; obesity; diabetes;
KM hypotension; hyperlipidaemia; anti-pyretic; da.
XX
OS Homo sapiens.
XX
PN WO200039315-A1.
XX
PD 06-JUL-2000.
XX
PF 22-DEC-1999; 99WO-JP007198.
XX
PR 24-DEC-1998; 98JP-00366719.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Toyoda Y, Kobayashi M, Igaki S;
XX
DR WPI; 2000-452407/39.
XX
PT DNA with promoter region containing regulator sequence of uncoupling
PT protein-2 (UCP-2), applicable in screening anti-obesity, anti-diabetic,
PT hypotensive, anti-hyperlipidemic and anti-pyretic drugs for use in
PT therapy.
XX
PS Claim 4; Fig 1-6; 43p; Japanese.
XX
CC This invention relates to DNA comprising a promoter region containing the
CC regulatory sequences of human uncoupling protein-2 (UCP-2). Included in
CC the invention are a recombinant vector containing the DNA sequence, cells
CC transformed by the vector, and a method for screening for compounds or
CC salts that can promote or inhibit the UCP-2 promoter activity using the

Aal05930 Human rep
Ab198494 Human tes
Ad889097 Human ESR
Abt44365 Partial g
Acn45170 Human gen
Aas43104 Human Oes
Adq59416 Human can
Adz13691 Human can
Acn43868 Mouse gen
Aak72395 Human imm
Aak72396 Human imm
Acc85730 Human kin
Ad18715 Human lim
Ab162910 Breast ca
Ab164414 Stomach c
Ab167668 Oesophagu
Aed18286 Fibroblc
Aak65423 Human imm
Aak84439 Human imm
Abd32620 Human can
Acn44566 Human gen
Adz13027 Human can
Abd33624 Human can
Aef80127 Cancer-as
Adq80254 Hermansky
Continuation (4 of

CC transformants. The DNA and cells transformed using it can be used to
CC screen for anti-obesity, anti-diabetic, hypotensive, anti-hyperlipidemic
CC and anti-pyretic drugs. The present sequence represents DNA containing
CC the UCP-2 promoter sequences

XX SQ Sequence 3505 BP; 671 A; 1053 C; 894 G; 887 T; 0 U; 0 Other;

Query Match 100.0%; Score 257; DB 3; Length 3505;

Best Local Similarity 100.0%; Pred. No. 1,2e-80;

Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCCTGGCAGTCTCTTCTGCTGTGTAACATATGCGCGGCTTGACCGGTGTA 60

DB 1133 TTCCCTGGCAGTCTCTTCTGCTGTGTAACATATGCGCGGCTTGACCGGTGTA 1192

QY 61 AGTGTGATATACAGAGATGACTGAAAGTCTTTGGGACTCGTTTCTCATTTGTA 120

DB 1193 AGTGTGATATACAGAGATGACTGAAAGTCTTTGGGACTCGTTTCTCATTTGTA 1252

QY 121 ATGGAAGTTAATACAGACCTTCTTCTACTCCCAACGCAAGTGTGTTGCCGCGCAGAG 180

DB 1253 ATGGAAGTTAATACAGACCTTCTTCTACTCCCAACGCAAGTGTGTTGCCGCGCAGAG 1312

QY 181 GGGCCAAATTGTTGGCTGTTCAAGCATCAGTACCCCAACAGCGGCTGAGCCCAATTAA 240

DB 1313 GGGCCAAATTGTTGGCTGTTCAAGCATCAGTACCCCAACAGCGGCTGAGCCCAATTAA 1372

QY 241 GGGCAACACAGCGCCGGT 257

DB 1373 GGGCAACACAGCGCCGGT 1389

RESULT 2

ADQ62971/c

ID ADQ62971 standard; cDNA; 3506 BP.

AC ADQ62971;

DT 07-OCT-2004 (first entry)

XX Novel human cDNA sequence #132.

XX ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian;
XX cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis;
XX neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
XX cancer.

OS Homo sapiens.

XX EP1440981-A2.

XX 28-JUL-2004.

XX 21-JUN-2004; 2004EP-00001196.

XX 21-JAN-2003; 2003JP-00102206.

XX 09-MAY-2003; 2003JP-00131392.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Tsogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

XX Yamamoto J, Isono Y, Negai K, Irie R;

XX WPI; 2004-535376/52.

XX P-PSDB; ADQ65159.

XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
XX Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

XX Claim 1; SEQ ID NO 132; 2449bp; English.

XX The invention relates to 2495 novel polynucleotides (I) and their encoded
XX polypeptides, sequences hybridizing to these nucleotides, sequences

CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a nucleotide
CC sequence of the invention.

XX SQ Sequence 3506 BP; 647 A; 1039 C; 1184 G; 636 T; 0 U; 0 Other;

Query Match 16.2%; Score 41.6; DB 12; Length 3506;

Best Local Similarity 63.7%; Pred. No. 0.0013;

Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 12 TTCCCTTCTGCTGTGTAACATATAGCGCGGCTGACAGAGGTGTAAGTGTGAAT 71

DB 146 TTCCCTTGTCTTTTGAAGCCACACAGGATGGGCTTGAACAGGCTAGCTGTG-AC 88

QY 72 ATCAGAGAATGACTGAACGCTCTTTGGGACTCGCTTCTCATTTGTAATAAGAGTTAA 131

DB 87 CTGGGCAAGTTACTGAACCTCTTTGAGGCTCAGCTTCTCATTTGTAATAAGAGCTAA 28

QY 132 TACC 135

DB 27 CAAAC 24

ADQ6818/c

ID ADQ6818 standard; DNA; 16256 BP.

AC ADQ6818;

DT 01-JAN-2004 (first entry)

XX Human GPCR gene SEQ ID NO:1271.

XX ds; gene; human; GPCR;

XX guanosine triphosphate-binding protein coupled receptor; gene therapy.

XX Homo sapiens.

XX EP1270724-A2.

XX 02-JAN-2003.

XX 18-JUN-2002; 2002EP-00013517.

XX 18-JUN-2001; 2001JP-00246789.

XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX Suwa M, Asai K, Akiyama Y, Aburatani H;

XX WPI; 2003-315783/31.

XX P-PSDB; ADQ6819.

XX Claim 1; SEQ ID NO 1271; 28pp; English.

XX The invention relates to a novel polynucleotide encoding a guanosine

XX triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of

XX the invention may have a use in gene therapy. The polynucleotide and

XX polypeptide are useful for preparing a composition for treating a patient

XX in need of increased or suppressed activity or expression of the

XX guanine triphosphate-binding protein coupled receptor. The

XX polynucleotide sequences shown in ADQ6818-ADQ67616 encode GPCR's of the

XX invention.

Sequence 16256 BP; 3574 A; 4360 C; 4175 G; 3847 T; 0 U; 300 Other;
Query Match 16.2%; Score 41.6; DB 10; Length 16256;
Best Local Similarity 63.7%; Pred. No. 0.0025;
Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;
QY 12 TCCCTTCTGCTGTGAAACATATAGCGCGGCTGACCGAGGTGTAAGTGTGAAT 71
DB 13196 TCCCTTGTGCTTTTGAAGCCACACAGGCATGGGCTTGAACACGGCTCAGCTGTGTG-AC 13138
QY 72 ATCAGGAAGATGACTGACGCTTTGGAGCTCCGCTTCCCATCTGTAATAATGAGGTTAA 131
DB 13137 CTGGGGAGGTTACTGTAACCTTTGAGGCTCAGCTTTCATCTGGAACGAGGCTAA 13078
QY 132 TACC 135
DB 13077 CAAAC 13074
RESULT 4
AAK64094/c
ID AAK64094 standard; cDNA; 332 BP.
XX AAK64094;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:9154.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytosolic; gene therapy; vaccine; metastasis; ss.
OS Homo sapiens.
XX
PN WC0200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WC-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
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PH	Key	Location/Qualifiers
FT	CDS	2032..2274 /*tag=8 /product="8.8"
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PN	CN1355192-A.	
XX		
PD	26-JUN-2002.	
XX		
PF	01-DEC-2000; 2000CN-00127648.	
XX		
PR	01-DEC-2000; 2000CN-00127648.	
PA	(UYFU-) UNIV FUDAN.	
XX		
P1	Mao Y, Xie Y;	
XX		
DR	WPI, 2003-000129/01. P-PsDB; ABP60159.	
XX		
PT	Polypeptide-lipocyte differentiation associated protein 8.8 and polynucleotide for coding it.	
PS	Claim 6; Page 26-27 (disclosure); 34pp; Chinese.	
CC	The invention relates to a lipocyte differentiation associated protein designated 8.8. Also disclosed are the polynucleotide encoding the CC polypeptide, and the process for preparing this polypeptide using DNA recombination techniques. The application of the polypeptide is in CC treating diseases such as obesity and Alexander disease. The current sequence represents the lipocyte differentiation associated protein 8.8 encoding cDNA	
SQ	Sequence 2425 BP; 910 A; 361 C; 439 G; 715 T; 0 U; 0 Other;	
Query Match	13.9%; Score 35.6; DB 10; Length 2425;	
Best Local Similarity	58.5%; Pred No. 0.15; Mismatches 44; Indels 0; Gaps 0	
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DB	903 TAGAGCCCTGGCTGCGCACTTACTTCGGTGTAATGTAACAAGTTGCTCAATTCTT 962	
OY	95 TTGGAGCTCCGTTTCTCATTTGTAATAAGAGTTAATCCAGCCT 140	
DB	963 ATTGTCTCAGTTTCTTCATTATATAAAGAAGATAATATGGCAT 1008	
RESULT 9		
ID	AAS30048/c	
XX	AAS30048 standard; DNA; 4673 BP.	
XX		
AC	AAS30048;	
XX		
DT	21-NOV-2001 (first entry)	
XX		
DE	Human lung antigen genomic DNA #118.	
XX		
KM	Lung antigen protein; human; mouse; rabbit; goat; horse; cat; dog;	
KM	chicken; sheep; immunosuppressive; antiathritic; vasotropic;	
KM	antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective;	
KM	cerebroprotective; nootropic; antibacterial; vinicide; fungicide; cancer;	
KM	ophthalmological; vulnery; gene therapy; autoimmune disease; neoplasm;	
KM	hyperproliferative disorder; breast; liver; cardiovascular disorder; de;	
KM	cerebrovascular disorder; nervous system disorder; bacterial infection;	
KM	fungal infection; viral infection; ocular disorder; endocrine disorder;	
KM	gastrointestinal disorder; renal disorder; respiratory disorder;	
KM	wound healing; skin aging; organ transplantation; food preservative;	
XX	tissue regeneration; anti-infertility; food additive.	
OS	Homo sapiens.	
XX		
PN	WO200155303-A2.	

XX	02 -AUG-2001.	
PD		
XX	17 -JUN-2001,	2001MO-US01301.
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 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 PT Rosen CA, Barash SC, Ruben SM;
 XX

DR WPI; 2001-457723/49.
 XX
 XX Isolated polypeptide for treating, preventing and/ or prognosing
 PT respiratory disorders related to the lung including lung cancers and also
 PT for testing and detection e.g. diagnosis.
 XX
 PS Claim 1; SEQ ID NO 312; 507bp; English.
 XX
 CC Sequences AAS29931-AS30164 represent genomic DNA molecules, which encode
 CC the lung antigen polypeptides of the invention. Lung antigen polypeptides
 CC and their associated polynucleotides are useful in the diagnosis,
 CC treatment and prevention of various types of disorders in e.g. humans,
 CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A
 CC pathological condition can be determined by detecting the presence or
 CC absence of a mutation in a lung antigen polynucleotide. The treatable
 CC disorders include autoimmune diseases such as rheumatoid arthritis,
 CC hyperproliferative disorders such as neoplasms of the breast or liver,
 CC cardiovascular disorders such as cardiac arrest, cerebrovascular
 CC disorders such as cerebral ischaemia, nervous system disorders such as
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi,
 CC ocular disorders such as corneal infection, endocrine disorders such as
 CC premature labour and infertility, gastrointestinal disorders such as
 CC Crohn's disease, renal disorders such as glomerulonephritis and
 CC respiratory disorders such as asthma and pleurisy. The polypeptides can
 CC also be used to aid wound healing, to prevent skin aging due to sunburn,
 CC to maintain organs before transplantation, to regenerate tissues and in
 CC chemotaxis. The polypeptides can also be used as a food additive or
 CC preservative to increase or decrease storage capabilities. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

Query Match 13.8%; Score 35.4; DB 5; Length 4673;
 Best Local Similarity 55.2%; Pred. No. 0.24;
 Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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 Db 141 TAAACGTTAACTTTGGAATGTGCTTAAACGTGTGTCTCACTTCCTCATCTTT 82
 QY 119 AAATGAGCTTATACCAAGCTTCTTACTCCCAACGACGCTTTGTCCGGCAG 178
 Db 81 AAAGAAAGGATATGACACTGTATGATATTAATCATATACATATGAGACACTTCAAC 22
 QY 179 AGGAC 183
 Db 21 AGTGC 17

RESULT 10
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 ID ADB33385 standard; DNA; 4673 BP.

AC ADB33385;

DT 04-DEC-2003 (first entry)

DE Human novel lung related polypeptide DNA SEQ ID NO 312.

XX gene therapy; lung antigen; neoplasia; acute myelogenous leukemia;
 KW adenocarcinoma; respiratory disorder; chronic rhinitis; sinusitis;
 KW immunodeficiency; X-linked agammaglobulinemia;
 KW X-linked infantile agammaglobulinemia; inflammatory disorder;
 KW adrenailitis; alveolitis; immune complex disease; serum sickness;
 KW polyarteritis nodosa; bleeding disorder; thrombocytopenia;
 KW Von Willebrand's disease; acquired platelet dysfunction; kidney failure;
 KW multiple myeloma; macropilage related disorder; Gaucher's disease;
 KW Meilman-Pick disease; tumour; colon cancer; pancreatic cancer;
 KW renal disorder; nephritis; bone disorder; Albers-Schönberg disease;
 KW bowleg; muscle disorder; Becker's muscular dystrophy;
 KW Duchenne's muscular dystrophy; nervous disorder; ischaemic lesion;
 KW traumatic lesion; endocrine disorder; Cushing's syndrome;
 KW corticosteroid deficiency; gastrointestinal disorder; dysphagia;

KW gastric reflux; human; da.
XX
OS Homo sapiens.
XX
PN US2003054368-A1.
XX
PD 20-MAR-2003.
XX
PF 22-FEB-2002; 2002US-00079854.
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XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX WPI; 2003-695900/66.
DR
PT Novel isolated lung antigen polypeptides useful for treating, preventing,
PT diagnosing acute myelogenous leukemias, adenocarcinoma, thrombocytopenia,
PT von Willebrand's disease.
XX
PS Disclosure; SEQ ID NO 312; 178bp; English.
XX
XX The invention relates to an isolated lung antigen polypeptide sequence or
CC encoded sequence in a cDNA clone. The polypeptide and its polynucleotide
CC are useful for treating, preventing, diagnosing and/or prognosing
CC diseases and/or disorders such as pathological cell proliferative
CC neoplasias e.g. acute myelogenous leukemias, adenocarcinoma; respiratory
CC disorders such as chronic rhinitis, sinusitis; immunodeficiencies such as
CC X-linked agammaglobulinaemia, X-linked infantile agammaglobulinaemia;
CC inflammatory disorders such as adenitis, alveolitis; immune complex
CC diseases such as serum sickness; polyarteritis nodosa; bleeding disorders
CC such as thrombocytopenia, von Willebrand's disease; acquired platelet
CC dysfunction such as kidney failure, multiple myeloma; disorders
CC associated with macrophage numbers and/or macrophage function such as
CC Gaucher's disease, Neimann-Pick disease; tumors such as colon cancer,
CC pancreatic cancer; renal disorders such as kidney failure, nephritis;
CC bone disorders such as Albers-Schonberg disease, bowlegs; muscle
CC disorders such as Becker's muscular dystrophy, Duchenne's muscular
CC dystrophy; nervous disorders such as ischemic lesions, traumatic lesions
CC ; endocrine disorders such as Cushing's syndrome, corticosteroid

Query Match 13.8%; Score 35.4; DB 10; Length 4673;
Best Local Similarity 55.2%; Pred. No. 0.24;
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 59 TAAGTGTGATATATCAGGAAGATGACGCTTTGGAGCTCCGTTCTCATTTGTA 118
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DB 81 AAGAAGGAGTATGACACTGTATGATTAATACATATATGAGGACACTTTCAC 22
QY 179 AGGCG 183
DB 21 AGTGC 17

RESULT 11
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AC AAK84030;
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DT 07-NOV-2001 (first entry)
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DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38842.
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XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KM cytostatic; gene therapy; vaccine; metastasis; ds.
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OS Homo sapiens.
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XX WO200157182-A2.
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PF 17-JAN-2001; 2001WO-US001354.
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XX	PR	05-JAN-2001;	2001US-0259678P.
XX	PA	(HUMA-) HUMAN GENOME SCI INC.	
XX	PT	Rosen CA, Barash SC, Ruben SM;	
XX	DR	WPI; 2001-483426/52.	
XX	PT	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	
XX	PS	useful for preventing, diagnosing and/or treating cancers and metastasis	
XX	PS	Disclosure; SEQ ID NO 38842; 3071pp + Sequence Listing; English.	

CC	AAK54951. to AAK44702 encode the human immune/haematopoietic antigen (I)
CC	amino acid sequences given in AAK82170 to AAK91921. (I) have cytotoxic
CC	activity, and can be used in gene therapy and vaccine production. (I)
CC	proteins and polynucleotides may be used in the prevention, diagnosis and
CC	treatment of diseases associated with inappropriate (I) expression. For
CC	example, they may be used to treat disorders associated with decreased
CC	expression by rectifying mutations or deletions in a patient's genome
CC	that affect the activity of (I) by expressing inactive proteins or to
CC	supplement the patients own production of (I). Additionally, (I)
CC	polynucleotides may be used to produce the secreted (I), by inserting the
CC	nucleic acids into a host cell and culturing the cell to express the
CC	protein. (I) proteins and polynucleotides may be used to prevent,
CC	diagnose and treat immune/haematopoietic-related diseases, especially
CC	cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC	to AAK87694 represent human immune/haematopoietic antigen genomic
CC	sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC	represent sequences used in the exemplification of the present invention
XX	
SO	Sequence 7220 BP; 2177 A; 1230 C; 1433 G; 2380 T; 0 U; 0 Other;
Query Match	13.8%; Score 35.4; DB 4; Length 7220;
Best Local Similarity	55.2%; Pred. No. 0.29;
Matches	69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
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OY	119 AAATGGAGGTTAATACGAGCCTTCTTACTCCCCANAAGCAGCGTGTTCGCCGGCAG 178
DB	4809 AAGAAGAGGATATATGACACTGTTTATGATTAATTACATATATACATTTGGAGACATTTTAA 4750
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DB	4749 AGTGC 4745
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XX	
DT	15-JUL-2002 (first entry)
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XX	
KM	Human, ds; gene; transporter; transgenic; transporter mediated disease;
KM	drug screening; pharmacogenomic analysis; chromosome 18; SNP;
KM	single nucleotide polymorphism.
XX	
OS	Homo sapiens.
XX	
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XX AEP74705;
AC
XX
XX 06-APR-2006 (first entry)
DT
XX
XX Human polynucleotide #219.
DB
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XX Diagnosis; gene regulation; gene expression;
KM post traumatic stress disorder; psychiatric disorder; tranquilizer; gene;
KM ds.
XX
XX Homo sapiens.
OS
XX
XX MO2006013561-A2.
PN
XX
XX 09-FEB-2006.
PD
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XX 02-AUG-2005; 2005MO-IL000824.
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XX 02-AUG-2004; 2004US-0592408P.
XX
XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.
XX
XX Segman R, Shalev A, Goltser T, Friedman N, Shefi N, Kaminski N;
PI
XX WPI; 2006-145797/15.
DR
XX
XX New kit comprising 10 and no more than 574 polynucleotides capable of
PT specifically binding at least one specific polynucleotide sequence,
PT useful for determining predisposition of a subject to develop PTSD, or
PT for diagnosing PTSD.
XX
XX Claim 1, SEQ ID NO 219, 157BP; English.
PS
XX
XX The invention relates to a kit for determining predisposition of a
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CC subject to developing post-traumatic stress disorder (PTSD) comprising at
CC least 10 and no more than 574 polynucleotides, where each of the
CC polynucleotides is capable of specifically binding at least one specific
CC polynucleotide sequence. The invention also relates to a kit for
CC diagnosing PTSD in a subject, agents for the manufacture of the kit
CC cited comprising the polynucleotides cited, and a microarray comprising
CC at least 10 and no more than 904 oligonucleotides where each of the
CC oligonucleotides is capable of specifically binding at least one specific
CC polynucleotide sequence. The kit comprises each of the polynucleotides
CC selected from an oligonucleotide molecule, a cDNA molecule, a genomic
CC molecule and an RNA molecule. Each of the polynucleotides is at least 10
CC and no more than 50 nucleic acids in length. Each of the polynucleotides
CC is bound to a solid support. The kit also comprises at least one reagent
CC suitable for detecting hybridization of the polynucleotides and at least
CC one RNA transcript. The kit further comprises packaging materials
CC packaging the at least one reagent and instructions for using the kit in
CC determining predisposition of the subject to developing PTSD or for
CC diagnosing the disease. The microarray comprises oligonucleotides of at
CC least 10 and no more than 40 nucleic acids in length. The agent is
CC capable of regulating an expression level of at least one gene as a
CC pharmaceutical or for the manufacture of a medicament identified for
CC preventing PTSD. The kit is useful for determining predisposition of a
CC subject to developing PTSD or for diagnosing PTSD. This sequence
CC represents a human polynucleotide of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
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Sequence 152037 BP; 44112 A; 33269 C; 33124 G; 41532 T; 0 U; 0 Other;

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Query Match 13.8%; Score 35.4; DB 15; Length 152037;
Best Local Similarity 69.6%; Pred. No. 1.1;
Matches 48; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
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DB 22903 AATCTCAGGCAAGTACTGACCTCTGTGACTCAGTGTCCATCTTAAATGAGCA 22962
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OY 129 TAATACCAG 137
DB 22963 TAATAATAG 22971
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XX ADZ04285;
AC
XX
XX 16-JUN-2005 (first entry)
DT
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XX Human leukotriene A4 hydrolase (LTA4H) gene Seg1D1.
DB
XX
XX myocardial infarction; cardiac; vasotropic; antianginal;
KM antiarteriosclerotic; antidiabetic; hypotensive; antilipemic; anorectic;
KM diabetes; hypertension; hypercholesterolemia; obesity; unstable angina;
KM blood; chromosome-12; gene; ds.
XX
XX Homo sapiens.
OS
XX
XX MO2005027886-A2.
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XX
XX 31-MAR-2005.
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PA
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XX Helgadóttir A, Gurney ME, Hakonarson H, Gulcher JR;
PI
XX WPI; 2005-262656/27.
XX
```

DR P-PSDB; AD204287.

XX Use of leukotriene inhibitor for preventing or treating myocardial
PT infarction or decreasing susceptibility to myocardial infarction and
PT acute coronary syndrome.

PS Example 1; SEQ ID NO 1; 201pp; English.

CC This invention relates to a novel method of preventing or treating
CC myocardial infarction (MI) or decreasing susceptibility to MI or acute
CC coronary syndrome (ACS) in an individual which comprises administration
CC of a leukotriene inhibitor. The invention may be useful for the
CC development of compounds with a cardiant, vasotropic, antianginal,
CC antiarteriosclerotic, antidiabetic, hypotensive, antileptic or anorectic
CC activity acting as a leukotriene inhibitor. The invention is useful for
CC preventing or treating myocardial infarction or decreasing susceptibility
CC to myocardial infarction in an individual, who has at least one risk
CC factor of haplotype or other variant for myocardial infarction (MI) in
CC any MI disease gene, haplotype or variant in 5-lipoxygenase activating
CC protein (FLAP), haplotype or other variant in the leukotriene A4
CC hydroxylase (LTA4H) gene or a polymorphism in an LTA4H nucleic acid. The
CC method of the invention may also be useful for preventing or treating
CC diabetes, hypertension, hypercholesterolemia, elevated lip(a), obesity,
CC past/current smoker, acute coronary syndrome such as unstable angina, non
CC -ST-elevation myocardial infarction (NSTEMI) or ST-elevation MI (STEMI)
CC in an individual who has atherosclerosis or who requires treatment (for
CC example angioplasty, stents, coronary artery bypass graft) to restore
CC blood flow in arteries, and for decreasing risk of a subsequent
CC myocardial infarction in an individual who has had at least one
CC myocardial infarction. The present sequence is that of the human
CC leukotriene A4 hydroxylase (LTA4H) gene, located on chromosome 12q23, which
CC was used during the development of the method of the invention. Note: The
CC present sequence contains introns, the number and location of which are
CC not provided in the specification.

XX SQ Sequence 100000 BP; 29762 A; 21176 C; 20553 G; 28509 T; 0 U; 0 Other;

Query Match 13.6%; Score 35; DB 14; Length 100000;

Best Local Similarity 61.5%; Pred. No. 1.3; Matches 56; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 42 CCGGCTGACCGAGGTGTAAGTGTGAATATACGAAGATGACTGAACGCTTTGGGAC 101

Db 22966 CTGGCTCTGCGCATTTGGTATGATGACTTGTGGCGAAGGATTGACTTCTCTGGGCC 23025

QY 102 TCCGTTTCTCATTTGTAATAATGAGGTTAAT 132

Db 23026 TCAGTTGCTCATCTGTAAATGAAGATAAT 23056

RESULT 15

AEF72834 ID AEF72834 standard; DNA; 100001 BP.

XX AEF72834;

DT 06-APR-2006 (first entry)

XX Human leukotriene A4 hydroxylase (LTA4H) gene - SEQ ID 718.

XX propylaxis; SNP detection; myocardial infarction; cardiant;

KM leukotriene A4 hydroxylase; LTA4H; gene; ds.

XX Homo sapiens.

XX US2006019269-A1.

XX 26-JAN-2006.

XX 30-MAR-2005; 2005US-00096191.

XX 17-OCT-2002; 2002US-0419433P.

XX 21-FEB-2003; 2003US-0449331P.

PR 17-SEP-2003; 2003US-0503587P.
PR 16-OCT-2003; 2003WO-US032556.
PR 30-JAN-2004; 2004US-00769744.
PR 22-APR-2004; 2004US-00830477.
PR 17-SEP-2004; 2004WO-US030582.
PR 10-JAN-2005; 2005US-0642909P.
PR 31-JAN-2005; 2005WO-US003312.

XX (DECO-) DECODE GENETICS INC.

PI Helgadottir A, Hakonarson H, Gulcher JR, Gurney ME;

DR WPI; 2006-124282/13.

DR P-PSDB; AEF72836.

PT Prophylaxis therapy for myocardial infarction comprises selecting a human
PT by screening for genetic variation in e.g. 5-lipoxygenase activating
PT protein gene, administering a composition comprising a agent and
PT monitoring inflammatory marker.

PS Disclosure; SEQ ID NO 718; 134pp; English.

CC The invention comprises a method of prophylaxis therapy for myocardial
CC infarction. The method involves selecting a human subject susceptible to
CC myocardial infarction by screening for a genetic variation in either the
CC 5-lipoxygenase activating protein (FLAP) gene or the leukotriene A4
CC hydroxylase (LTA4H) gene. The method further involves administration of a
CC therapeutic agent and monitoring at least one inflammatory marker in the
CC subject before and during the prophylaxis treatment. The method of the
CC invention is useful for prophylaxis therapy for myocardial infarction.
CC The present DNA sequence represents the human LTA4H gene. NOTE: The
CC present sequence is not shown in the specification, but has been
CC retrieved from the USPTO website.

XX SQ Sequence 100001 BP; 29763 A; 21176 C; 20553 G; 28509 T; 0 U; 0 Other;

Query Match 13.6%; Score 35; DB 15; Length 100001;

Best Local Similarity 61.5%; Pred. No. 1.3; Matches 56; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 42 CCGGCTGACCGAGGTGTAAGTGTGAATATACGAAGATGACTGAACGCTTTGGGAC 101

Db 22966 CTGGCTCTGCGCATTTGGTATGATGACTTGTGGCGAAGGATTGACTTCTCTGGGCC 23025

QY 102 TCCGTTTCTCATTTGTAATAATGAGGTTAAT 132

Db 23026 TCAGTTGCTCATCTGTAAATGAAGATAAT 23056

Search completed: June 5, 2006, 16:57:58
Job time : 227.597 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:39:00 ; Search time 1779.61 Seconds
(without alignments)
8075.514 Million cell updates/sec

Title: US-09-869-098a-1_COPY_1133_1389

Perfect score: 257
Sequence: 1 ttcctcgcagctccctctcg.....aaagcgaccagcccgct 257

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	255.4	99.4	941	2	BG720951 602692616
2	77	30.0	314	1	AA903751 0K64C05.8
3	41.6	16.2	555	8	CN282871 170004245
4	41.6	16.2	558	9	DA094053 DA094053
5	40	15.6	855	1	AJ817111 AJ817111
6	38.6	15.0	444	8	CV402643 CV402643
7	38.6	15.0	685	12	CE142616 CE142616
8	37.6	14.6	777	12	CC004107 PUGJ51TB
9	36.8	14.3	641	13	DU383369 DU383369
10	36.8	14.3	749	14	DU516086 109860979
11	36.4	14.2	374	11	AQ024482 HS_2180_B
12	36.4	14.2	707	14	CR095999 Forward_B
13	36.2	14.1	571	11	AZ412085 IM015SH19
14	36	14.0	810	13	CL654603 PRI0121a
15	35	14.0	906	14	CT069763 Sus scrofa
16	35	14.0	1163	12	CG745747 P038-4-A1
17	35.8	13.9	614	11	AQ315012 RBC111-94
18	35.8	13.9	870	14	CT256996 Sus scrofa
19	35.6	13.9	268	13	CZ414110 1009813 R

20	35.6	13.9	397	11	AQ428350	AQ428350	CTBT1-E1-
21	35.6	13.9	516	11	AQ428343	AQ428343	CTBT1-E1-
22	35.6	13.9	523	9	DA589393	DA589393	CTBT1-E1-
23	35.4	13.8	760	14	CT184624	CT184624	Sus scrofa
24	35.4	13.8	792	14	CR795773	CR795773	GR0AA13C
25	35.4	13.8	810	1	AU119919	AU119919	AU119919
26	35	13.6	335	11	AQ018075	AQ018075	CTBT1-E1-
27	35	13.6	417	11	AQ020685	AQ020685	CTBT1-E1-
28	35	13.6	572	14	DU513025	DU513025	109860962
29	35	13.6	644	14	AG158418	AG158418	Pan trogl
30	34.8	13.5	434	2	BG952217	BG952217	CM4-CT062
31	34.8	13.5	592	11	AQ423759	AQ423759	CTBT1-E1-
32	34.8	13.5	655	14	DU481223	DU481223	109841594
33	34.8	13.5	676	13	DU233749	DU233749	109857402
34	34.8	13.5	680	14	AG092833	AG092833	Pan trogl
35	34.8	13.5	711	13	DU438587	DU438587	109842102
36	34.8	13.5	737	12	CE199080	CE199080	tigr-gss-
37	34.8	13.5	755	14	CT180346	CT180346	Sus scrofa
38	34.8	13.5	780	13	DU176408	DU176408	109853345
39	34.8	13.5	833	13	DU193469	DU193469	109855323
40	34.6	13.5	266	1	AA091849	AA091849	mm0333.se
41	34.6	13.5	327	12	CG891660	CG891660	Ycm1330E3
42	34.6	13.5	480	11	AQ332789	AQ332789	HS 5008 A
43	34.6	13.5	589	11	AQ625001	AQ625001	CTBT1-E1-
44	34.6	13.5	593	11	AQ628004	AQ628004	CTBT1-E1-
45	34.6	13.5	727	11	AQ417175	AQ417175	RBC11-11-2

ALIGNMENTS

RESULT 1
BG720951/c
LOCUS
DEFINITION
602692616F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4825178 5',
mRNA sequence.
ACCESSION
BG720951 GI:14000138
VERSION
BG720951.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
1 (bases 1 to 941)
NIH-MGC <http://mgc.ncl.nih.gov/>
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LHAM10737 row: O column: 03
High quality sequence stop: 666.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4825178"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTVN-3', size-selected for average
insert size 2.2 kb and normalized to R0T 5. This is a

ORIGIN

primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

Query Match 99.4%; Score 255.4; DB 2; Length 941;
Best Local Similarity 99.6%; Pred. No. 8e-71;
Matches 256; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCCCTGGAGTCCTCTTCTGCTGTAACACATATGCGCGGCTTACCGAGGTGA 60
DB 324 TTCCCTGGAGTCCTCTTCTGCTGTAACACATATGCGCGGCTTACCGAGGTGA 265
QY 61 AGTGTGAATATCAGAGAATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 264 AGTGTGAATATCAGAGAATGATGATGATGATGATGATGATGATGATGATGAT 205
QY 121 ATGAGAGTTAATACCAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 180
DB 204 ATGAGAGTTAATACCAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 145
QY 181 GGGCCAAATGTTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 240
DB 144 GGGCCAAATGTTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 85
QY 241 GGGCAACACAGCGCCGT 257
DB 84 GGGCAACACAGCGCCGT 68

RESULT 2
AA903751 314 bp mRNA linear EST 09-JUN-1998
LOCUS AA903751
DEFINITION ok6405.81 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1518728.3,
similar to gb:K17360.1_mal HOMBOX PROTEIN HOX-D4 (HUMAN);, mRNA
sequence.

ACCESSION AA903751
VERSION AA903751.1 GI:3038874
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 314)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@ds-rs@mail.nih.gov
Tissue Procurement: Christopher A. Moshaluk, M.D., Ph.D., Michael
Bumett-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www.bio.linn.gov/bdrp/image/image.html
Insert length: 521 Std Error: 0.00
Seq primer: -40ml3 fwd. ST from Amerisham
High quality sequence stop: 297.

FEATURES
source

1. 314
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ORIGIN

/note="Vector: pT7T3D-Pact; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 30.0%; Score 77; DB 1; Length 314;
Best Local Similarity 98.9%; Pred. No. 2e-13;
Matches 88; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTCCCTGGAGTCCTCTTCTGCTGTAACACATATGCGCGGCTTACCGAGGTGA 60
DB 227 TTCCCTGGAGTCCTCTTCTGCTGTAACACATATGCGCGGCTTACCGAGGTGA 285
QY 61 AGTGTGAATATCAGAGAATGATGATGATGATGATGATGATGATGATGATGAT 89
DB 286 AGTGTGAATATCAGAGAATGATGATGATGATGATGATGATGATGATGATGAT 314

RESULT 3
CN282871/c 555 bp mRNA linear EST 16-MAY-2004
LOCUS CN282871
DEFINITION 17000424523059 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN282871
VERSION CN282871.1 GI:4729285
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 555)
Brandenberger R., Wei, H., Zhang, S., Lei, S., Murage, J., Fiek, G., J.,
Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M. S., Mandalam, R.,
Lebkowski, J. and Stanton, L. W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
JOURNAL 15146197
PUBMED
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 555 Std Error: 0.00.

FEATURES
source

1. 555
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_id="GRN_EB"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowth derived from h9s cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

ORIGIN

Query Match 16.2%; Score 41.6; DB 8; Length 555;
Best Local Similarity 63.7%; Pred. No. 0.061;
Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 12 TTCCCTGCTGCTGTAACACATATGCGCGGCTTACCGAGGTGAAGTGTGAAT 71
DB 176 TTCCCTGCTGCTTGTGAAGCCACACAGGATGGCTTGAACACAGGCTCACTGTGTC-AC 118
QY 72 ATCAGAGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 131

Db 117 CTGGGGAGGTTACTGAACCTTTGAGGCTTTCATCTGTGAAAAACGAGGCTAA 58
QY 132 TACC 135
Db 57 CAAC 54

RESULT 4
DA094053/c
LOCUS DA094053 558 bp mRNA linear EST 31-OCT-2005
DEFINITION DA094053 BRACE3 Homo sapiens cDNA clone BRACE3003192 5', mRNA
sequence.
ACCESSION DA094053
VERSION DA094053.1 GI:78418757
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 558)

REFERENCE
AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Matsushima, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Pujili, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560

JOURNAL
PUBMED
COMMENT Contact: Takao Isogai;
PLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
Location/Qualifiers
1. 558
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/note="Vector: PME18SFL3"

ORIGIN
Query Match 16.2%; Score 41.6; DB 9; Length 558;
Best Local Similarity 63.7%; Pred. No. 0.061;
Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

Db 12 TCCCTCTGCTGGTGAACACATATGCGCGCCGCTGACACAGGAGTAAAGTGAAT 71
Db 146 TCCCTTGTCTGTTTGAAGCCACACAGGCAATGGCTTGAACACGGCTCAGCTGTGTG-AC 88
QY 72 ATCAGAAAGATGACTGAACGTTTGGAGCTCCGTTTCTCATTTGAAATGAGAGTTAA 131
Db 87 CTGGGGAGGTTACTGAACCTTTGAGGCTCAGCTTTCATCTGTGAAAAACGAGGCTAA 28
QY 132 TACC 135
Db 27 CAAC 24

RESULT 5
AJ817111
LOCUS AJ817111 855 bp mRNA linear EST 12-MAY-2005
DEFINITION AJ817111 KN206 Bos sp. cDNA clone C0006007111, mRNA sequence.
ACCESSION AJ817111
VERSION AJ817111.1 GI:51884587
KEYWORDS EST.
SOURCE Bos sp.
ORGANISM Bos sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
1 (bases 1 to 855)
1 (bases 1 to 855)
McGuire, K. and Glass, E.J.
The expanding role of microarrays in the investigation of
macrophage responses to pathogens
Vec. Immunol. Immunopathol. 105 (3-4), 259-275 (2005)
Contact: McGuire K
Genomics and Genetics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -mismatches 20
and -mismatch 12 options. Vector: pBluescriptII(SK+) R. Site
1: EcoRV(lost) R. Site 2: NotI Seg Primer: T7 Normalised library
constructed from pooled monocytes from Bos taurus (Holstein) and
Bos indicus (Sahiwal) cattle subjected to various stimuli,
including infection with the protozoan parasite Theileria annulata.
Location/Qualifiers
1. 855
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/note="Vector: pBluescriptII(SK+); Site 1: EcoRV(lost);
Site 2: NotI; Normalised library constructed from pooled
monocytes from Bos taurus (Holstein) and Bos indicus
(Sahiwal) cattle subjected to various stimuli, including
infection with the protozoan parasite Theileria annulata"

ORIGIN
Query Match 15.6%; Score 40; DB 1; Length 855;
Best Local Similarity 57.0%; Pred. No. 0.22;
Matches 73; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Db 4 CCTGCAAGTCCCTTCTGCTGGTGAACACATATGCGCGCCGCTGACACAGGAGTAAAGT 63
Db 416 CTTAGCAAGTCTGCGACCCACAGTCATAGCTTAAAGTTTATAGTAGTAGT 475
QY 64 GTGTGAATATCAGAAAGATGACTGAACGTTTGGAGCTCCGTTTCTCATTTGAAATG 123
Db 476 GTGCAACCTCAGGACATGCTTAATCTCTAGGCTCAACTTCTCATCTATAAAGT 535
QY 124 GAGGTTAA 131
Db 536 GGGAGTTAA 543

RESULT 6
CV402643
LOCUS CV402643 444 bp mRNA linear EST 28-SEP-2004
DEFINITION RC0-BN0248-310700-025-a04 BN0248 Homo sapiens cDNA, mRNA sequence.
ACCESSION CV402643
VERSION CV402643.1 GI:52798116
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

Hominidae; Homo.
1 (bases 1 to 444)
Dias Neto,B., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongseneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. <http://www.ludwig.org.br>.
Location/Qualifiers
1..444
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="BN0248"
/note="Organ: breast normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 15.0%; Score 38.6; DB 8; Length 444;
Best Local Similarity 59.6%; Pred. No. 0.53;
Matches 65; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 38 GGGCCCGGCTGACCGAGGTGAAGTGTGAATATGAGAAGTACGACTCTTTG 97
DB 66 GACTCTGCTTTGCGATATACGAGTGCCTGACCCCTGTGCAGATGCTTAAATCCCTTC 125
QY 98 GGACTCCGTTTCCCATTTGAATAAGGAGGTAAATACGACCTTTCTTCT 146
DB 126 GGCTCAGATTTCATCTGAAAAGTGGGTTAATGCCATCTGCTTCT 174

RESULT 7
CE142616/c 685 bp DNA linear GSS 25-SEP-2003
LOCUS CE142616
DEFINITION tigr-gss-dog-17000371256164 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE142616
VERSION CE142616.1 GI:35254038
KEYWORDS GSS
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 685)
Kirchner,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Ruesch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
14512627
Contact: Kirchner EF
The Institute for Genomic Research

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirchner@tigr.org
Class: Shotgun.
Location/Qualifiers
1..685
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_1lb="dog library"
/note="Site_1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 15.0%; Score 38.6; DB 12; Length 685;
Best Local Similarity 52.9%; Pred. No. 0.6; 74; Indels 0; Gaps 0;
Matches 83; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 18 CTGCTGTGAAAACACATATGCGCGCGCTGACCGAGGTGAAGTGTGAATATCAGG 77
DB 651 CTGACCTGAGGCAATCTGCTGGGCTATGATCATTCCTGTGTGATTTTGGG 592
QY 78 AAGATGACGTGACGCTTTGGGAGCTCCGTTCTCATTTGAATGAGTTAATACAG 137
DB 591 AAATATTGAACCTGATGAACCTCAGTTTCTCATAGGAATGGGATATATACAG 532
QY 138 CTTCTTTACCTCCCAACGCGAGTGTTCGCGG 174
DB 531 TACACTGGTTTGAGGACACAGAGACTATTTCTGG 495

RESULT 8
CC004107/c 777 bp DNA linear GSS 31-MAR-2003
LOCUS CC004107
DEFINITION PUGJ51TB_ZM_0.6_1.0_KB Zee mays genomic clone ZMBR440106,
genomic survey sequence.
ACCESSION CC004107
VERSION CC004107.1 GI:29382667
KEYWORDS GSS.
SOURCE Zee mays
Zee mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zee.
1 (bases 1 to 777)
White,J.C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennettzen,J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSes: PUGJ51TD
Contact: Cathy WhiteJaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitejaw@tigr.org
Seq primer: TK
Class: sheared ends.
Location/Qualifiers
1..777
/organism="Zee mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_1lb="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high Cor selected genomic DNA library"

ORIGIN

Query Match 14.6%; Score 37.6; DB 12; Length 777;
Best Local Similarity 72.1%; Pred. No. 1.3;
Matches 49; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 54 GGGTGAAGTGTGATATCAGGAAGTACGCTCTTGGGACTCCGTTCTCA 113
DB 718 GGGGGAAGGGGTGGAATAATCAGGAACAGGTGATCATGTGTGTTACTCCATTCAGAA 659
QY 114 TTGTAAA 121
DB 658 TTATPAAA 651

RESULT 9
DU383369/c
LOCUS 1098313087090 CHORI-243 Ovis aries genomic clone CH243-86D11,
DEFINITION genomic survey sequence.
ACCESSION DU383369
VERSION DU383369.1 GI:77113232
KEYWORDS GSS.
SOURCE Ovis aries (sheep)
ORGANISM Ovis aries

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
1 (bases 1 to 641)
Kirckness, E., Shetty, J., de Jong, P., McEwan, J.C., Oddy, H. and
Cockett, N.

AUTHORS
TITLE Ovine BAC End Sequences from Library CHORI-243
JOURNAL Unpublished (2004)
COMMENT Other GSSs: 1098313044849
Contact: Ewen Kirkness
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-795-7536
Email: ekirknes@tigr.org

Sequences generated at the J. Craig Venter Institute Joint
Technology Center (JCVI/JTC; http://www.venterlinstitute.org/).
Original Trace: 1098313087090 Trace TI: gnl|ti|918927275
Insert Length: 184000 Std Error: 0.00 row: D column: 11
Seq primer: T7
Class: BAC ends.

FEATURES
source location/Qualifiers

1..641
/organism="Ovis aries"
/mol_type="genomic DNA"
/strain="Texel breed"
/db_xref="taxon:9940"
/clone="CH243-86D11"
/sex="Male"
/cell_type="Blood"
/clone_1lb="CHORI-243"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
The CHORI-243 sheep (M) (Ovis aries) BAC library produced
by Pieter de Jong's lab at CHORI
http://bacpac.chori.org/library.php?id=162"

ORIGIN

Query Match 14.3%; Score 36.8; DB 13; Length 641;
Best Local Similarity 69.4%; Pred. No. 2.2;
Matches 50; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 69 AATATCAGGAAGATGACTGAACGCTTTGGGACTCCGTTCTCATTTGTAATGAGCT 128
DB 324 AATATCAGGAAGATGAGATGACATCTGTGCTCCTCATTCTCTTTTAAATGAGAT 265
QY 129 TAATACAGCCT 140
DB 264 CAATATATGCT 253

RESULT 10
DU516086/c
LOCUS 1098609797641 CHORI-243 Ovis aries genomic clone CH243-514E4,
DEFINITION genomic survey sequence.
ACCESSION DU516086
VERSION DU516086.1 GI:77341805
KEYWORDS GSS.
SOURCE Ovis aries (sheep)
ORGANISM Ovis aries

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
1 (bases 1 to 749)
Kirckness, E., Shetty, J., de Jong, P., McEwan, J.C., Oddy, H. and
Cockett, N.

AUTHORS
TITLE Ovine BAC End Sequences from Library CHORI-243
JOURNAL Unpublished (2004)
COMMENT Other GSSs: 1098609881785
Contact: Ewen Kirkness
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-795-7536
Email: ekirknes@tigr.org

Sequences generated at the J. Craig Venter Institute Joint
Technology Center (JCVI/JTC; http://www.venterlinstitute.org/).
Original Trace: 1098609797641 Trace TI: gnl|ti|958319337
Insert Length: 184000 Std Error: 0.00 row: E column: 4
Seq primer: T7
Class: BAC ends.

FEATURES
source location/Qualifiers

1..749
/organism="Ovis aries"
/mol_type="genomic DNA"
/strain="Texel breed"
/db_xref="taxon:9940"
/clone="CH243-514E4"
/sex="Male"
/cell_type="Blood"
/clone_1lb="CHORI-243"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
The CHORI-243 sheep (M) (Ovis aries) BAC library produced
by Pieter de Jong's lab at CHORI
http://bacpac.chori.org/library.php?id=162"

ORIGIN

Query Match 14.3%; Score 36.8; DB 14; Length 749;
Best Local Similarity 69.4%; Pred. No. 2.3;
Matches 50; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 69 AATATCAGGAAGATGACTGAACGCTTTGGGACTCCGTTCTCATTTGTAATGAGCT 128
DB 440 AATATCAGGAAGATGAGATGACATCTGTGCTCCTCATTCTCTTTTAAATGAGAT 381

QY 129 TAATACAGCCT 140
DB 380 CAATATATGCT 369

RESULT 11
A0024482/c
LOCUS A0024482 374 bp DNA linear GSS 23-JUN-1998
DEFINITION HS 2180 B2 H07 MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2180 Col=14 Row=P, genomic survey
sequence.

ACCESSION A0024482
VERSION A0024482.1 GI:3243707
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 374)
AUTHORS Mahitras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahitras GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2180 row: P Column: 14
Class: BAC ends
High quality sequence stop: 374.

FEATURES
source
1..374
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=2180 Col=14 Row=P"
/sex="male"
/clone_1lb="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

ORIGIN

Query Match 14.2%; Score 36.4; DB 11; Length 374;
Best Local Similarity 70.0%; Pred. No. 2.6;
Matches 49; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 76 GGAAGATGACTGAACGCTTTGGACTCCGTTCTCTATTGTAAATGAGGTTAATACC 135
Db 133 GGAAGATTAAATGAACCTCTGCTGCTCAGATTTCTTCAATTTGAATAATGATGTT 74
QY 136 AGCCTCTTC 145
Db 73 AACTCTCTCC 64

RESULT 12 707 bp DNA linear GSS 05-JUL-2004
LOCUS CR095999
DEFINITION Forward strand read from insert in 5'HRT insertion targeting and chromosome engineering clone MHPN181020, genomic survey sequence.
ACCESSION CR095999
VERSION CR095999.1 GI:49833534
KEYWORDS GSS; genome survey sequence; MICR.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 707)
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,T., Yu,Y., Rogers,J., and Bradley,A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, UK. http://www.sanger.ac.uk/MICR

FEATURES
source
1..707
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN181020"
/clone_1lb="MHPN"

ORIGIN

Query Match 14.2%; Score 36.4; DB 14; Length 707;
Best Local Similarity 59.8%; Pred. No. 3.1;
Matches 61; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 60 AAGTGTGAATATACGGAAGATGACTGAACGCTTTGGAGCTCCGTTCTATTGTAA 119
Db 504 AGGTGTGATACCTTTAGGAAGATTATGAACCTTTTAGAGCTTCAGAAATCCCATGTAA 445
QY 120 AATGAGATTAAATACCAAGCTTTCTTCTACTCCCAACGAC 161
Db 444 AACCGAATTAATTAATGCTACTAGTCTATTAACTAAC 403

RESULT 13 571 bp DNA linear GSS 03-OCT-2000
LOCUS AZ412085
DEFINITION 1M0185H19F Mouse 10kb plasmid UGCGM library Mus musculus genomic
clone UGCGM0185H19 F, genomic survey sequence.
ACCESSION AZ412085
VERSION AZ412085.1 GI:10536098
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0185 row: H Column: 19
Seq primer: CGTTGTAAACGACGCGCACT
Class: Plasmid ends
High quality sequence stop: 571.

FEATURES
source
1..571
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0185H19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F."
/note="Vector: PMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI4732114|BP|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptor and purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 14.1%; Score 36.2; DB 11; Length 571;
Best Local Similarity 53.1%; Pred. No. 3.4;
Matches 77; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 106 TTTCCTCATGTAAATGAGGTTAATACAGCCTTTCTTACTCCCAAGCAGCTGT 165
DB 219 TCTCTCTTTCTTAAAGAAAAAACAACCTATTTTATTATTAATATTTGCGT 278
QY 166 TTGTCCCGGCGCAGAGGGCCCAATGTGTGCTGATCAGCATTCAGTACCCCAAGAGC 225
DB 279 TTTTCCGCGGTATATCTGTAGATGTGATCAACAGCTGTATCCCATCATGTGG 338
QY 226 GGTACGCAATTAAGGCGAACCG 250
DB 339 GAGCAGGAAATTGAACGAGATCTG 363

RESULT 14
CL654603/c 810 bp DNA linear GSS 09-JUL-2004
LOCUS PRI0121a.B01 - PRI0121a.B21 (810) Mixed stage fosmid library of *P. pacificus* var. California Pristionchus pacificus genomic, genomic
DEFINITION survey sequence.
ACCESSION CL654603 GI:50133560
VERSION CL654603.1
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 810)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppADB: an Acedb database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
JOURNAL 14681447
PUBMED Contact: Sommer RJ
COMMENT Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
source
1. 810
Location/Qualifiers
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of *P. pacificus*
var. California"
/note="Vector: pB1fos-5 Fosmid vector"

ORIGIN

Query Match 14.0%; Score 36; DB 13; Length 810;
Best Local Similarity 54.5%; Pred. No. 4.3;
Matches 72; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 108 TCGTCATTTGAATGAGGTTAATACAGCTTCTTACTCCCAAGCAGCTTT 167
DB 714 TTCCCATTTTACATTCAGGGAATACGAGCATCTTCTCTCAATATCAAGGAAA 655
QY 168 GTCCCGGCGCAGAGGCCCAATTTGGCTGTTCAGCATGATTACCCCAAGAGCGG 227

DB 654 AGATGAGCAGCGTCCCGAATTTTACGTCAAAATGAAGCCCGAAGGACTAACTGT 595
QY 228 TCAGCCCAATTAA 239
DB 594 ACTTCTCAATTGA 583

RESULT 15
CT069763 906 bp DNA linear GSS 01-NOV-2005
LOCUS CT069763
DEFINITION *Sus scrofa* genomic clone Pigf-66B15, genomic survey sequence.
ACCESSION CT069763
VERSION CT069763.1 GI:78627896
KEYWORDS GSS.
SOURCE *Sus scrofa* (pig)
ORGANISM *Sus scrofa*
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 906)
Humphray,S.J., Plumb,R.W. and Durham,J.L.
Direct Submission
Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 66B15. 66B15 is
part of the PigBAC BAC library created by Roslin Institute/RFCGR.
Further details: http://www.sanger.ac.uk/Projects/S_susrofa/.

REFERENCE 1 (bases 1 to 906)
AUTHORS Humphray,S.J., Plumb,R.W. and Durham,J.L.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 66B15. 66B15 is
part of the PigBAC BAC library created by Roslin Institute/RFCGR.
Further details: http://www.sanger.ac.uk/Projects/S_susrofa/.

FEATURES
source
1. 906
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="taxon:9823"
/clone_lib="Pigf-66B15"
/tissue_type="Blood cells"
/note="vector pbelOBAC11
sex male"

ORIGIN

Query Match 14.0%; Score 36; DB 14; Length 906;
Best Local Similarity 62.0%; Pred. No. 4.5;
Matches 57; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 42 CCGAGCTGACGAGGAGTGAAGTGTGTAATATCAGGAAGTGAAGCTTTGGGAC 101
DB 515 CTGGCTTGCCATTTATCACTGTGACCTTTTGGCAAGTATTATCTCTCGGTC 574
QY 102 TCGTTTCTCATTTGAATGAGGTTAATA 133
DB 575 TTGGTTTCTCATTCATTAATGAGGATATA 606

Search completed: June 6, 2006, 00:08:50
Job time: 1782.61 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:58:22 / Search time 65.8364 Seconds
(without alignments)
7304.087 Million cell updates/sec

Title: US-09-869-098A-1_COPY_1133_1389

Perfect score: 257
Sequence: 1 tccctcgagctccctctcg.....aaagcgcaaccagcccggt 257

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents_NA:*

- 1: /EMC_Celerra_SIDS3/prodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/prodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/prodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/prodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/prodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/prodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/prodata/2/ina/PP_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/prodata/2/ina/RE_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/prodata/2/ina/backfiles1.seq:*
- 10: /EMC_Celerra_SIDS3/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	255.4	99.4	11808	3	US-09-949-016-15281 Sequence 15281, A
2	255.4	99.4	39754	3	US-09-949-016-14689 Sequence 14689, A
3	39.4	15.3	93920	3	US-09-949-016-12461 Sequence 12461, A
4	39.4	15.3	93920	3	US-09-949-016-16853 Sequence 16853, A
5	38.2	14.9	128470	3	US-09-949-016-13765 Sequence 13765, A
6	36.8	14.3	36103	3	US-09-949-016-16382 Sequence 16382, A
7	36.8	14.3	133613	3	US-09-949-016-15894 Sequence 15894, A
8	36.4	14.2	109038	3	US-09-949-016-12159 Sequence 12159, A
9	36	14.0	25166	3	US-09-949-016-16072 Sequence 16072, A
10	35.4	13.8	601	3	US-09-949-016-51777 Sequence 51777, A
11	35.4	13.8	21136	3	US-09-949-016-13748 Sequence 13748, A
12	35.4	13.8	146095	3	US-09-949-016-12872 Sequence 12872, A
13	35.4	13.8	146104	3	US-09-949-016-13239 Sequence 13239, A
14	35	13.6	601	3	US-09-949-016-17171 Sequence 17171, A
15	35	13.6	26933	3	US-09-949-016-12045 Sequence 12045, A
16	35	13.6	26933	3	US-09-949-016-15872 Sequence 15872, A
17	35	13.6	298336	3	US-09-949-016-16600 Sequence 16600, A
18	34.6	13.5	56131	3	US-09-949-016-12944 Sequence 12944, A
19	34.4	13.4	601	3	US-09-949-016-84988 Sequence 84988, A
20	34.4	13.4	601	3	US-09-949-016-85139 Sequence 85139, A
21	34.4	13.4	68452	3	US-09-949-016-13305 Sequence 13305, A
22	34.4	13.4	109159	3	US-09-949-016-14159 Sequence 14159, A
23	34.4	13.4	109159	3	US-09-949-016-14170 Sequence 14170, A

ALIGNMENTS

24	34.4	13.4	325791	3	US-09-768-185A-1	Sequence 1, Appli
25	34.2	13.3	601	3	US-09-949-016-127649	Sequence 127649, A
26	34.2	13.3	601	3	US-09-949-016-127650	Sequence 127650, A
27	34.2	13.3	601	3	US-09-949-016-127651	Sequence 127651, A
28	34.2	13.3	601	3	US-09-949-016-127985	Sequence 127985, A
29	34.2	13.3	601	3	US-09-949-016-127987	Sequence 127987, A
30	34.2	13.3	601	3	US-09-949-016-127988	Sequence 127988, A
31	34.2	13.3	304533	3	US-09-949-016-15371	Sequence 15371, A
32	34.2	13.3	345533	3	US-09-949-016-15372	Sequence 15372, A
33	33.6	13.1	33112	3	US-10-429-873A-3	Sequence 3, Appli
34	33.6	13.1	42633	3	US-09-949-016-17317	Sequence 17317, A
35	33.6	13.1	42633	3	US-09-949-016-17318	Sequence 17318, A
36	33.6	13.1	93894	3	US-09-949-016-17318	Sequence 15929, A
37	33.4	13.0	239527	3	US-09-949-016-15980	Sequence 15980, A
38	33.2	12.9	46118	3	US-09-949-016-15703	Sequence 17003, A
39	33	12.8	84916	3	US-09-949-016-14736	Sequence 14736, A
40	33	12.8	118136	3	US-09-949-016-12429	Sequence 14239, A
41	32.8	12.8	36016	3	US-09-949-016-14223	Sequence 14223, A
42	32.8	12.8	421491	3	US-09-949-016-12805	Sequence 12805, A
43	32.8	12.8	421494	3	US-09-949-016-14060	Sequence 14060, A
44	32.6	12.7	601	3	US-09-949-016-43267	Sequence 43267, A
45	32.6	12.7	601	3	US-09-949-016-43456	Sequence 43456, A

RESULT 1
US-09-949-016-15281
Sequence 15281, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTNER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL0001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15281
LENGTH: 11808
TYPE: DNA
ORGANISM: Human
US-09-949-016-15281

Query Match 99.4%; Score 255.4; DB 3; Length 11808;
Best Local Similarity 99.6%; Pred. No. 5.3e-81;
Matches 256; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	TTCCCTGGGCGAGCTCCCTTGGCTGGTGAACATATATGGCGCGGCTGACGAGGTGA	60
DB	901	TTCCCTGGGCGAGCTCCCTTGGCTGGTGAACATATATGGCGCGGCTGACGAGGTGA	960
QY	61	AGTGTGATATATCAGAGATGATGACGAGCTTTGGAGCTCCGTTCTCTCATTTGAA	120
DB	961	AGTGTGATATATCAGAGATGATGACGAGCTTTGGAGCTCCGTTCTCTCATTTGAA	1020
QY	121	ATGAGGTTATATCAGAGCTTTCTTACTCCCAAGCAGCTGTTTGTCCGCGCAG	180
DB	1021	ATGAGGTTATATCAGAGCTTTCTTACTCCCAAGCAGCTGTTTGTCCGCGCAG	1080
QY	181	GGCCCAATGTTGGCTGTTTACGATCATGTTACCCCAAGAGCGGTGACCATTTAA	240
DB	1081	GGCCCAATGTTGGCTGTTTACGATCATGTTACCCCAAGAGCGGTGACCATTTAA	1140
QY	241	GGCGAACGAGCCCGGT 257	

Db 1141 GCGGAACGAGCCCGGT 1157

RESULT 2

US-09-949-016-14689
; Sequence 14689, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14689
; LENGTH: 39754
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) - (39754)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14689

Query Match 99.4%; Score 255.4; DB 3; Length 39754;
Best Local Similarity 99.6%; Pred. No. 9,4e-81;
Matches 256; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCCTGGAGTCCTCTTCTGCTGTAACACATATGCGCGGCTTGAACGAGGTGA 60
DB 28816 TTCCTGGAGTCCTCTTCTGCTGTAACACATATGCGCGGCTTGAACGAGGTGA 28875
QY 61 AGTGTGTAATATCAGGAAGATGACTGAACTGTTGGAGCTCCGTTCTCAATTGAAA 120
DB 28876 AGTGTGTAATATCAGGAAGATGACTGAACTGTTGGAGCTCCGTTCTCAATTGAAA 28935
QY 121 ATGAGAGTTAATACGAGCTCTTCTTACTCCCAAAAGCAGTGTGTTCCCGGACAG 180
DB 28936 ATGAGAGTTAATACGAGCTCTTCTTACTCCCAAAAGCAGTGTGTTCCCGGACAG 28995
QY 181 GGGCCAAATTGTTGCTGTTTACGCGATCAGTTAACCCCAAGAGCGGTCAAGCAATTAAA 240
DB 28996 GGGCCAAATTGTTGCTGTTTACGCGATCAGTTAACCCCAAGAGCGGTCAAGCAATTAAA 29055
QY 241 GGGGAACGAGCCCGGT 257
DB 29056 GGGGAACGAGCCCGGT 29072

RESULT 3

US-09-949-016-12461/C
; Sequence 12461, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12461
; LENGTH: 93920
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12461

Query Match 15.3%; Score 39.4; DB 3; Length 93920;
Best Local Similarity 62.9%; Pred. No. 0.0087;
Matches 61; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 50 ACCAGGGTGAAGTGTGTAATATCAGGAAGATGACTGAACGCTTTGGAGACTCCGTTTC 109
DB 63793 ACCATTATTAAGCTGTGACTTGTGGAAGAGTTACTTAACCTCTGTGATTCACTTTC 63734
QY 110 CTCATTGTAATAATGAGGTTAATACAGCCTTCTCT 146
DB 63733 TTCATTGTAAATAAAGAAATAACAGTCTATCCT 63697

RESULT 4

US-09-949-016-16853/C
; Sequence 16853, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16853
; LENGTH: 93920
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16853

Query Match 15.3%; Score 39.4; DB 3; Length 93920;
Best Local Similarity 62.9%; Pred. No. 0.0087;
Matches 61; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 50 ACCAGGGTGAAGTGTGTAATATCAGGAAGATGACTGAACGCTTTGGAGACTCCGTTTC 109
DB 63793 ACCATTATTAAGCTGTGACTTGTGGAAGAGTTACTTAACCTCTGTGATTCACTTTC 63734
QY 110 CTCATTGTAATAATGAGGTTAATACAGCCTTCTCT 146
DB 63733 TTCATTGTAAATAAAGAAATAACAGTCTATCCT 63697

RESULT 5

US-09-949-016-13765/C
; Sequence 13765, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13765
;; LENGTH: 128470
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-13765

Query Match 14.3%; Score 38.2; DB 3; Length 128470;
Best Local Similarity 73.1%; Pred. No. 0.027;
Matches 49; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 70 ATATCAGAGAGTGAACGCTTTGGGACTCCGTTCTCTCATTTGTAATAATGAGGCTT 129
DB 61211 ATCTGGGACATGACTTAACCTCTCTGAGCCTCAGTTCTCATTTTAAAGAGATGAG 61152
QY 130 AATACCA 136
DB 61151 AATCCA 61145

RESULT 6
US-09-949-016-16382/c
; Sequence 16382, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16382
; LENGTH: 36103
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16382

Query Match 14.3%; Score 36.8; DB 3; Length 36103;
Best Local Similarity 63.6%; Pred. No. 0.048;
Matches 56; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 59 TAAGTGTGTAATATCAGAAAGTGAACGCTTTGGGACTCCGTTCTCATTTGTA 118
DB 3675 TAAAGATTACCTGCTCAGCAATTTGTAATCTTTGGGCTCAGTTCTCATTTGTA 616
QY 119 AAATGAGTTAATACCAAGCCTTCTTCT 146
DB 3615 AAAAGTGGGATTAACAGAGCCTGCTCT 3588

RESULT 7
US-09-949-016-15824/c
; Sequence 15824, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307

;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 15824
;; LENGTH: 133613
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-15824

Query Match 14.3%; Score 36.8; DB 3; Length 133613;
Best Local Similarity 69.4%; Pred. No. 0.088;
Matches 50; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 70 ATATCAGAGAGTGAACGCTTTGGGACTCCGTTCTCTCATTTGTAATAATGAGGCTT 129
DB 83380 ATTCAGAGAGTGAACGCTTAACCTCTGATATCTCATTTCTCATTTAAATGGGATC 83321
QY 130 AATACCA 141
DB 83320 AGTATTTACCTT 83309

RESULT 8
US-09-949-016-12199
; Sequence 12199, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12199
; LENGTH: 109038
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(109038)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12199

Query Match 14.2%; Score 36.4; DB 3; Length 109038;
Best Local Similarity 70.0%; Pred. No. 0.11;
Matches 49; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 67 TGAATATCAGAGAGTGAACGCTTTGGGACTCCGTTCTCTCATTTGTAATAATGAG 126
DB 79268 TGAACCTTGGAGAGTACTCACTCTCTGGGCCCCAGTTCTCATTTGTAATAATGAG 79327
QY 127 GTTAATACCA 136
DB 79328 GTGTTAATCA 79337

RESULT 9
US-09-949-016-16072

```
/ Sequence 16072, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 16072
/ LENGTH: 25166
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(25166)
/ OTHER INFORMATION: n = A,T,C or G
/
/ US-09-949-016-16072
```

```
Query Match          14.0%; Score 36; DB 3; Length 25166;
Best Local Similarity 60.0%; Pred. No. 0.078;
Matches 60; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
```

```
QY 52 CAGGGTGTAAAGTGTGATATATCAGAGAGTGAAGTGAAGCTCTTTGGAGCTCCGTTTCTT 111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 10238 CAGACGCGCTGGCTTGATCTCAGCTCCATCTGTGTACGTGTGAGTCCGCTTTTCT 10297
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 112 CATTGTAATGAGGTATATACAGCTCTTCTTACTCC 151
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 10298 CACCTGTAATGTGGGATATATACAATAGTTTCACTCC 10337
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 10

```
/ US-09-949-016-51777
/ Sequence 51777, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 51777
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
/
/ US-09-949-016-51777
```

```
Query Match          13.8%; Score 35.4; DB 3; Length 601;
Best Local Similarity 69.6%; Pred. No. 0.022;
Matches 48; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
```

```
QY 69 AATATCAGAAGATGATGTAAGCTCTTGGAGTCCGTTTCTTCAATGTAATGAGGT 128
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 139 AATACCGGAGATTAATTAATCTTCTGGGCTCAGTCTTTCATAGATTAATGAGGC 198
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
QY 129 TAATACAG 137
    ||| ||| |||
DB 199 TAATACAG 207
    ||| ||| |||
```

RESULT 11

```
/ US-09-949-016-13748/C
/ Sequence 13748, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13748
/ LENGTH: 21136
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(21136)
/ OTHER INFORMATION: n = A,T,C or G
/
/ US-09-949-016-13748
```

```
Query Match          13.8%; Score 35.4; DB 3; Length 21136;
Best Local Similarity 55.2%; Pred. No. 0.12;
Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
```

```
QY 59 TAAGTGTGATATATCAGAGAGTGAAGTGAAGCTCTTTGGAGTCCGTTTCTTCAATGTA 118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 17934 TAACGCTGTACCTTTTGAATGTGCTTAACCTGTGTCTCAGTTTCTTCATCTT 17875
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 119 AATGAGGTATATACAGCTCTTCTACTCCCAAGCAGTGTGTCGCCGCCAG 178
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 17874 AAGAAAGGATATGACCTGTTATGATATATACATATACATATGAGAGCACTTCAAC 17815
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 179 AGGAC 183
    ||| |||
DB 17814 AGTGC 17810
    ||| |||
```

RESULT 12

```
/ US-09-949-016-12872/C
/ Sequence 12872, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12872
/ LENGTH: 146095
/ TYPE: DNA
```



```
; ORGANISM: Human
US-09-949-016-12872
Query Match      13.8%; Score 35.4; DB 3; Length 146095;
Best Local Similarity 69.6%; Pred. No. 0.29;
Matches 48; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 69 AATATCAGGAAGATGACTGAAAGCTTTGGGACTCCGTTCCATTTGTAATAATGAGGT 128
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98177 AATACCGGCAAGTATTTAACCTCTCGGGCCCTCAGCTTCTCATGATAAATGAGGC 98118

QY 129 TAATACCAG 137
      ||||| |||||
Db 98117 TAATACACG 98109

RESULT 13
US-09-949-016-13239/c
; Sequence 13239, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13239
; LENGTH: 146104
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13239

Query Match      13.8%; Score 35.4; DB 3; Length 146104;
Best Local Similarity 69.6%; Pred. No. 0.29;
Matches 48; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 69 AATATCAGGAAGATGACTGAAAGCTTTGGGACTCCGTTCCATTTGTAATAATGAGGT 128
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98177 AATACCGGCAAGTATTTAACCTCTCGGGCCCTCAGCTTCTCATGATAAATGAGGC 98118

QY 129 TAATACCAG 137
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Db 98117 TAATACACG 98109

RESULT 14
US-09-949-016-171471/c
; Sequence 171471, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 171471
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-171471

Query Match      13.6%; Score 35; DB 3; Length 601;
Best Local Similarity 66.7%; Pred. No. 0.031;
Matches 50; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 69 AATATCAGGAAGATGACTGAAAGCTTTGGGACTCCGTTCCATTTGTAATAATGAGGT 128
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 534 AATCTGGGAAGGTACTTAATAATCCTGAGCCCTCAGTTTCTCATTTAAATGGA 475

QY 129 TAATACCAGCTTCT 143
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Db 474 TAATACAGGCTTGT 460

RESULT 15
US-09-949-016-12045/c
; Sequence 12045, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12045
; LENGTH: 26933
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(26933)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12045

Query Match      13.6%; Score 35; DB 3; Length 26933;
Best Local Similarity 61.5%; Pred. No. 0.19;
Matches 56; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 42 CCGGCTGACGAGGTGTAAGTGTGAATATGAGGAAGTGAAGCTCTTTGGGAC 101
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1575 CTGGCTCTGCAATTTGCTAAGTATGACTGTGGGCAAGTATGACTTCTCTGGGCC 1516

QY 102 TCCGTTTCCATTTGTAATAATGAGCTTAT 132
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1515 TCAGTTGCCATCTGTAATAATGAGATTAAT 1485

Search completed: June 5, 2006, 22:39:42
Job time : 69.8364 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 22:40:12 ; Search time 511.092 Seconds
(without alignments)
6178.780 Million cell updates/sec

Title: US-09-869-098a-1_COPY_1133_1389

Perfect score: 257
Sequence: 1 ttccttcgacgagccctctg.....aaagcgacacagcccgct 257

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA Main:*

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- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	256.6	100.0	562	4	US-09-925-065A-566754
2	256.6	100.0	562	5	US-09-925-065A-566754
3	244.6	95.2	554	4	US-09-925-065A-177131
4	244.6	95.2	554	5	US-09-925-065A-177131
5	244.6	95.2	561	12	US-10-301-480-268288
6	244.6	95.2	561	12	US-10-301-480-881697
7	41.6	16.2	16256	7	US-10-017-161-1597
8	41.6	16.2	16256	7	US-10-282-198-1271
9	41.6	16.0	459	12	US-10-301-480-456533
10	41.6	16.0	459	12	US-10-301-480-456533
11	41.6	16.0	484	6	US-10-027-632-187045
12	41.6	16.0	484	7	US-10-027-632-187045
13	38.8	15.1	1664	10	US-10-750-185-50997
14	38.8	15.1	1664	10	US-10-750-623-50997
15	37.4	14.6	407	4	US-09-925-065A-496734
16	37.4	14.6	407	5	US-09-925-065A-496734
17	37.4	14.4	1510	10	US-10-450-763-20121

C 18	36.8	14.3	57013	6	US-10-087-192-1798	Sequence 1798, Ap
C 19	36.8	14.3	149612	6	US-10-087-192-1960	Sequence 1960, Ap
C 20	36.6	14.2	640	4	US-09-925-065A-501248	Sequence 501248, A
C 21	36.6	14.2	640	5	US-09-925-065A-501248	Sequence 501248, A
C 22	36.4	14.2	177175	15	US-11-121-086-79	Sequence 79, Appl
C 23	36.2	14.1	28499	9	US-10-741-600-17869	Sequence 17869, A
C 24	36.2	14.1	28499	10	US-10-995-561-13420	Sequence 13420, A
C 25	36.2	14.0	564	6	US-10-027-632-321496	Sequence 321496, A
C 26	36.2	14.0	564	7	US-10-027-632-321496	Sequence 321496, A
C 27	36.2	14.0	35956	7	US-10-017-161-761	Sequence 761, App
C 28	36.2	14.0	167891	15	US-11-121-086-14	Sequence 14, Appl
C 29	35.6	13.9	627	6	US-10-027-632-228402	Sequence 228402, App
C 30	35.6	13.9	627	7	US-10-027-632-228402	Sequence 228402, App
C 31	35.4	13.8	4673	3	US-09-764-878-312	Sequence 312, App
C 32	35.4	13.8	4673	6	US-10-079-854-312	Sequence 312, App
C 33	35.4	13.8	143306	3	US-09-729-920-3	Sequence 3, Appl
C 34	35.4	13.8	143306	9	US-10-887-932-3	Sequence 3, Appl
C 35	35.4	13.8	152037	10	US-10-756-149-198	Sequence 198, App
C 36	35.2	13.7	524	6	US-10-027-632-273815	Sequence 273815, App
C 37	35.2	13.7	524	7	US-10-027-632-273815	Sequence 273815, App
C 38	35.2	13.7	691	12	US-10-301-480-571176	Sequence 571176, App
C 39	35.2	13.7	691	12	US-10-301-480-1186585	Sequence 1186585, App
C 40	35.2	13.7	849	6	US-10-027-632-169223	Sequence 169223, App
C 41	35.2	13.7	849	6	US-10-027-632-169224	Sequence 169224, App
C 42	35.2	13.7	849	7	US-10-027-632-169223	Sequence 169223, App
C 43	35.2	13.7	849	7	US-10-027-632-169224	Sequence 169224, App
C 44	35.2	13.7	996	12	US-10-301-480-581001	Sequence 581001, App
C 45	35.2	13.7	996	12	US-10-301-480-1194410	Sequence 1194410, App

ALIGNMENTS

RESULT 1
US-09-925-065A-566754
Sequence 566754, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Mang, David G.
TITLE OR INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925, 065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243, 096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289, 846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 566754
LENGTH: 562
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-566754

Query Match 100.0%; Score 257; DB 4; Length 562;
Best Local Similarity 99.6%; Pred. No. 1.7e-83;
Matches 256; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TTCCCTGAGAGTCCCTTCTGCTGATGAAACATATGCGCGGCTGACGAGGCTA	60
Db	228	TTCCCTGAGAGTCCCTTCTGCTGATGAAACATATGCGCGGCTGACGAGGCTA	287
Qy	61	AGTGTGATATATGAGAGATGATGATGATGATGATGATGATGATGATGATGAT	120
Db	288	AGTGTGATATATGAGAGATGATGATGATGATGATGATGATGATGATGATGAT	347

OY	121	ATGAGGGTTAAATACGAGCCTTCTCTACATCCCCAAAGGACGGTTGTCGCCGCCAGAG	180
Db	348	ATGGAGGTTAAATACGAGCCTTCTCTACATCCCCAAAGGACGGTTGTCGCCGCCAGAG	407
OY	181	GGCCCAATTGTTGGCTGTTACGCAATCAGTAAACCCACAGAGCGGGTCAGCCAAATTAAA	240
Db	408	GGCCCAATTGTTGGCTGTTACGCAATCAGTAAACCCACAGAGCGGGTCAGCCAAATTAAA	467
OY	241	GGCGAACCGAGCCCGGT	257
Db	468	GGCGAACCGAGCCCGGT	484

RESULT 2

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US-09-925-065A-566754
/ Sequence 566754, Application US/09925065A
/ Publication No. US20050228172A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.115
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 566754
/ LENGTH: 562
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-566754

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Query Match	100.0%	Score 257	DB 5	Length 562
Best Local Similarity	99.6%	Pred. No. 1.7e-83		
Matches 256	Conservative 1	Mismatches 0	Indels 0	Gaps 0

Accession	Sequence	Length
QY	TTCCCTGGGAGAGTCCCTTGTGCTGTGTAAAAACAATATGAGGCGCGCTGACACAGGGGTGA	60
Db	228 TTCCCTGGGAGAGTCCCTTGTGCTGTGTAAAAACAATATGAGGCGCGCGCTGACACAGGGGTGA	287
QY	61 AGTGTGTGATATCAGGAAGATGACTGAACGTCGTTTGGGACTCCGTTTCTCAATTGTAAA	120
Db	288 AGTGTGTGATATCAGGAAGATGACTGAACGTCGTTTGGGACTCCGTTTCTCAATTGTAAA	347
QY	121 ATGAGAGGTAAATACCAAGCCTCTCTTACACGCCCAACGCAAGGTTTGTCCGGCCAGAG	180
Db	348 ATGAGAGGTAAATACCAAGCCTCTCTTACACGCCCAACGCAAGGTTTGTCCGGCCAGAG	407
QY	181 GGCCCAATTGTTGGCTGTTCAACGATCAGTTACCCCCACAGGAGCGGTCAACCAATTTAAA	240
Db	408 GGCCCAATTGTTGGCTGTTCAACGATCAGTTACCCCCACAGGAGCGGTCAACCAATTTAAA	467
QY	241 GGCGAACCAGGCCCGGT	257
Db	468 GGCGAACCAGGCCCGGT	484

RESULT 3

US-09-925-065A-177131/C
; Sequence 177131, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:

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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 106827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 171131
LENGTH: 554
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-171131

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US-09-925-065A-177131

Query Match	95.2%	Score 244.6;	DB 4;	Length 554;
Best Local Similarity	99.2%	Pred. No. 4.6e-79;		
Matches 255; Conservative	1;	Mismatches 0;	Indels 1;	Gaps 1;

Oy	TTCCCTGGCAGTCCCTTCTGCTGTGAAAAACAATATGCGCGGCTGACAGGGGTGTA	60
Db	552 TTCCCTGGCAGTCCCTTCTGCTGTGAAAAACAATATGCGCGGCTGACAGGGGTGTA	493
Oy	61 AGTGTGTAATATCAGGAAGATGACTGAACGTCCTTGGGATCCCGTTTCTCATTTGTAAA	120
Db	492 AGTGTGTAATATCAGGAAGATGACTGAACGTCCTTGGGATCCCGTTTCTCATTTGTAAA	433
Oy	121 ATGGAAGTTAATACAGACCTTCTTACTACCCCAAAGCAGTGTGTGCCCGGCGAG	180
Db	432 ATGGAAGTTAATACAGACCTTCTTACTACCCCAAAGCAGTGTGTGTGCCCGGCGAG	373
Oy	181 GGCCCAATTTGGCTGTTACGACATCAGTTAACCCCAACAGGACGGGTCAAGCCAAATTTAAA	240
Db	372 GG-CAATTGTTGGCTGTTACGACATCAGTTAACCCCAACAGGACGGGTCAAGCCAAATTTAAA	314
Oy	241 GGCGAACACAGGCCCGGT	257
Db	313 GGCGAACACAGGCCCGGT	297

RESULT 4

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US-09-925-065A-177131/c
/ Sequence 177131, Application US/09925065A
/ Publication No. US20050228172A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925, 065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243, 096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252, 147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250, 092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261, 766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/269, 846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 177131

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LENGTH: 554
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-177131

Query Match 95.2%; Score 244.6; DB 5; Length 554;
Best Local Similarity 99.2%; Pred. No. 4.7e-79;
Matches 255; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTCCCTGGCAGTCCCTTCTGCTGTAACACATATATGCGCGGCTGACGAGGGTGA 60
DB 552 TTCCCTGGCAGTCCCTTCTGCTGTAACACATATATGCGCGGCTGACGAGGGTGA 493
QY 61 AGTGTGAATATCAGAGAGATGACGTGACGCTTTGGGACCTCCGTTTCTCATTTGTA 120
DB 492 AGTGTGAATATCAGAGAGATGACGTGACGCTTTGGGACCTCCGTTTCTCATTTGTA 433
QY 121 ATGAGAGTTAATACGAGCCTTTCTTACTCCCAACGCGTGTGTTGTCGGCCAGAG 180
DB 432 ATGAGAGTTAATACGAGCCTTTCTTACTCCCAACGCGTGTGTTGTCGGCCAGAG 373
QY 181 GGCCCAATTGGTGGCTTACGATCAGTTACCCCAAGAGAGGGGTGAGCAATTAA 240
DB 372 GG-CAATTGGTGGCTTACGATCAGTTACCCCAAGAGAGGGGTGAGCAATTAA 314
QY 241 GGCGAACAGGCGCCGGT 257
DB 313 GGCGAACAGGCGCCGGT 297

RESULT 5
US-10-301-480-268288/c
Sequence 268288, Application US/10301480
Publication No. US20060057564A1

GENERAL INFORMATION:
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 268288
LENGTH: 561

TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-268288

Query Match 95.2%; Score 244.6; DB 12; Length 561;
Best Local Similarity 99.2%; Pred. No. 4.7e-79;
Matches 255; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTCCCTGGCAGTCCCTTCTGCTGTAACACATATATGCGCGGCTGACGAGGGTGA 60
DB 559 TTCCCTGGCAGTCCCTTCTGCTGTAACACATATATGCGCGGCTGACGAGGGTGA 500
QY 61 AGTGTGAATATCAGAGAGATGACGTGACGCTTTGGGACCTCCGTTTCTCATTTGTA 120
DB 499 AGTGTGAATATCAGAGAGATGACGTGACGCTTTGGGACCTCCGTTTCTCATTTGTA 440
QY 121 ATGAGAGTTAATACGAGCCTTTCTTACTCCCAACGCGTGTGTTGTCGGCCAGAG 180
DB 439 ATGAGAGTTAATACGAGCCTTTCTTACTCCCAACGCGTGTGTTGTCGGCCAGAG 380
QY 181 GGCCCAATTGGTGGCTTACGATCAGTTACCCCAAGAGAGGGGTGAGCAATTAA 240
DB 379 GG-CAATTGGTGGCTTACGATCAGTTACCCCAAGAGAGGGGTGAGCAATTAA 321

QY 241 GGCGAACAGGCGCCGGT 257
DB 320 GGCGAACAGGCGCCGGT 304

RESULT 6
US-10-301-480-881697/c
Sequence 881697, Application US/10301480
Publication No. US20060057564A1

GENERAL INFORMATION:
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 881697
LENGTH: 561

TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-881697

Query Match 95.2%; Score 244.6; DB 12; Length 561;
Best Local Similarity 99.2%; Pred. No. 4.7e-79;
Matches 255; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTCCCTGGCAGTCCCTTCTGCTGTAACACATATATGCGCGGCTGACGAGGGTGA 60
DB 559 TTCCCTGGCAGTCCCTTCTGCTGTAACACATATATGCGCGGCTGACGAGGGTGA 500
QY 61 AGTGTGAATATCAGAGAGATGACGTGACGCTTTGGGACCTCCGTTTCTCATTTGTA 120
DB 499 AGTGTGAATATCAGAGAGATGACGTGACGCTTTGGGACCTCCGTTTCTCATTTGTA 440
QY 121 ATGAGAGTTAATACGAGCCTTTCTTACTCCCAACGCGTGTGTTGTCGGCCAGAG 180
DB 439 ATGAGAGTTAATACGAGCCTTTCTTACTCCCAACGCGTGTGTTGTCGGCCAGAG 380
QY 181 GGCCCAATTGGTGGCTTACGATCAGTTACCCCAAGAGAGGGGTGAGCAATTAA 240
DB 379 GG-CAATTGGTGGCTTACGATCAGTTACCCCAAGAGAGGGGTGAGCAATTAA 321
QY 241 GGCGAACAGGCGCCGGT 257
DB 320 GGCGAACAGGCGCCGGT 304

RESULT 7
US-10-017-161-1597/c
Sequence 1597, Application US/10017161
Publication No. US20030143668A1

GENERAL INFORMATION:
APPLICANT: SWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161

CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1597
LENGTH: 16256
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: source
LOCATION: (1)..(16256)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(306)
FEATURE:
NAME/KEY: CDS
LOCATION: (760)..(918)
FEATURE:
NAME/KEY: CDS
LOCATION: (1009)..(1194)
FEATURE:
NAME/KEY: CDS
LOCATION: (1602)..(1618)
FEATURE:
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NAME/KEY: CDS
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LOCATION: (6999)..(7197)
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NAME/KEY: CDS
LOCATION: (7651)..(7809)
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NAME/KEY: CDS
LOCATION: (15950)..(16056)
FEATURE:
NAME/KEY: modified_base
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OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (10323)..(10422)
OTHER INFORMATION: a, t, c, g, unknown or other
US-10-017-161-1597

Query Match 16.2%; Score 41.6; DB 7; Length 16256;
Best Local Similarity 63.7%; Pred. No. 0.0015;
Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 12 TCCTCTCTGCTGTAACATATAGCGCCGCTGACCAAGGTGTAAGTGTGAAT 71
DB 13196 TCCTCTCTGCTTGTGAAGCCACACAGCATGGCTTGAACAGCTGCTG-AC 13138
QY 72 ATCAGGAAGATGACGTAACGTCCTTGGAGCTCCGTTCTCATTTGAAATGAGGTTAA 131
DB 13137 CTGGGGCAGGTTACTGAACCTCTTGAAGGCTCAGCTTCTCATCTGAAACGAGGCTAA 13078
QY 132 TACC 135
DB 13077 CAAC 13074

RESULT 8

US-10-292-798-1271/c
Sequence 1271, Application US/10292798
Publication No. US2003023583A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1271
LENGTH: 16256
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: source
FEATURE:
LOCATION: (1)..(16256)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(306)
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LOCATION: (760)..(918)
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LOCATION: (1837)..(2040)
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LOCATION: (3954)..(4181)
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LOCATION: (8742)..(8932)
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NAME/KEY: CDS
LOCATION: (14104)..(14223)
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LOCATION: (14326)..(14487)
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NAME/KEY: CDS
LOCATION: (14579)..(14707)
FEATURE:
NAME/KEY: CDS
LOCATION: (15950)..(16056)
FEATURE:
NAME/KEY: modified base
LOCATION: (3847)..(3946)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (10323)..(10422)
OTHER INFORMATION: a, t, c, g, unknown or other
US-10-292-798-1271
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Best Local Similarity 63.7%; Pred. No. 0.0015;
Matches 79; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 12 TCCCTTCTGCTGTAACATATGCGCCGCTGACCAAGCTGTAGTGTGAAT 71
Db 13196 TCCCTTGTGTTTGAAGCCCAACAGGCAATGGCTTGAACAGGCTGCTGTGTC-AC 13138

QY 72 ATCAGAAAGTATGACTGAAAGCTCTTTGGAGCTCCGTTTCTCATTTGTAATAATGAGAGTTAA 131
Db 13137 CTGGGACAGGTACTGAACTCTTTGAGGCTCAGCTTTCATCTGGAATAACAGAGGCTAA 13078

QY 132 TACC 135
Db 13077 CAAC 13074
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RESULT 9
US-10-301-480-4563
Sequence 45633, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45633
LENGTH: 459
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-45633
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Query Match 16.0%; Score 41; DB 12; Length 459;
Best Local Similarity 61.9%; Pred. No. 0.00059;
Matches 65; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 26 GAAACACATATGCGCCGCTGACCAAGGTGTAATGTAATATCAGAGATGAC 85
Db 76 GAAACAGCTCAGAGCCAGACTGCCAGGTTGAACTCTTCCACGTAAGCAATTAC 135

QY 86 TGAACGCTTTGGGACTCCGTTCTCATTTGTAATAATGAGAGTTA 130
Db 136 TTAACCTTTTGAGCCTCACTTCTCTCTTTAAATGAATCA 180
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RESULT 10
US-10-301-480-659042
Sequence 659042, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 659042
LENGTH: 459
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-659042
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Query Match 16.0%; Score 41; DB 12; Length 459;
Best Local Similarity 61.9%; Pred. No. 0.00059;
Matches 65; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 26 GAAACACATATGCGCCGCTGACCAAGGTGTAATGTAATATCAGAGATGAC 85
Db 76 GAAACAGCTCAGAGCCAGACTGCCAGGTTGAACTCTTCCACGTAAGCAATTAC 135

QY 86 TGAACGCTTTGGGACTCCGTTCTCATTTGTAATAATGAGAGTTA 130
Db 136 TTAACCTTTTGAGCCTCACTTCTCTCTTTAAATGAATCA 180
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RESULT 11
US-10-027-632-187045/c
Sequence 187045, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
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/ TITLE OF INVENTION: Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ PRIOR FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 187045
/ LENGTH: 484
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-187045
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Query Match          16.0%; Score 41; DB 6; Length 484;
Best Local Similarity 61.9%; Pred. No. 0.0006;
Matches 65; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
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QY 26 GAAACACATATGCGCCGCGCTGACGAGGTGTAAGTGTGAATTCAGGAATGAC 85
DB 409 GAAACAGCTCAGAGCCAGACAGCTGCGAGGTTGAATCCCTGCCAGTAGGCAATTAC 350
QY 86 TGAACGCTTTGGAGCTCCGTTCTTCATGTGTAATGAGGTTA 130
DB 349 TTAAGCTTTGAGCCTCAGCTTCTCTCTTAATGAAATCA 305
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RESULT 12
US-10-027-632-187045/c
/ Sequence 187045, Application US/10027632
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ PRIOR FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 187045
/ LENGTH: 484
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-187045
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Query Match          16.0%; Score 41; DB 7; Length 484;
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Best Local Similarity 61.9%; Pred. No. 0.0006;
Matches 65; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 26 GAAACACATATGCGCCGCGCTGACGAGGTGTAAGTGTGAATTCAGGAATGAC 85
DB 409 GAAACAGCTCAGAGCCAGACAGCTGCGAGGTTGAATCCCTGCCAGTAGGCAATTAC 350
QY 86 TGAACGCTTTGGAGCTCCGTTCTTCATGTGTAATGAGGTTA 130
DB 349 TTAAGCTTTGAGCCTCAGCTTCTCTCTTAATGAAATCA 305
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RESULT 13
US-10-750-185-50997/c
/ Sequence 50997, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ PRIOR FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 50997
/ LENGTH: 1664
/ TYPE: DNA
/ ORGANISM: Bovine
US-10-750-185-50997
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Query Match          15.1%; Score 38.8; DB 10; Length 1664;
Best Local Similarity 70.3%; Pred. No. 0.0065;
Matches 52; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
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QY 73 TCAGGAAGATGACTGAACGCTTTGGAGCTCCGTTCTTCATGTGTAATGAGGTTAAT 132
DB 439 TCAGGAGGTCGATGAACCTTTGGCTCAGCTTCTTAATGAAGAAATGCGATTAAT 380
QY 133 ACCAGCCTTCTTCT 146
DB 379 AATAGCCTTACCT 366
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RESULT 14
US-10-750-623-50997/c
/ Sequence 50997, Application US/10750623
/ Publication No. US20050287531A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-1
/ CURRENT APPLICATION NUMBER: US/10/750,623
/ PRIOR FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 50997
/ LENGTH: 1664
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TYPE: DNA
ORGANISM: Bovine 19866881425868
US-10-750-623-50997

Query Match 15.1%; Score 38.8; DB 10; Length 1664;
Best Local Similarity 70.3%; Pred. No. 0.0065;
Matches 52; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 73 TCAGAGATGATGACGTAAGCTTTGGGACCTCCGTTTCCTCATTTGTAATGAGGTTAAT 132
DB 439 TCAGGCGAGCTCGATGACCTCTTTGCTCCTCAGTTTCTTAATGAGAAATGCGATTAAT 380

QY 133 ACCAGCCTTCTCT 146
DB 379 AATAGCCCTACCT 366

RESULT 15
US-09-925-065A-496734/c
Sequence 496734, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957066
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 496734
LENGTH: 407
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-496734

Query Match 14.6%; Score 37.4; DB 4; Length 407;
Best Local Similarity 61.6%; Pred. No. 0.012;
Matches 77; Conservative 0; Mismatches 46; Indels 2; Gaps 1;

QY 47 CTGACCAAGGCTGTAAGTGTGAATATCAGAAAGATGTAACGCTTTGGGACTCCGT 106
DB 385 CTGACTTACTCTATATATATATGCTTAAGCAATGACTTAACCTTTCAGAGCTCAGT 326

QY 107 TTCTCATTTGTAATGAGGTTAATACCA--GGCTTCTCTACTCCCAAGCAAGCAAGT 164
DB 325 TTCTCATTTTATTAATGAGGATATATACAGTGCCTTCTTTCTCTTCAATGAATTA 266

QY 165 TTTGT 169
DB 265 TGTGT 261

Search completed: June 6, 2006, 00:20:59
Job time: 513.092 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 22:44:48 ; Search time 7.49143 Seconds
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Scoring table: IDENTITY_NUC
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Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31.8	12.4	151830	6 US-10-519-335-37	Sequence 37, App1
2	30.6	11.9	1780	7 US-11-293-697-1981	Sequence 181, Ap
3	30.6	11.9	3719	6 US-10-529-452-49	Sequence 49, App1
4	30	11.7	3646	6 US-10-511-937-358	Sequence 358, App
5	29.8	11.6	6035	7 US-11-293-383-12	Sequence 12, App1
6	29.6	11.5	3646	7 US-11-293-697-1350	Sequence 150, Ap
7	29	11.3	258	7 US-11-304-129-58	Sequence 58, App1
8	28	10.9	1458	6 US-10-511-937-598	Sequence 598, App
9	28	10.9	1830	7 US-11-293-697-1731	Sequence 1731, Ap
10	28	10.9	3252	7 US-11-293-697-604	Sequence 604, App
11	28	10.9	9973	6 US-10-857-260-29	Sequence 29, App1
12	27.6	10.7	56580	6 US-10-553-298-1	Sequence 1, App1
13	27.4	10.7	3165	7 US-11-293-697-1501	Sequence 1501, Ap
14	27.2	10.6	591	6 US-10-488-619-1537	Sequence 1537, Ap
15	27.2	10.6	2788	7 US-11-293-697-1674	Sequence 1674, Ap
16	27	10.5	1389	7 US-11-217-529-75896	Sequence 75896, A
17	27	10.5	2940	7 US-11-302-678-13	Sequence 13, App1
18	26.8	10.4	1479	6 US-10-526-538-15	Sequence 15, App1
19	26.6	10.4	256	7 US-11-301-554-423	Sequence 423, App
20	26.6	10.4	3500	6 US-10-525-126-89	Sequence 89, App1
21	26.4	10.3	3106	7 US-11-293-697-565	Sequence 565, App
22	26.2	10.2	2190	7 US-11-293-697-2423	Sequence 2423, App
23	26.2	10.2	16125	7 US-11-236-238-1	Sequence 1, App1
24	26	10.1	454	7 US-11-301-554-1557	Sequence 1557, Ap
25	25.8	10.0	1491	7 US-11-217-529-81443	Sequence 81443, A

26	25.8	10.0	2378	7 US-11-293-697-1075	Sequence 1075, Ap
27	25.8	10.0	15314	6 US-10-501-834-218	Sequence 218, App
28	25.8	10.0	394191	6 US-10-506-549-3	Sequence 3, App1
29	25.6	10.0	1922	6 US-10-526-538-1	Sequence 1, App1
30	25.6	9.9	1703	6 US-10-953-349-11062	Sequence 11062, A
31	25.4	9.9	1813	7 US-11-293-697-1815	Sequence 1815, Ap
32	25.4	9.9	2256	6 US-10-505-928-657	Sequence 657, App
33	25.4	9.9	2646	7 US-11-293-697-1153	Sequence 1153, App
34	25.4	9.9	3524	6 US-10-511-937-390	Sequence 390, App
35	25.4	9.9	3541	6 US-10-505-928-113	Sequence 113, App
36	25.2	9.8	9730	6 US-10-501-834-219	Sequence 219, App
37	25	9.7	726	7 US-11-145-307A-33	Sequence 33, App1
38	25	9.7	759	7 US-11-217-529-4431	Sequence 4431, App
39	25	9.7	824	6 US-10-488-619-1933	Sequence 1933, App
40	25	9.7	1321	6 US-10-196-749-371	Sequence 371, App
41	25	9.7	1587	7 US-11-293-697-1139	Sequence 1139, App
42	25	9.7	2892	7 US-11-293-697-235	Sequence 235, App
43	25	9.7	3486	7 US-11-302-678-25	Sequence 25, App1
44	25	9.7	3934	6 US-10-196-749-349	Sequence 349, App
45	24.8	9.6	597	7 US-11-217-529-705	Sequence 705, App

ALIGNMENTS

RESULT 1
US-10-519-335-37/c
Sequence 37, Application US/10519335
Publication NO. US20060099210A1
GENERAL INFORMATION:
APPLICANT: Cavaire, Laurent
APPLICANT: Chumakov, Ilya
APPLICANT: Destenaves, Benoit
APPLICANT: Gonthier, Catherine
APPLICANT: Elias, Isabelle
TITLE OF INVENTION: NOVEL KNOX POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES IN THE TREATMENT OF MENTAL DISORDERS
FILE REFERENCE: G-194US03PCT
CURRENT APPLICATION NUMBER: US/10/519,335
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 60/391,359
PRIOR FILING DATE: 2002-06-25
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
LENGTH: 151830
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_freature
LOCATION: (10)..(110)
OTHER INFORMATION: n = a or c or g or t
NAME/KEY: misc_freature
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (119115)..(119121)
/ OTHER INFORMATION: n = a or c or g or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (119123)..(119123)
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/ NAME/KEY: misc_feature
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/ NAME/KEY: misc_feature
/ LOCATION: (142063)..(142063)
/ OTHER INFORMATION: n = a or c or g or t
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/ NAME/KEY: misc_feature
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/ NAME/KEY: misc_feature
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/ NAME/KEY: misc_feature
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/ LOCATION: (149079)..(149079)
/ OTHER INFORMATION: n = a or c or g or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (5363)..(5363)
/ OTHER INFORMATION: n = a or c or g or t
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/ NAME/KEY: misc_feature
/ LOCATION: (8080)..(8080)
/ OTHER INFORMATION: n = a or c or g or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (10296)..(10296)
/ OTHER INFORMATION: n = a or c or g or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (14528)..(14528)
/ OTHER INFORMATION: n = a or c or g or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (15336)..(15336)
/ OTHER INFORMATION: n = a or c or g or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (15457)..(15457)
/ OTHER INFORMATION: n = a or c or g or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (16288)..(16288)
/ OTHER INFORMATION: n = a or c or g or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (16307)..(16307)
/ OTHER INFORMATION: n = a or c or g or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (16316)..(16316)
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/ NAME/KEY: misc_feature
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (57662)..(57662)
/ OTHER INFORMATION: n = a or c or g or t
/ FEATURE:
/ NAME/KEY: 5' UTR
/ LOCATION: (1)..(54)
/ OTHER INFORMATION: exon 1
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (55)..(124)
/ OTHER INFORMATION: exon 1
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (91147)..(91244)
/ OTHER INFORMATION: exon 2
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (93669)..(93834)
/ OTHER INFORMATION: exon 3
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (96310)..(96422)
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; OTHER INFORMATION: exon 4
; FEATURE:
; NAME/KEY: exon
; LOCATION: (99546)..(99723)
; OTHER INFORMATION: exon 5
; FEATURE:
; NAME/KEY: exon
; LOCATION: (125441)..(125605)

Query Match      12.4%; Score 31.8; DB 6; Length 151830;
Best Local Similarity 58.3%; Pred. No. 0.43;
Matches 74; Conservative 0; Mismatches 52; Indels 1; Gaps 1;

QY 18 CTGCTGATGAAACACATATGCGCCGCTGACCAAGGATGTAAGTGTGAATATCAGG 77
DB 25888 CTCACCTGACACGCGACGAGGGGACGACGCGACGAGGGGGAACAGACGATCCTTGCA 25829

QY 78 AAGATGACGACGCTCTTTGGGACTCCGTTTCTCAT-TGTAAATGAGGTTAATACCA 136
DB 25828 AAGATCAGCTTGCTGCTCCCTGAGCTTCAGTTTCTCATCTGTACAAAGAGATGAATATCA 25769

QY 137 GCCTTCT 143
DB 25768 CTCTTCT 25762
```

```

RESULT 2
US-11-293-697-1981
; Sequence 1981, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; PRIOR FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1981
; LENGTH: 1780
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1981

Query Match      11.9%; Score 30.6; DB 7; Length 1780;
Best Local Similarity 65.2%; Pred. No. 0.13;
Matches 45; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 62 GTCTGGAATATCAGGAAGTGAAGTGAAGTCTTTGGGACTCCGTTTCTCATTTGTAA 121
DB 1415 GTCTCTTGAAGTGGGCAAGTACTTCACTCTGCGGCTCAGTTTCTCATAGAAA 1474

QY 122 TGGAGTTA 130
DB 1475 TAGCGTTA 1483
```

```

; PRIOR APPLICATION NUMBER: JP 2002-288394
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 3719
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)...(2205)
US-10-529-452-49

Query Match      11.9%; Score 30.6; DB 6; Length 3719;
Best Local Similarity 65.2%; Pred. No. 0.19;
Matches 45; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 76 GGAAGTACTGAAGCTCTTTGGGACTCCGTTTCTCATTTGTAAATGAGGTTAATAC 135
DB 2963 GGAAGTCAATGAGCCTTTGAGCTTCAGTTTCTCATCTGTAAATGAGGATTAATAC 2904

QY 136 AGCCTTCT 144
DB 2903 CAACCTCAT 2895
```

```

RESULT 4
US-10-511-937-358
; Sequence 358, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 358
; LENGTH: 3646
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-358

Query Match      11.7%; Score 30; DB 6; Length 3646;
Best Local Similarity 64.3%; Pred. No. 0.31;
Matches 45; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 69 AATATCAGGAAGTGAAGTGAAGTCTTTGGGACTCCGTTTCTCATTTGTAAATGAGG 128
DB 3158 AACCTTGGGACATTAATATATCTTTGAGCCTTAGTTTTCATCTGTAAACAGGGA 3217

QY 129 TAATACAG 138
DB 3218 TAATACAG 3227
```

```

RESULT 5
US-11-297-383-12/C
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/ Sequence 12, Application US/11297383
/ Publication No. US20060110813A1
/ GENERAL INFORMATION:
/ APPLICANT: Ajinomoto Co., Inc.
/ TITLE OF INVENTION: Process for Producing L-Glutamic Acid
/ FILE REFERENCE: C210MOPC4045
/ CURRENT APPLICATION NUMBER: US/11/297,383
/ PRIOR FILING DATE: 2005-12-09
/ PRIOR APPLICATION NUMBER: 2003-165545
/ PRIOR FILING DATE: 2003-06-10
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 12
/ LENGTH: 6035
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: plasmid pSTVCB
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (2129)..(3439)
US-11-297-383-12
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Query Match 11.6%; Score 29.8; DB 7; Length 6035;
Best Local Similarity 58.4%; Pred. No. 0.47;
Matches 52; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
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```
QY 143 TTCTACCCCAAGCAGGTGTTGTCGGCCAGAGGCCCAATTGTTGGCTTCAAC 202
DB 1834 TTCTGACCTTCAGGCGACCATTTCAACCCCGCTAGAGGTGAAATGCTGGCTTTAAG 1775
QY 203 GCATCAGTTACCCCAAGAGCGGCTCAG 231
DB 1774 GCATTAATAATCCACATATAAGTGACTG 1746
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```
RESULT 6
US-11-293-697-1350
/ Sequence 1350, Application US/11293697
/ Publication No. US20060105376A1
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: Novel full length cDNA
/ FILE REFERENCE: H1-A0106
/ CURRENT APPLICATION NUMBER: US/11/293,697
/ PRIOR FILING DATE: 2005-12-05
/ PRIOR APPLICATION NUMBER: US/10/108,260
/ PRIOR FILING DATE: 2002-03-28
/ NUMBER OF SEQ ID NOS: 5458
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1350
/ LENGTH: 3646
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-293-697-1350
```

```
Query Match 11.5%; Score 29.6; DB 7; Length 3646;
Best Local Similarity 51.5%; Pred. No. 0.43;
Matches 66; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
```

```
QY 94 TTGGAGCTCCGTTTCTCTCAATTGTAATGAGGTTAATACAGCCCTTCTTCACTCCC 153
DB 774 TCTGGGCTCCAGTTTCCCAATTGTGATGAGGCACTTCCAAATGCTCTCTAGGCCCT 833
QY 154 AAAGCAGCTGTTTGTCCCGGCGAGAGGCCCAATTGTTGGCTGTTACGCATCAGTTAC 213
DB 834 GCAAGTAAGTAATTTTTCAGTTCAAGTCAAGCAGGTAAGGAGCATTCATCATTTGTG 893
QY 214 CCCACAGAGAG 225
DB 894 CTCATATCAAG 905
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```
RESULT 7
US-11-304-129-58/c
/ Sequence 58, Application US/11304129
/ Publication No. US20060088915A1
/ GENERAL INFORMATION:
/ APPLICANT: OHTAKI, Tetuya
/ APPLICANT: MASUDA, Yasuhide
/ APPLICANT: TAKATSU, Yoshinori
/ APPLICANT: MATANABE, Takuya
/ APPLICANT: TERAU, Yasuko
/ APPLICANT: SHINTANI, Yasuhide
/ APPLICANT: HINUMA, Syuji
/ TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
/ FILE REFERENCE: 2762USOP
/ CURRENT APPLICATION NUMBER: US/11/304,129
/ PRIOR FILING DATE: 2005-12-15
/ PRIOR APPLICATION NUMBER: US/10/333,192
/ PRIOR FILING DATE: 2003-09-29
/ PRIOR APPLICATION NUMBER: JP 2000-217442
/ PRIOR FILING DATE: 2000-07-18
/ PRIOR APPLICATION NUMBER: JP 2001-26779
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: PCT/JP01/06162
/ PRIOR FILING DATE: 2001-07-17
/ NUMBER OF SEQ ID NOS: 58
/ SEQ ID NO 58
/ LENGTH: 258
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic DNA
US-11-304-129-58
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```
Query Match 11.3%; Score 29; DB 7; Length 258;
Best Local Similarity 55.4%; Pred. No. 0.2;
Matches 56; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
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```
QY 137 GCCTTCTTACTTCCCAAGCAGCGTGTGTTGTCGGCCAGAGGCCCAATTGTTGGCT 196
DB 123 GCATCTTCACTTCAAGCAGCCCGGGGTGCATACGACGACGACGAGCCAGCGCT 64
QY 197 GTTCAGCATCATGTTACCCCAAGAGCGGCTCAGCATTT 237
DB 63 AATCGCAGCAGTATCCCGCACCGCATGTCATCATCGTT 23
```

```
RESULT 8
US-10-511-937-598/c
/ Sequence 598, Application US/10511937
/ Publication No. US2006008836A1
/ GENERAL INFORMATION:
/ APPLICANT: EXPRESSION DIAGNOSTICS, INC.
/ APPLICANT: Wohlgemuth, Jay
/ APPLICANT: Fry, Kirk
/ APPLICANT: Woodward, Robert
/ APPLICANT: Ly, Ngoc
/ APPLICANT: Prentice, James
/ APPLICANT: Morris, Macdonald
/ APPLICANT: Rosenberg, Steven
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
/ TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
/ FILE REFERENCE: 5061200104
/ CURRENT APPLICATION NUMBER: US/10/511,937
/ PRIOR FILING DATE: 2004-10-19
/ PRIOR APPLICATION NUMBER: PCT/US2003/012946
/ PRIOR FILING DATE: 2003-04-24
/ PRIOR APPLICATION NUMBER: US 10/131,831
/ PRIOR FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: US 10/325,899
/ PRIOR FILING DATE: 2002-12-20
/ NUMBER OF SEQ ID NOS: 3117
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 598
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LENGTH: 1458
TYPE: DNA
ORGANISM: Homo sapiens
US-10-511-937-598

Query Match 10.9%; Score 28; DB 6; Length 1458;
Best Local Similarity 53.7%; Pred. No. 1.1;
Matches 58; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 66 GTGAATATCGAAGATGATGACGCTTTGGACCTCCGTTTCCTATGTAAATGA 125
DB 380 GTGACATATCGAATCGCTGAAAGTTCTCTGTTCATTCCTTTAGCTCCACA 321

QY 126 GGTAAATACGAGCCTTCTTACTCCCAACGACGTTTGTCCG 173
DB 320 GAGTCTCTCCACGACTTCTTAGCTTAATCCCAAGTTTGGTACAG 273

RESULT 9

US-11-293-697-1731/c
Sequence 1731, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
PRIOR FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1731
LENGTH: 1830
TYPE: DNA
ORGANISM: Homo sapiens
US-11-293-697-1731

Query Match 10.9%; Score 28; DB 7; Length 1830;
Best Local Similarity 53.7%; Pred. No. 1.2;
Matches 58; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 66 GTGAATATCGAAGATGATGACGCTTTGGACCTCCGTTTCCTATGTAAATGA 125
DB 438 GTGACATATCGAATCGCTGAAAGTTCTCTGTTCATTCCTTTAGCTCCACA 379

QY 126 GGTAAATACGAGCCTTCTTACTCCCAACGACGTTTGTCCG 173
DB 378 GAGTCTCTCCACGACTTCTTAGCTTAATCCCAAGTTTGGTACAG 331

RESULT 10

US-11-293-697-604/c
Sequence 604, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
PRIOR FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 604
LENGTH: 3252
TYPE: DNA
ORGANISM: Homo sapiens
US-11-293-697-604

Query Match 10.9%; Score 28; DB 7; Length 3252;
Best Local Similarity 63.2%; Pred. No. 1.6;

Matches 43; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 70 ATATCAGAGATGATGACGCTTTGGACCTCCGTTTCCTATGTAAATGAGATT 129
DB 877 ATCTGGGATGTTACTTACTCTCTATGCTCTGTTCTCATTTGTAAATAGGAT 818

QY 130 AATACAG 137
DB 817 AATACAG 810

RESULT 11

US-10-857-260-29
Sequence 29, Application US/10857260
Publication No. US20060110742A1
GENERAL INFORMATION:
APPLICANT: Lyons, Leslie A.
APPLICANT: Grah, Robert
APPLICANT: Erdman, Carolyn
TITLE OF INVENTION: The Regents of the University of California
FILE REFERENCE: 023070-146800US
CURRENT APPLICATION NUMBER: US/10/857,260
PRIOR FILING DATE: 2004-05-28
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 9973
TYPE: DNA
ORGANISM: Felis catus
FEATURE:
OTHER INFORMATION: Genbank Accession No. AC145332.28 genomic DNA for
OTHER INFORMATION: PKD1 9973 bp contig
NAME/KEY: modified base
LOCATION: (1)..(9973)
OTHER INFORMATION: n = g, a, c or t
US-10-857-260-29

Query Match 10.9%; Score 28; DB 6; Length 9973;
Best Local Similarity 60.5%; Pred. No. 2.7;
Matches 46; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 61 AGTGTGAAATATCAGAGATGATGACGCTTTGGACCTCCGTTTCCTATGTAA 120
DB 8374 AGCTGTGATTTTGGACGCTCCCTTCGCTCTGAGGCTCAGTTTCCATCTAAC 8433

QY 121 ATGAGGTTAATACA 136
DB 8434 ATTGGGATCATACGA 8449

RESULT 12

US-10-553-298-1
Sequence 1, Application US/10553298
Publication No. US20060110385A1
GENERAL INFORMATION:
APPLICANT: NeuroNova AG
TITLE OF INVENTION: A Method for Diagnosing and Treating Affective Disorders
FILE REFERENCE: XXX
CURRENT APPLICATION NUMBER: US/10/553,298
PRIOR FILING DATE: 2005-10-14
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 56580
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: exon1
LOCATION: (3000)..(3124)
OTHER INFORMATION:
FEATURE:

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/ NAME/KEY: exon2
/ LOCATION: (24841).. (25009)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: exon3
/ LOCATION: (26134).. (26202)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: exon4
/ LOCATION: (30958).. (31030)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: exon5
/ LOCATION: (32481).. (32577)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: exon6
/ LOCATION: (35416).. (35496)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: exon7
/ LOCATION: (36113).. (36242)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: exon8
/ LOCATION: (37541).. (37677)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: exon9
/ LOCATION: (45470).. (45560)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: exon10
/ LOCATION: (47229).. (47295)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: exon11
/ LOCATION: (47380).. (47529)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: exon12
/ LOCATION: (50438).. (50539)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: exon13
/ LOCATION: (54392).. (54889)
/ OTHER INFORMATION:
/ US-10-553-298-1

Query Match          10.7%; Score 27.6; DB 6; Length 56580;
Best Local Similarity 67.2%; Pred. No. 8.7;
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 76 GGAAGATGACTGAACGCTTGGGACCTCCGTTTCCTATTGTAATAATGAGGTTAATA 133
Db 33237 GGAATAATGCTTAACCTCTCTGAGTTTCAGTGCTCCTCACTGTAATAAGCAATAATA 33234

RESULT 13
US-11-293-697-1501
/ Sequence 1501, Application US/11293697
/ Publication No. US20060105376A1
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: Novel full length cDNA
/ FILE REFERENCE: HI-A0106
/ CURRENT APPLICATION NUMBER: US/11/293,697
/ PRIOR FILING DATE: 2005-12-05
/ PRIOR APPLICATION NUMBER: US/10/108,260
/ PRIOR FILING DATE: 2002-03-28
/ NUMBER OF SEQ ID NOS: 5458
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 1501
```

```
/ LENGTH: 3165
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-11-293-697-1501

Query Match          10.7%; Score 27.4; DB 7; Length 3165;
Best Local Similarity 50.4%; Pred. No. 2.5;
Matches 67; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 69 AATATCAGGAAGATGACTGAACGCTTTGGGACCTCCGTTTCCTATTGTAATAATGAGGT 128
Db 1610 AAGATTACAGAAAGACGGGACACCCGAGAGCTGTGTCTGTCTGACTGTGACCGG 1669

QY 129 TAATACCAAGCTTTCTTCTACTCCCAACGACGTTGTTGCCGGCCAGAGGCCCAAT 188
Db 1670 TCAGGGCATTCATCTTGCTCCCAATTACCCCGTATGATGCGGCAATGAGACATAC 1729

QY 189 TGTGGCTGTCA 201
Db 1730 CGCTGGCAGTGCA 1742

RESULT 14
US-10-488-619-1537/c
/ Sequence 1537, Application US/10488619
/ Publication No. US20060099578A1
/ GENERAL INFORMATION:
/ APPLICANT: Greenlee, Wanner and Sullivan, P.C.
/ TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
/ FILE REFERENCE: 98-01 WO
/ CURRENT APPLICATION NUMBER: US/10/488,619
/ PRIOR FILING DATE: 2004-03-01
/ NUMBER OF SEQ ID NOS: 3040
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 1537
/ LENGTH: 591
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ US-10-488-619-1537

Query Match          10.6%; Score 27.2; DB 6; Length 591;
Best Local Similarity 48.7%; Pred. No. 1.3;
Matches 74; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 96 TGGAGCTCCGTTCCATTCATTAATAATGAGGTTAATACAGGCTTCTTACTCCCA 155
Db 213 TCGCCATAGGCTGTTCACTTGAAGAAGTCTACAGACCATCCCAAGGGCCGAG 154

QY 156 ACGCAGGTGTTTGTCCCGGCGAGAGGCCCAATGTTGCTGTTCACGATCAGTTACC 215
Db 153 GCACCCCTCTTCCCTGCTGTGCTCCCTGGGTGTGTGACTCGTACAGGTCCT 94

QY 216 CCACAGACGGGTCCAGCCAATTAAAGCGAAC 247
Db 93 GCCAGGGCGGGGTGGGCGAGAGCAGTGACAC 62

RESULT 15
US-11-293-697-1674
/ Sequence 1674, Application US/11293697
/ Publication No. US20060105376A1
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: Novel full length cDNA
/ FILE REFERENCE: HI-A0106
/ CURRENT APPLICATION NUMBER: US/11/293,697
/ PRIOR FILING DATE: 2005-12-05
/ PRIOR APPLICATION NUMBER: US/10/108,260
/ PRIOR FILING DATE: 2002-03-28
/ NUMBER OF SEQ ID NOS: 5458
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 1674
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LENGTH: 2788
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-11-293-697-1674

Query Match 10.6%; Score 27.2; DB 7; Length 2788;
 Best Local Similarity 61.1%; Pred. No. 2.8;
 Matches 44; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY	62	GTGTGGAATATCAGAGATGACTGACCTTTGGACTCCGTTCTCATTTGTAAA	121
Db	2031	GTATGAAACTTATAGGTAATTTACTTAACCTCTGACCTCAGTTTCTCATCTGTAAA	2090
QY	122	TGAGGTTAATA	133
Db	2091	ACAGGATAACA	2102

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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1587.8	99.1	32270	5	AF306570 Homo sapi
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5	1575.8	98.3	156370	5	AP003717 Homo sapi
6	1563.8	97.6	155668	12	AC024029 Homo sapi
7	1547.4	96.5	197031	12	AC019121 Homo sapi
8	1251.6	78.1	3301	5	AF208500 Homo sapi
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15	158.4	9.9	235330	12	AC140522 Homo sapi
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20	156.8	9.8	173271	12	AC141623 Homo sapi
21	156.8	9.8	173912	12	AC141075 Homo sapi
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28	155.8	9.7	190144	5	AL590080 Human DNA
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39	151	9.4	171833	5	AC146953 Homo sapi
40	151	9.4	178820	5	AC020552 Homo sapi
41	150.8	9.4	56912	5	AL160176 Human DNA
42	150.6	9.4	184041	5	AC093496 Homo sapi
43	150.6	9.4	187159	5	AC090941 Homo sapi
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ALIGNMENTS

RESULT 1	ES4511	3505 bp	DNA	linear	PAT 31-JAN-2002
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DEFINITION	UCP-2 promoter and use thereof.				
ACCESSION	ES4511.1	GI:18629692			
VERSION	JP 2000236886-A/1.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				

REFERENCE
1 (bases 1 to 3505)
AUTHORS Toyota, Y., Kobayashi, M. and Igaki, S.
TITLE UCP-2 promoter and use thereof
JOURNAL Patent: JP 2000236886-A 1 05-SEP-2000;
TAKEDA CHEM IND LTD
OS Homo sapiens (human)
PN JP 2000236886-A/1
PD 05-SEP-2000
PF 22-DEC-1999 JP 1999364724
PR

PI YUKIO TOYOTA, MAKOTO KOBAYASHI, SHIGERU IGAKI
PC C12N15/09, A61K45/00, A61P3/04, A61P3/06, A61P9/10, A61P9/12, PC
A61P29/00, C12N1/21,
PC C12N5/10, C12N1/02, G01N33/15, G01N33/50//A61K31/711, A61K38/00,
PC A61K48/00,
PC (C12N15/09, C12R1:19), (C12N15/09, C12R1:91), (C12N1/21, C12R1:19),
PC (C12N5/10, C12R1:91), (C12N15/00, C12N5/00, A61K37/02, (C12N15/00,
PC C12R1:19),
PC (C12N15/00, C12R1:91), (C12N5/00, C12R1:91)
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ORIGIN

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Matches 1603; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1141 TCTGAGCCCTTTTCTCATCCAGAGCTGAGAGAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1200
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DEFINITION complete sequences.
ACCESSION AP003531
VERSION AP003531.2 GI:20334341
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
1 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
Published Only in Database (2001)
2 (bases 1 to 199384)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (18-APR-2001) Masahiro Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suenho-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
On Apr 26, 2002 this sequence version replaced GI:1369094.
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VERSION AF306570.1 GI:11037742  
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SOURCE  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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Hominiidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 3270)  
TITLE Schmeitler, C., Oberkofler, H., Esterbauer, H. and Patsch, W.  
JOURNAL UCP2 promoter region and exon 1  
REFERENCE  
AUTHORS 2 (bases 1 to 3270)  
TITLE Unpublished  
AUTHORS Schmeitler, C., Oberkofler, H., Esterbauer, H. and Patsch, W.  
JOURNAL Direct Submision  
SUBMITTED (18-SEP-2000) Laboratory Medicine, LandesKliniken  
Salzburg, Melchner Hauptstr. 48, Salzburg A-5020, Austria  
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Query Match 99.1%; Score 1587.8; DB 5; Length 3270;
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mRNA

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2490 ACCGGGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2549
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2610 ACAGCAGAGCGGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2669
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2730 ACTTAAGACAGCGGCGCGCTGAGAGGCTGTTGTTAGAAAACCGTCT 2771

RESULT 4
DQ087219 12177 bp DNA linear PRI 18-JUN-2005
LOCUS Homo sapiens uncoupling protein 2 (mitochondrial, proton carrier) (UCP2) gene, complete cds; nuclear gene for mitochondrial product.
DEFINITION DQ087219
VERSION DQ087219.1 GI:67515418
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 12177) Shaffer, T., Bertucci, C., Baler, C.N., Livingston, R.J., Rieder, M.J., Daniel, M., Downing, T.K., Stansbury, I.B., Nguyen, C.P., Gilderbieve, H., Cassidy, C.M., Johnson, E.J., Swanson, J.E., McFarland, T., Yoo, B., Park, C. and Nickerson, D.A. Direct Submission Submitted (07-JUN-2005) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA
COMMENT To cite this work please use: NIH/NIHES, Environmental Genome Project, NIH/NIHES ES15478, Department of Genome Sciences, Seattle, WA

(URL: http://egp.gs.washington.edu) .
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OY	61	AAGAGCACCCTGGACAACACAGGAGACCTGTCACTAACAAAGAATAAATTAATTAGCCAG	120			
Db	113	AAGAGCACCTGGACAACATATAGGAGAGACCTGTCACTAACAAAGAATAAATTAATTAGCCAG	172			
OY	121	GCTTAGTGCTCATCTCCCTGTGTGCCCACTACTAGGAGGCGAAGTAGTGTCTC	180			
Db	173	GCTTAGTGCTCATCTCCCTGTGTGCCCACTACTAGGAGGCGAAGTAGTGTCTC	232			
OY	181	CCAGAGGCTCAAGACTGACGTGAGCTGAGACCCAGCCACCTGCATTCCAGCCTGGCAAC	240			
Db	233	CCAGAGGCTCAAGACTGACGTGAGCTGAGACCCAGCCACCTGCATTCCAGCCTGGCAAC	292			
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OY	301	CCTAAACACATCTTTTTCAAAGAGACTTTAAAGACTTCATGCTGGTCTCTGTG	360			
Db	353	CCTAAACACATCTTTTTCAAAGAGACTTTAAAGACTTCATGCTGGTCTCTGTG	412			
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Db	413	ATCTCCACTCCCTTTTCAGGTCACACTTTTAACAGTCCTTTTSCCAAGGTAATA	472			
OY	421	AGTATATAGTTCTTGAATCCAGATTCCTCTGTTTSGACAGCCAGGGGCAATTTT	480			
Db	473	AGTATATAGTTCTTGAATCCAGATTCCTCTGTTTSGACAGCCAGGGGCAATTTT	532			
OY	481	GGTCTGACAGCCTTGATCTGTTCTGCTGTGCTCAGCAATCTCACAGCAAAATTTGCG	540			
Db	533	GGTCTGACAGCCTTGATCTGTTCTGCTGTGCTCAGCAATCTCACAGCAAAATTTGCG	592			

QY	541	AGCCTCTCCGGAATGACAGACCCAGACAGAGCTCAGGCGCAAAAGCTAGAGAAACCTGGGCGA	600
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QY	781	TCCTGTTTCCAGCTGCTTGCACAGACCAATGCGCTCGAGTGTCTTTCCGCTATA	840
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LOCUS AP003717 Homo sapiens genomic DNA, chromosome 11q clone:RP11-167N4, complete
DEFINITION sequences.
ACCESSION AP003717 GI:20334343
VERSION AP003717.3
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in Database (2001)
REFERENCE 2 (bases 1 to 156370)
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (04-JUN-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
[E-mail: hattori@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
Tel: 81-45-503-9111, Fax: 81-45-503-9170]
COMMENT On Apr 26, 2002 this sequence version replaced gi:16904692.
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RESULT 6
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LOCUS Homo sapiens chromosome 11 clone RP11-167N4, WORKING DRAFT
DEFINITION
AC024029
SEQUENCE 15 unordered pieces.
AC024029 GI:7230916
AC024029.3 GI:7230916
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 155668)
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 155668)
Waterston,R.H.
Direct Submission
Submitted (20-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Mar 13, 2000 this sequence version replaced gi:7109555.

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information -----
Center project name: H_NH0167N04
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990119
Consensus quality: 146450 bases at least Q40
Consensus quality: 149629 bases at least Q30
Consensus quality: 151087 bases at least Q20
Insert size: 16800; agarose-fp
Insert size: 154268; sum-of-contigs
Quality coverage: 3.98 in Q20 bases; sum-of-contigs
Quality coverage: 4.38 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1806: contig of 1806 bp in length
* 1807 1906: gap of unknown length
* 1907 4798: contig of 2892 bp in length
* 4799 4898: gap of unknown length
* 4899 7312: contig of 2414 bp in length
* 7313 7412: gap of unknown length
* 7413 11277: contig of 3865 bp in length
* 11278 11377: gap of unknown length
* 11378 14368: contig of 2991 bp in length
* 14369 14468: gap of unknown length
* 14469 20130: contig of 5662 bp in length
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Best Local Similarity 99.7%; Pred. No. 0;
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QY 781 TCTGTTTCAAG 840
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QY 1321 ACCGAG 1380
DB 68841 ACCGAG 68782
QY 1381 CTTGTGCTCAGATTCATGATTTGTTTCTTCCCTCCCAAGAGAGAGAGAGAGAGAGAGAGAG 1440
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LOCUS Homo sapiens chromosome 11 clone Rn11-535C12, WORKING DRAFT
DEFINITION
SEQUENCE 23 unordered pieces.
AC019121
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AC019121.3 GI:8440022
VERSION HTG; HTGS PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 197031)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 197031)
AUTHORS Waterston,R.H.
TITLE Direct Submission

JOURNAL
Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 10, 2000 this sequence version replaced gi:7105573.

COMMENT

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
Project Information -----
Center project name: H_NH0535C12
----- Summary Statistics -----
Sequencing vector: M13, 55%
Sequencing vector: plasmid, 45%
Chemistry: Dye-terminator Big Dye, 45% of reads
Chemistry: Dye-terminator Big Dye, 45% of reads
Assembly program: Phrap, version 0.990319
Consensus quality: 182418 bases at least Q40
Consensus quality: 187565 bases at least Q30
Consensus quality: 190012 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 194831; sum-of-contigs
Quality coverage: 4.10 in Q20 bases; agarose-fp
Quality coverage: 4.05 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Matches 1588; Conservative 0; Mismatches 11; Indels 4; Gaps 3;
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ACCESSION	AF208500				
VERSION	AF208500.1	GI:6684000			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.				
REFERENCE	1 (bases 1 to 3301) Tu,N., Chen,H., Winkles,U., Reinert,I., Marmann,G., Pirke,K.M. and Lense,K.U. Molecular cloning and functional characterization of the promoter region of the human uncoupling protein-2 gene Biochem. Biophys. Res. Commun. 265 (2), 326-334 (1999)				
JOURNAL	2 (bases 1 to 3301) Tu,N., Chen,H., Winkles,U., Reinert,I., Pirke,K.M. and Lense,K.U. Functional characterization of the 5'-flanking and promoter regions of the human UCP2 gene Biochem. Biophys. Res. Commun. (2000) In press				
PUBMED	3 (bases 1 to 3301) Lense,K.-U., Tu,N. and Chen,H. Direct Submission Submitted (26-NOV-1999) Laboratory of Molecular Neurogenetics, Center for Psychobiological and Psychosomatic Research, University of Trier, Friedrich-Wilhelm-Strasse 23, Trier D-54290, Germany				
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QY	1370	TTGCGGGGCCACCTGTTGCTGCACTTCTGATTTGTTCCTTCCCGCAACACGGCGGCGCT	14229
Db	2697	TTGCGGGGCCACCTGTGTCTGGA--TTCTGATTTGTTCTTCCCGGCAACACCGGCGCTT	2754
QY	1430	GTAACCAATTCGACACGAGGCGCGGTCTCGGAGAGGCCCACTCCCGCTCTCAGAGATCAACC	14889
Db	2755	TAAACCAATTGACAGCGA-GGCCGTGAGAGGCCCACTCCCGCTCTCAGAGATCAACC	2813
QY	1490	GCG-----CGCTCGCTCGAGAGGGGTAGTTGCTCCAGCGT--AGGGGCGCTGGGC	15428
Db	2814	GCGCGCGCTCGCTCGAGAGGGGTGTGTTAGTTTGTCCCAAGCGTTAGGGGGCTCGGGCC	28737
QY	1543	CCATTAAGAGAGAGATGCACTTTAAGACACGCGCCCGCTGGAACGCTTGTTAAGAACCGTCC	16021
Db	2874	CCATTAAGAGAGAGATGCACTTTAAGACACGCGCCCGCTGGAACGCTTGTTAAGAACCGTCC	29333
QY	1603	T 1603	
Db	2934	T 2934	

RESULT 9			
LOCUS	AC136431		
DEFINITION	AC136431	168721 bp	DNA linear PRI 21-DEC-2002
	Homo sapiens chromosome 16 clone RP11-148M17, complete sequence.		

	Query Match	9.9%;	Score 158.4;	DB 5;	Length 168721;
	Best Local Similarity	73.9%;	Pred. No-1e-34;		
	Matches 229;	Conservative 0;	Mismatches 76;	Indels 5;	Gaps 2;
OY	2 CCTGTATATTCAGTACTGTGAGAGTCCGAGGCTCAGAGGACCTGTTGAGGCCAGAGTTCA	61			
Db	18726 CCGTATATCCCAACACTTTTGAGAGGGCCAAGGCAGGTGATTGCTTGAGCCAGAGATTGG	18785			
OY	62 AGAGCAGCCTTGACAACAACAGGGAGACCCTGTCACTACAAAGAATAAATTAAATTAGCCAGG	121			
Db	18786 AGACCAAGCCTGGGGCAACATAGAGAGCTCATCTTACAAAATAATCAAAAAATTACCTAGG	18845			
OY	122 CTTAGTGGCTCATCCCGTGGTCCACGTACTACAGGAGGACAGAGTAGGA-----CTGGTT	177			
Db	18846 CGTGTGTGACATGCTCTGTATGTCCAGCTACTAGGGAGGCTGAGTGGGAGGATGGCTTG	18905			
OY	178 GTCCACAGAGGTCAAGACTGACAGTAGAGTGAAGCCAGCCACTGTGATTCAGCCTGGGC	237			
Db	18906 AGCCCAAAGAGTGTGAAGATGSCAGTAGCCGAGATTGCAACA-CTGCACTCCAGCCTGGGT	18964			
OY	238 AACCAAAAAGACCCCTGTCTCAAAAAATAAGTTAAATTAAATTAAATTATATATTTAAATAGTTTA	297			
Db	18965 GACAGAGCAAGACCTGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCAG	19024			
OY	298 AACCTTAAC 307				
Db	19025 ATCCCTAGAC 19034				

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGTTCA 61
 Db 131562 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGTTTG 131503
 QY 62 AGAGCAGCCTTGAGCAACACAGGAGAGCTGTCTACTACAAAGATTAATAATTAGCCAGG 121
 Db 131502 AGAGCAGCCTTGAGCAACACAGGAGAGCTGTCTACTACAAAGATTAATAATTAGCCAGG 131443
 QY 122 CTGATGGGCTCATCCCTGTGTGCTCCAGCTACTAGAGGAGCAGAGTAGA-----CTGCTT 177
 Db 131442 CGTGTGGGCAATGCTGTGATGCTCCAGCTACTAGAGGAGCTGAGTGGGAGAGATGGCTTG 131383
 QY 178 GTCCAGAGAGTCAAGACTGCACTGAGCTGAGCCAGCCAGCTGCAATTCAGCTGGGC 237
 Db 131382 AGCCCAAGAGGTGAGAGATGCACTGAGCCAGATTTGACCA-CTGCACTCAGCTGGGT 131324
 QY 238 AACAAAAAGAGACCTGTCTCAAAAAATAATTAAATAATAATAATAATAGTTTA 297
 Db 131323 GACAGAGCAGAGACCTGTCTCAAAAAATAATAATAATAATAATAATAATAATAAGCAG 131264
 QY 298 AACCTTAAC 307
 Db 131263 ATCCCTAGAC 131254

RESULT 12
 AC138897/c 175785 bp DNA linear HTG 21-JAN-2003
 LOCUS AC138897 Homo sapiens chromosome 16 clone RP11-482B16, WORKING DRAFT
 DEFINITION AC138897
 SEQUENCE 3 unordered pieces.
 AC138897.1 GI:27805309
 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS DOE Joint Genome Institute.
 TITLE Sequencing of Human Chromosome 16
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 175785)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-2003) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 COMMENT -----Genome Center
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: http://www.jgi.doe.gov

Project Information
 Center Project Name: 591493
 Center clone name: RPC1-11_482B16

Summary Statistics
 Consensus quality: 175156 bases at least Q40
 Consensus quality: 175239 bases at least Q30
 Consensus quality: 175390 bases at least Q20
 Estimated insert size: 180000; agarose-fp estimation
 Estimated insert size: 175585; sum-of-contigs estimation
 Quality coverage: 16.07 in Q20 bases; agarose-fp estimation
 Quality coverage: 16.47 in Q20 bases; sum-of-contigs estimation.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 3 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 1 47298: contig of 47298 bp in length

FEATURES
 source
 * 47299 47398: gap of unknown length
 * 47399 106534: contig of 59136 bp in length
 * 106535 106634: gap of unknown length
 * 106635 175785: contig of 69151 bp in length.
 location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="16"
 /clone="RP11-482B16"
 /clone_1lb="RPC1 human BAC library 11"
 /clone_2lb="47398"
 /estimated_length=unknown
 /estimated_length=106634
 /estimated_length=unknown

ORIGIN
 Query Match 9.3%; Score 158.4; DB 12; Length 175785;
 Best Local Similarity 73.9%; Pred. No. 1e-34;
 Matches 229; Conservative 0; Mismatches 76; Indels 5; Gaps 2;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGTTCA 61
 Db 108733 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGGCCAGAGTTTG 108674
 QY 62 AGAGCAGCCTTGAGCAACACAGGAGAGCTGTCTACTACAAAGATTAATAATTAGCCAGG 121
 Db 108673 AGAGCAGCCTTGAGCAACACAGGAGAGCTGTCTACTACAAAGATTAATAATTAGCCAGG 108614
 QY 122 CTGATGGGCTCATCCCTGTGTGCTCCAGCTACTAGAGGAGCAGAGTAGA-----CTGCTT 177
 Db 108613 CGTGTGGGCAATGCTGTGATGCTCCAGCTACTAGAGGAGCTGAGTGGGAGAGATGGCTTG 108554
 QY 178 GTCCAGAGAGTCAAGACTGCACTGAGCTGAGCCAGCCAGCTGCAATTCAGCTGGGC 237
 Db 108553 AGCCCAAGAGGTGAGAGATGCACTGAGCCAGATTTGACCA-CTGCACTCAGCTGGGT 108495
 QY 238 AACAAAAAGAGACCTGTCTCAAAAAATAATTAAATAATAATAATAATAGTTTA 297
 Db 108494 GACAGAGCAGAGACCTGTCTCAAAAAATAATAATAATAATAATAATAATAATAAGCAG 108435
 QY 298 AACCTTAAC 307
 Db 108434 ATCCCTAGAC 108425

RESULT 13
 AC136434 189911 bp DNA linear HTG 01-NOV-2002
 LOCUS AC136434 Homo sapiens chromosome 16 clone RP11-261E14, WORKING DRAFT
 DEFINITION AC136434
 SEQUENCE 4 unordered pieces.
 AC136434
 AC136434.1 GI:24462324
 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS DOE Joint Genome Institute.
 TITLE Sequencing of Human Chromosome 16
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 189911)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (01-NOV-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 COMMENT -----Genome Center
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: http://www.jgi.doe.gov

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2006, 16:15:11 ; Search time 1394.65 Seconds
(without alignments)
8013.826 Million cell updates/sec

Title: US-09-869-098a-1_COPY_255_1857

Perfect score: 1603
Sequence: 1 acctgtaattccagctactgt.....cgcttgtagaaccgtcct 1603

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1603	100.0	3505	3	AAA62932
2	433.8	27.1	9314	12	ADG65405
3	152	9.5	135005	12	ADQ19501
4	150.4	9.4	23579	10	ADQ87112
5	149.4	9.3	186510	10	ADQ824797
6	148.8	9.3	151909	14	ABE86535
7	147.4	9.2	81099	11	ACN45018
8	147.2	9.2	110000	14	AE61124-0
9	147	9.2	110000	10	ADG70447-0
10	147	9.2	110000	10	ABZ79565-0
11	146.8	9.2	7739	4	AA136824
12	146.8	9.2	7739	8	ABX59812
13	146.8	9.2	7739	12	ADJ30562
14	146.8	9.2	226475	9	AAE58279
15	146.4	9.1	41150	10	ADL13819
16	146.4	9.1	41150	14	AE018343
17	146.4	9.1	44348	12	ADN48556
18	145.4	9.1	31749	4	AAK72959

C	19	145.4	9.1	78925	3	AAC98888
C	20	145.4	9.1	143947	15	AER38790
C	21	145.4	9.1	143947	15	AER38751
C	22	145.4	9.1	143947	15	AER35247
C	23	145.4	9.1	143947	15	AER64068
C	24	145.4	9.1	143947	15	AER63985
C	25	144.8	9.0	53122	11	ACN43998-6
C	26	144.8	9.0	110000	11	ACN43998-5
C	27	144.6	9.0	2096	8	ACT72436
C	28	144.6	9.0	93500	13	ADT77142
C	29	144.4	9.0	32169	5	AB14358
C	30	144	9.0	109906	6	ABK94411
C	31	144	9.0	109906	12	ADJ08112
C	32	144	9.0	158417	13	AD536461
C	33	143.8	9.0	11006	14	AE61101
C	34	143.6	9.0	58822	9	ADA02540
C	35	143.6	9.0	58822	10	ADA72278
C	36	143.6	9.0	58822	10	AD85788
C	37	143.6	9.0	110000	12	ADN06353-0
C	38	143.6	9.0	110000	13	ADN94372-0
C	39	143.6	9.0	145616	14	ABD17971
C	40	143.6	9.0	174472	14	ADZ13139
C	41	143.6	9.0	174703	11	ACN44738
C	42	143.6	9.0	276276	11	ACN44350
C	43	143.4	8.9	2005	5	AAF93841
C	44	143.4	8.9	2005	14	ADY63190
C	45	143.4	8.9	22428	4	AA541759

ALIGNMENTS

RESULT 1	AAA62932	standard; DNA; 3505 BP.
ID	AAA62932	
AC	AAA62932;	
XX		
DT	02-NOV-2000	(first entry)
DE	DNA containing human uncoupling protein-2 (UCP-2) promoter region.	
XX		
KM	Promoter; human; uncoupling protein-2; UCP-2; obesity; diabetes;	
XX	hypotension; hyperlipidaemia; anti-pyretic; de.	
OS	Homo sapiens.	
XX		
PN	WO200039315-A1.	
XX		
PD	06-JUL-2000.	
XX		
PF	22-DEC-1999;	99WO-JP007198.
XX		
PR	24-DEC-1998;	98JP-00366719.
XX		
PA	(TAKE) TAKEIDA CHEM IND LTD.	
XX		
PI	Toyoda Y, Kobayashi M, Igaki S;	
XX		
DR	WPI; 2000-452407/39.	
XX		
PT	DNA with promoter region containing regulator sequence of uncoupling	
PT	protein-2 (UCP-2), applicable in screening anti-obesity, anti-diabetic,	
PT	hypotensive, anti-hyperlipidemic and anti-pyretic drugs for use in	
PT	therapy.	
XX		
PS	Claim 4; Fig 1-6; 43pp; Japanese.	
XX		
CC	This invention relates to DNA comprising a promoter region containing the	
CC	regulatory sequences of human uncoupling protein-2 (UCP-2). Included in	
CC	the invention are a recombinant vector containing the DNA sequence, cells	
CC	transformed by the vector, and a method for screening for compounds or	
CC	salts that can promote or inhibit the UCP-2 promoter activity using the	

CC transformants. The DNA and cells transformed using it can be used to
 CC screen for anti-obesity, anti-diabetic, hypotensive, anti-hyperlipidemic
 CC and anti-pyretic drugs. The present sequence represents DNA containing
 CC the UCP-2 promoter sequences

XX Sequence 3505 BP; 671 A; 1053 C; 894 G; 887 T; 0 U; 0 Other;

Query Match 100.0%; Score 1603; DB 3; Length 3505;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1603; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ACCGTGAATTCAGTACTGTGAGAGTCCGAGTCAAGAGCTGCTTGAGGCCAGAGTTC 60
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Db 255 ACCGTGAATTCAGTACTGTGAGAGTCCGAGTCAAGAGCTGCTTGAGGCCAGAGTTC 314
   |||

QY 61 AAGAGAGCCTGGAACAACAGGAGAGCCTGTCATCAAGAATTAATTAATTAAGCAG 120
   |||
Db 315 AAGAGAGCCTGGAACAACAGGAGAGCCTGTCATCAAGAATTAATTAATTAAGCAG 374
   |||

QY 121 GCTTAATGAGTCAATCCCTGTGTGTCCAGTACTAAGGAGGAGAGAGTGAAGTGTGTC 180
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Db 375 GCTTAATGAGTCAATCCCTGTGTGTCCAGTACTAAGGAGGAGAGAGTGAAGTGTGTC 434
   |||

QY 181 CCAAGAGGTGAACATGCACTGAGTGAAGACCCAGCCACTGCAATTCAGCTGGGCAAC 240
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Db 435 CCAAGAGGTGAACATGCACTGAGTGAAGACCCAGCCACTGCAATTCAGCTGGGCAAC 494
   |||

QY 241 AAAAAGAGACCCGTGTCAAAAAATATAATTAATTAATTAATTAATTAATTAATTAAT 300
   |||
Db 495 AAAAAGAGACCCGTGTCAAAAAATATAATTAATTAATTAATTAATTAATTAATTAAT 554
   |||

QY 301 CCTAAACAATCTCTTTTCAAGAGAGCTTTAAGAGCTTCATGCTGCTGTGTC 360
   |||
Db 555 CCTAAACAATCTCTTTTCAAGAGAGCTTTAAGAGCTTCATGCTGCTGTGTC 614
   |||

QY 361 ATCTCACTTCCCTTTTCAAGCTCCAGACTTTTAAGAGTCTCTTTGCAAGATATA 420
   |||
Db 615 ATCTCACTTCCCTTTTCAAGCTCCAGACTTTTAAGAGTCTCTTTGCAAGATATA 674
   |||

QY 421 AGTATATAGTTTTCGGAATCAGATTTCTTCCGTTTGAAGAGGAGGAGCAATTTT 480
   |||
Db 675 AGTATATAGTTTTCGGAATCAGATTTCTTCCGTTTGAAGAGGAGGAGCAATTTT 734
   |||

QY 481 GGTCTGAGAGCCTTTGATCTGTTCTGCTGTGCTGCAATCTCACAGCAAAATTTGCG 540
   |||
Db 735 GGTCTGAGAGCCTTTGATCTGTTCTGCTGTGCTGCAATCTCACAGCAAAATTTGCG 794
   |||

QY 541 AGCTCTCCGGAATGCAAGCCAGACAGAGCTCAGCCAAAGCTAGAGAACTGGCGGA 600
   |||
Db 795 AGCTCTCCGGAATGCAAGCCAGACAGAGCTCAGCCAAAGCTAGAGAACTGGCGGA 854
   |||

QY 601 GGGAGACTCAGAGGCGACAAAAAACTTATATCTTTTCTTTTCTTTTCTTTTCTTTCT 660
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Db 855 GGGAGACTCAGAGGCGACAAAAAACTTATATCTTTTCTTTTCTTTTCTTTTCTTTCT 914
   |||

QY 661 TTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 720
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Db 915 TTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 974
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QY 721 TTTCTTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780
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QY 781 TCTGTTTCAAGGCTTCTGCAAGAGCAATGGGCTGGGGTGTGTTTCTTTCCGCTATA 840
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Db 1035 TCTGTTTCAAGGCTTCTGCAAGAGCAATGGGCTGGGGTGTGTTTCTTTCCGCTATA 1094
   |||

QY 841 ATTATCAGGCGCATCCAGCTGTGTCCCTCAGTGTTCCTTGAGAGTCCCTTCTGCT 900
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Db 1095 ATTATCAGGCGCATCCAGCTGTGTGTCCCTCAGTGTTCCTTGAGAGTCCCTTCTGCT 1154
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QY 901 GGTGAAAAACATATGGCGCGGCTTGAACAGAGGTGAAGTGTGTAATATCAGGAAGAT 960
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Db 1155 GGTGAAAAACATATGCGCGCGGCTGACCAAGGTTAAGTGTGTAATATCAGGAAGAT 1214
   |||
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QY 1021 TTCTACTCCCAACGACGTTGTTTCCCGGCAAGAGGCCCAATTTGTTGCTGTTTAC 1080
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Db 1275 TTCTACTCCCAACGACGTTGTTTCCCGGCAAGAGGCCCAATTTGTTGCTGTTTAC 1334
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QY 1081 GCATCAGTTTACCCCAACAGAGCGGTCAGCAATTAAGGCGAACAGAGCCGGTCCATC 1140
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Db 1335 GCATCAGTTTACCCCAACAGAGCGGTCAGCAATTAAGGCGAACAGAGCCGGTCCATC 1394
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QY 1141 TCTGAGGCTTTTCTCATCCAGGCTGGAACAGAGCTGAGCTGAGCCCGCTCTGCC 1200
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Db 1395 TCTGAGGCTTTTCTCATCCAGGCTGGAACAGAGCTGAGCTGAGCCCGCTCTGCC 1454
   |||

QY 1201 TTGTCAAGTGCAGGAGGCGGCGCTGTTGCTGTGTGTGTGTAAGAGCTGACAGCT 1260
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Db 1455 TTGTCAAGTGCAGGAGGCGGCGCTGTTGCTGTGTGTGTGTAAGAGCTGACAGCT 1514
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QY 1261 GGGTGTCCCGCGCCGCGCGGCGCTTTAGTGTCCGTGTCCTAAACGACAGGCGGCTGC 1320
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Db 1515 GGGTGTCCCGCGCCGCGCGGCGCTTTAGTGTCCGTGTCCTAAACGACAGGCGGCTGC 1574
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QY 1321 ACCGAGGAGAAAGGCGGAGCCAGCCAGCCAGCCAGCCAGCTGTGTGCTGCTGCGGCA 1380
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Db 1575 ACCGAGGAGAAAGGCGGAGCCAGCCAGCCAGCCAGCCAGCTGTGTGCTGCTGCGGCA 1634
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QY 1381 CCTGTTGCTGCAAGTTCTGATTTGTTCTTCTCCCGACAAAGCGGCGGCTCTAACCAATCG 1440
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QY 1441 ACAGAGAGGCGGCTGCGAGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCTGCT 1500
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Db 1695 ACAGAGAGGCGGCTGCGAGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCTGCT 1754
   |||

QY 1501 CGCAGAGAGGTTGGTATTTGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
   |||
Db 1755 CGCAGAGAGGTTGGTATTTGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1814
   |||

QY 1561 ACTTAAGACAGGCGCCGCTGAGCGCTGTTAGAAAACCGTCTT 1603
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Db 1815 ACTTAAGACAGGCGCCGCTGAGCGCTGTTAGAAAACCGTCTT 1857
   |||

RESULT 2
ADG65405
ID ADG65405 standard; DNA; 9314 BP.
XX
XX ADG65405;
AC
XX
DT 11-MAR-2004 (first entry)
XX
DE Human uncoupling protein 2 (UCP2) gene.
XX
XX anorectic; antidiabetic; immunomodulator; gene therapy; haplocloning;
KM uncoupling protein 2; mitochondrial; proton carrier; UCP2;
KM polymorphic site; haplotype; haploclon pair; obesity; diabetes;
KM immunological disorder; body mass defect; thermoregulation defect; human;
KM gene; de; SNP; single nucleotide polymorphism.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1283
FT variation
FT FT /*tag= a
FT FT /standard_name= "Single nucleotide polymorphism"
FT FT /tag= b
FT FT /standard_name= "Single nucleotide polymorphism"
FT variation 2051

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Db 1 GGTCATCTCTGACGCGCTTTTCTCATCCAGGAGCTGACAGGCAAGCTGAGCGCCG 60
OY 1193 GCTCTGCTTTGTCACGTGCGGAGGCGCGCCGCTTTCCTTGTGTGTGTAAGACCTGAG 1252
Db 61 GCTCTGCTTTGTCACGTGCGGAGGCGCGCCGCTTTCCTTGTGTGTGTAAGACCTGAG 120
OY 1253 GTGACGCTGAGGTCTCCCGCCCGCGGAGGCTTTAGTGTCTCTGTCTCTTAAACCCGAG 1312
Db 121 GTACACGCTGAGGTCTCCCGCCCGCGGAGGCTTTAGTGTCTCTGTCTCTTAAACCCGAG 180
OY 1313 GCGGCTCCACCGGAGGAGAAAGGCGGCGAACCCGAGCGGACCAAGCGGTGTGTGCGTTG 1372
Db 181 GCGGCTCCACCGGAGGAGAAAGGCGGCGAACCCGAGCGGACCAAGCGGTGTGTGCGTTG 240
OY 1373 CCGGAGCACTGTGTGTGTCAGATTCTGATTGTCTTCTCCCGCAACAACGCGGCTGTGA 1432
Db 241 CCGGAGCACTGTGTGTGTCAGATTCTGATTGTCTTCTCCCGCAACAACGCGGCTGTGA 300
OY 1433 ACCAATCGACAGGAGGCGCGGTGCGAGAGCCCGCCGCTGAGAGAGCCAGCGCG 1492
Db 301 ACCAATCGACAGGAGGCGCGGTGCGAGAGCCCGCCGCTGAGAGAGCCAGCGCG 360
OY 1493 CGCTCGCTGCGAGAGGAGGTGAGTTTGTCCAGCGTGAAGGAGGCTGAGCCCAATAAAGA 1552
Db 361 CGCTCGCTGCGAGAGGAGGTGAGTTTGTCCAGCGTGAAGGAGGCTGAGCCCAATAAAGA 419
OY 1553 GGAAGTGAAGCTTAAGACAGCGGCCCGCTGAGACGCTTGTGAACCGTCT 1603
Db 420 GGAAGTGAAGCTTAAGACAGCGGCCCGCTGAGACGCTTGTGAACCGTCT 468

RESULT 3
ADQ19501/c
ID ADQ19501 standard; DNA; 135005 BP.

XX AC ADQ19501;

XX DT 26-AUG-2004 (first entry)

XX DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2320.

KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human; ds.

XX OS Homo sapiens.

XX PN MO2004048938-A2.

XX PD 10-JUN-2004.

XX PF 26-NOV-2003; 2003MO-US038193.

XX PR 26-NOV-2002; 2002US-0429739P.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Aziz N, Ginsburg WM, Zlotnick A;

XX DR WPI; 2004-441208/41.

XX PT Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue sarcoma.

XX PS Example 2; SEQ ID NO 2320; 210pp; English.

XX CC The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the

CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.

XX SQ Sequence 135005 BP; 32951 A; 33605 C; 32661 G; 35788 T; 0 U; 0 Other;
Query Match 9.5%; Score 152; DB 12; Length 135005;
Best Local Similarity 80.0%; Pred. No. 4, 2e-22;
Matches 216; Conservative 0; Mismatches 50; Indels 4; Gaps 3;

OY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTGAGAGGACTGTTGAGGCCAGAGTTC 60

Db 84820 ATCTGTAATTCAGTACTGTGAGAGTCCGAGGTGAGAGGACTGTTGAGGCCAGAGTTC 84761

OY 61 AAGAGCAGCCTTGACAAACAGGAGAA--CTGTCTACTACAAAGATTAAATTATAGCC 118

Db 84760 AAGACTATCTCTGGGCAACATAGTGAAGACCCCTGTCTCTCAAAAAATAGAAAAATTAGTC 84701

OY 119 AGGCTTAGTGGCTCATCCCTGTGTGTCCAGCTACTAGGGAGGAGAGTAGAGTGGT 178

Db 84700 GGGTATGTGGACACATGCCCTGTATGTCCAGCTACTAGAGAGGCTGAGTAGATTGCTTG 84641

OY 179 -TCCAGAGAGTTCAGACAGTGAAGTGAAGCCAGCCACTGCAATTCAGCTGAGC 237

Db 84640 AGCTCAGAGAGTTCAGAGCGGCGAGTGAAGTGAAGCAGTGGCA-CTGTACTCAACTGGGC 84582

OY 238 AACAAAAAGAGACCTGTCTCAAAAAATTA 267

Db 84581 AACAGAAACAGACCTGTCTCAAAAAATA 84552

RESULT 4

ADQ87112
ID ADQ87112 standard; DNA; 23579 BP.

XX AC ADQ87112;

XX DT 01-JAN-2004 (first entry)

XX DE Human GPCR gene SEQ ID NO:1565.

XX KW ds; gene; human; GPCR;

XX KW guanosine triphosphate-binding protein coupled receptor; gene therapy.

XX OS Homo sapiens.

XX PN BP1270724-A2.

XX PD 02-JAN-2003.

XX PF 18-JUN-2002; 2002BP-00013517.

XX PR 18-JUN-2001; 2001JP-00246789.

XX PA (NRAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX PI Suwa M, Asai K, Akiyama Y, Aburatani H;

XX DR WPI; 2003-315783/31.

XX PS P-PSDB; ADQ87113.

XX PT New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.

XX PS Claim 1; SEQ ID NO 1565; 28pp; English.

XX CC The invention relates to a novel polynucleotide encoding a guanosine

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25-AUG-2005 (first entry)

Human SLC4A4 gene genomic sequence SEQ ID NO:34.

DNA methylation; biomarker; cancer; gene; ds; SLC4A4.

Homo sapiens.

US2005130172-A1.

16-JUN-2005.

27-JAN-2004; 2004US-00765790.

16-DEC-2003; 2003US-00737082.

(FARB) BAYER CORP.

Beard C, Burgess C, Gannon A, Harvey J, Lechner JF, Li Z; WPI; 2005-456991/46.

GENBANK; AF011390, NM_003759.

Identifying nucleic acid sequences as biomarker for disease, by identifying nucleic acid sequences comprising methylated CpG site and down-regulated in diseased cells and comparing its expression level with demethylated nucleic acid.

Claim 11; SEQ ID NO 34; 27bp; English.

The invention relates to a method (M1) for identifying one or more nucleic acid sequences useful as a biomarker for a disease to be detected. (M1) involves identifying nucleic acid sequences comprising methylated CpG site in promoter-first exon region and that are down-regulated in diseased cells, comparing expression level of nucleic acid sequences with that of demethylated nucleic acid sequences and identifying nucleic acid sequences exhibiting increase in expression after demethylation. Also described: (1) detecting (M2) the presence or stage of a disease in a subject, which involves determining the degree of methylation of one or more CpG sites on nucleic acid sequences in a biological sample obtained from the subject, and determining the presence of, predisposition to, or stage of the disease in the subject based on the degree of methylation; (2) monitoring the onset, progression, or regression of a disease in a subject; (3) determining the efficacy of a test compound for inhibiting a disease in a subject; and (4) a kit (I) useful for diagnosis, prognosis, staging, monitoring, and therapeutic treatment of a disease. (M1) is useful for identifying one or more nucleic acid sequences useful as a biomarker for a disease to be detected, where the nucleic acid sequences are useful for detecting, the presence or stage of a disease such as cancer e.g. colorectal cancer in a subject. The present sequence represents a specifically claimed human genomic sequence for use in the method of the invention. Note - The sequence data for this patent is not represented in the printed specification but was obtained in electronic format from the USPTO web site.

Sequence 383432 BP; 113010 A; 69169 C; 74959 G; 126294 T; 0 U; 0 Other;

Query Match 9.2%; Score 147.2; DB 14; Length 110000;

Best Local Similarity 74.0%; Pred. No. 4.3e-21;

Matches 213; Conservative 0; Mismatch 73; Indels 2; Gaps 2;

2 CCTGTAATTCACGACTGTGTAGAGTCCGAGGTCCAGAGACTGTGTAGGCCAGAGTTCA 61

Db CTTGTACTCCGACACTTTTGAAGGTGAGGTAGTGAATCCCTTGAGCCGACGAGTTG 90551

62 AGAGCAGCCTGAGCAACACAGAGGAGCC-TGTCACTCAAAAGATTAATTAATGACG 120

Db AGACCAAGCCTGGGCAATATGCAAAACCTTGTCTTCAAAAAAGACAAGATAAGCCAG 90621

121 GCTTATGAGCTCATCTCTGTGTGTCCGACTACTAGAGGAGGAGCAAGTAGACTGCTTGT 180

90622 GTGTGTGTGTGACACCTGTGTGTGTCCGACTTCTTGTGGAGGGGTGAGGTGTGACACTTGA 90681

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D6		90682	CCAGGAGGTGAGTGCTGTGATGTAGGCCAAGATTGTGTCCA-CTGCATCTCACGCTGGGTAAc	90740
Oy	241	AAAAAGACCCCTGCTCCAAAATAATTAAATTAAATTAATAATAA	288	
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RESULT 9
ADG70447_0/c

wf Sequence split info	5 fragments	LOCUS ADG70447	Accession Adg70447
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WP ADG70447_1	100001 210000		
WP ADG70447_2	200001 310000		
WP ADG70447_3	300001 410000		
WP ADG70447_4	400001 410846		
ID ADG70447 standard;	DNA; 410846 BP.		
XX ADG70447;			
AC			
DT	11-MAR-2004	(first entry)	
XX			
DE	Human ANGE-CILD8-CILD7 hybrid gene.		
XX			
KM	ANGE; CILD8; CILD7; ANGE-CILD8; ANGE-CILD7; CILD7-CILD8;		
KW	ANGE-CILD8-CILD7; anti-allergic; antihistaminic; dermatological;		
KX	antipyretic; anti-inflammatory; gene therapy; Igs-mediated disease;		
KM	ANGE 1; single nucleotide polymorphism; ds.		
XX			
OS	Chimeric.		
DS	Homo sapiens.		
XX			
FH Key	Location/Qualifiers		
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PN WO2003000727-A2.			
XX PD			
PD 03-JAN-2003.			
PF PF			
PR 21-JUN-2002; 2002WO-GB002859.			
XX PR			
PPR 21-JUN-2001; 2001GB-00015211.			
PR 21-JUN-2001; 2001GB-00015212.			
XX PA			
PA (ISIS-) ISIS INNOVATIONS LTD.			
XI Zhang Y,	Moffatt M,	Cookson W,	Tinsley J;
DR WIPI; 2003-201405/19.			
XX PT	New nucleic acid sequence comprising an ANGE, CILD8 or CILD7 mRNA, or		
PT their hybrid, useful for screening agents for treating IgE-mediated	diseases, e.g. asthma, atopy, hay fever, eczema, atopie dermatitis, or		
PS allergic rhinitis.			
XX Claim 12; Fig 5; 429pp; English.			
XX The invention relates to a novel isolated or recombinant nucleic acid	sequence comprising an ANGE, CILD8 or CILD7 mRNA, or ANGE-CILD8, ANGE-		
CC CILD7, CILD7-CILD8, or ANGE-CILD8-CILD7 hybrid mRNA sequence, its	complement, homologue or fragment. The novel nucleic acid sequences have		

KW	cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;	PR	21-SEP-2000;	2000US-0234274P.
KW	neurological disease; infection; human; secreted protein;	PR	25-SEP-2000;	2000US-023497P.
KW	musculoskeletal system; ds.	PR	25-SEP-2000;	2000US-023498P.
XX		PR	26-SEP-2000;	2000US-0235484P.
OS	Homo sapiens.	PR	27-SEP-2000;	2000US-0235834P.
XX		PR	27-SEP-2000;	2000US-0235836P.
PN	WO200155367-A1.	PR	29-SEP-2000;	2000US-0236327P.
XX		PR	29-SEP-2000;	2000US-0236367P.
PD	02-AUG-2001.	PR	29-SEP-2000;	2000US-0236368P.
XX		PR	29-SEP-2000;	2000US-0236369P.
PF	17-JAN-2001, 2001WO-US001338.	PR	29-SEP-2000;	2000US-0236370P.
XX		PR	02-OCT-2000;	2000US-0236802P.
XX		PR	02-OCT-2000;	2000US-0237037P.
PR	31-JUN-2000; 2000US-0179065P.	PR	02-OCT-2000;	2000US-0237038P.
PR	04-FEB-2000; 2000US-0180628P.	PR	02-OCT-2000;	2000US-0237039P.
PR	24-FEB-2000; 2000US-0184664P.	PR	02-OCT-2000;	2000US-0237040P.
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PR	18-APR-2000; 2000US-0198123P.	PR	20-OCT-2000;	2000US-0241221P.
PR	19-MAY-2000; 2000US-0205515P.	PR	20-OCT-2000;	2000US-0241785P.
PR	07-JUN-2000; 2000US-0209467P.	PR	20-OCT-2000;	2000US-0241786P.
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PR	30-JUN-2000; 2000US-0215135P.	PR	20-OCT-2000;	2000US-0241809P.
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PR	14-AUG-2000; 2000US-0225757P.	PR	08-NOV-2000;	2000US-0246610P.
PR	14-AUG-2000; 2000US-0225758P.	PR	08-NOV-2000;	2000US-0246611P.
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PR	18-AUG-2000; 2000US-0226279P.	PR	17-NOV-2000;	2000US-0249207P.
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PR	22-AUG-2000; 2000US-0226688P.	PR	17-NOV-2000;	2000US-0249209P.
PR	23-AUG-2000; 2000US-0227009P.	PR	17-NOV-2000;	2000US-0249210P.
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PR	01-SEP-2000; 2000US-0229287P.	PR	17-NOV-2000;	2000US-0249212P.
PR	01-SEP-2000; 2000US-0229343P.	PR	17-NOV-2000;	2000US-0249213P.
PR	01-SEP-2000; 2000US-0229344P.	PR	17-NOV-2000;	2000US-0249214P.
PR	01-SEP-2000; 2000US-0229345P.	PR	17-NOV-2000;	2000US-0249215P.
PR	05-SEP-2000; 2000US-0229509P.	PR	17-NOV-2000;	2000US-0249216P.
PR	05-SEP-2000; 2000US-0229513P.	PR	17-NOV-2000;	2000US-0249217P.
PR	06-SEP-2000; 2000US-0230437P.	PR	17-NOV-2000;	2000US-0249218P.
PR	06-SEP-2000; 2000US-0230438P.	PR	17-NOV-2000;	2000US-0249244P.
PR	08-SEP-2000; 2000US-0231242P.	PR	17-NOV-2000;	2000US-0249245P.
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PR	08-SEP-2000; 2000US-0231414P.	PR	17-NOV-2000;	2000US-0249299P.
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PR	12-SEP-2000; 2000US-0231968P.	PR	01-DEC-2000;	2000US-0251030P.
PR	14-SEP-2000; 2000US-0232397P.	PR	05-DEC-2000;	2000US-0251988P.
PR	14-SEP-2000; 2000US-0232398P.	PR	05-DEC-2000;	2000US-0256719P.
PR	14-SEP-2000; 2000US-0232399P.	PR	06-DEC-2000;	2000US-0251479P.
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PR	14-SEP-2000; 2000US-0232401P.	PR	08-DEC-2000;	2000US-0251868P.
PR	14-SEP-2000; 2000US-0233063P.	PR	08-DEC-2000;	2000US-0251869P.
PR	14-SEP-2000; 2000US-0233064P.	PR	08-DEC-2000;	2000US-0251869P.
PR	14-SEP-2000; 2000US-0233065P.	PR	08-DEC-2000;	2000US-0251990P.
PR	21-SEP-2000; 2000US-0234223P.			

PR 11-DEC-2000; 2000US-0254097P.
XX 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Baraesh SC, Ruben SM;
XX WPI; 2001-451937/48.
XX
PT Isolated polypeptide for treating, preventing and/or prognosing
PT disorders related to the musculoskeletal system including musculoskeletal
XX cancers and also for testing and detection e.g. diagnosis.
XX
PS Example 2; SEQ ID NO 3189; 781bp + Sequence Listing; English.
XX
CC The invention relates to novel genes (AAL34669-AAL37666) and proteins
CC (AAB03087-AAB04109) associated with the musculoskeletal system useful for
CC preventing, treating or ameliorating medical conditions e.g. by protein
CC or gene therapy. The genes are isolated from a range of human tissues
CC disclosed in the specification. The nucleic acids, proteins, antibodies
CC and (ant)agonists are useful in the diagnosis, treatment and prevention
CC of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as
CC myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g.
CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
CC bacterial, fungal and parasitic infections. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 7739 BP; 1963 A; 1731 C; 1890 G; 2155 T; 0 U; 0 Other;
XX
Query Match 9.2%; Score 146.8; DB 4; Length 7739;
Best Local Similarity 77.5%; Pred. No. 2,4e-21;
Matches 217; Conservative 0; Mismatches 57; Indels 6; Gaps 3;
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DB 5571 AGACCAAGCTTGGGCAACATAGGAGACCTGACTCTCAATATATTTAAAAATTCGCTGG 5512
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DB 5511 GTGTAGTGGACATACCTGTGTGTCCTCAGCTAGTGTGGAGGCGAGAGAGATGCTT 5452
QY 177 TGTCCAGAGAGTCAAGACTGCACTGAGCTGAGAGCCAGGCCAAGCTGCAATTCAGCCCTGG 236
DB 5451 GAGCCCAAGAGAGTCAAGGCTGCAATGAGCTGCAATCTTGGCA-CTGCACTTCAGACTGG 5393
QY 237 CAACAAAAAGAGACCTGTCTCAAAAAATAAGTTAATA 276
DB 5392 CAACAGACTGAGACCTGTCTCAAAAAACAACAAAA 5353
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RESULT 12
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ID ABX59812 standard; cDNA: 7739 BP.
XX
AC ABX59812;
XX
DT 26-FEB-2003 (first entry)
XX
DE cDNA encoding novel human musculoskeletal system antigen #2156.
XX
KM Gene; ss; musculoskeletal system antigen; cancer; metastasis;
KM re-vascularisation; thrombosis; arteriosclerosis; mineral content;
XX

KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
KW post-operative tissue repair; limb regeneration; neuronal growth;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW AIDS-related complex; chondrocyte growth; bone regeneration;
KW periodontal regeneration; tissue transport; bone graft; skin aging;
KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
KW cell growth; organ transplant; cell differentiation; body height; weight;
KW hair colour; eye colour; skin; percentage of adipose tissue;
KW pigmentation; cosmetic surgery; metabolism; biorhythm; cardiac rhythm;
KW depression; tendency for violence; pain; reproductive capability;
KW hormone level; endocrine level; appetite; libido; memory; stress;
KW storage capability; fat content; lipid content; protein content;
KW carbohydrate content; vitamin content; cofactor content;
KW nutritional component.
XX
OS Homo sapiens.
XX
XX US2002147140-A1.
XX
XX 10-OCT-2002.
XX
PF 17-JAN-2001; 2001US-00764877.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 28-JUN-2000; 2000US-0214886P.
XX 07-JUL-2000; 2000US-0216647P.
XX 07-JUL-2000; 2000US-0216880P.
XX 11-JUL-2000; 2000US-0217487P.
XX 11-JUL-2000; 2000US-0217496P.
XX 14-JUL-2000; 2000US-0218290P.
XX 26-JUL-2000; 2000US-0220963P.
XX 26-JUL-2000; 2000US-0220964P.
XX 14-AUG-2000; 2000US-0224518P.
XX 14-AUG-2000; 2000US-0224519P.
XX 14-AUG-2000; 2000US-0225287P.
XX 14-AUG-2000; 2000US-0225288P.
XX 14-AUG-2000; 2000US-0225270P.
XX 14-AUG-2000; 2000US-0225447P.
XX 14-AUG-2000; 2000US-0225757P.
XX 14-AUG-2000; 2000US-0225758P.
XX 22-AUG-2000; 2000US-0226888P.
XX 30-AUG-2000; 2000US-0228924P.
XX 01-SEP-2000; 2000US-0229287P.
XX 01-SEP-2000; 2000US-0229343P.
XX 01-SEP-2000; 2000US-0229344P.
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XX 05-SEP-2000; 2000US-0229509P.
XX 05-SEP-2000; 2000US-0229513P.
XX 08-SEP-2000; 2000US-0231413P.
XX 21-SEP-2000; 2000US-0234223P.
XX 21-SEP-2000; 2000US-0234274P.
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XX 29-SEP-2000; 2000US-0236367P.
XX 29-SEP-2000; 2000US-0236368P.
XX 29-SEP-2000; 2000US-0236369P.
XX 29-SEP-2000; 2000US-0236370P.
XX 02-OCT-2000; 2000US-0236802P.
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XX 08-DEC-2000; 2000US-0251856P.
XX 08-DEC-2000; 2000US-0251868P.
XX 08-DEC-2000; 2000US-0251869P.

XX (ROSE/) ROSEN C A.
PA (RUBEN/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX WPI; 2003-128199/12.
XX
PT Isolated nucleic acid molecules encoding musculoskeletal system
XX associated polypeptides, useful for detecting disorders, e.g. cancer.
XX
PS Disclosure; SEQ ID NO 3189; 321pp; English.
XX
XX The invention describes an isolated nucleic acid molecule comprising a
CC sequence encoding musculoskeletal system associated polypeptides useful
CC for detecting disorders, e.g., cancer or cancer metastases, in animals or
CC humans. The nucleic acid: stimulates re-vascularisation of ischaemic
CC tissues associated with conditions such as thrombosis, arteriosclerosis,
CC and other cardiovascular conditions; treats wounds due to injuries,
CC burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
CC and limb regeneration; stimulates neuronal growth; can treat and prevent
CC neuronal damage occurring in certain disorders or neurodegenerative
CC conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-
CC related complex; stimulates chondrocyte growth, thus they can be used to
CC enhance bone and periodontal regeneration and aid in tissue transports or
CC bone grafts; prevents skin aging due to sunburn by stimulating
CC keratinocyte growth; prevents hair loss, since FGF family members
CC activate hair-forming cells and promotes melanocyte growth; stimulates
CC growth and differentiation of hematopoietic cells and bone marrow cells
CC when used in combination with other cytokines; maintains organs before
CC transplantation or for supporting cell culture of primary tissues;
CC induces tissue of mesodermal origin to differentiate in early embryos;
CC increases or decreases the differentiation or proliferation of embryonic
CC stem cells, besides, hematopoietic lineage; modulates mammalian
CC characteristics, such as, body height, weight, hair colour, eye colour,
CC skin, percentage of adipose tissue, pigmentation, size, and shape (e.g.,
CC cosmetic surgery); modulates mammalian metabolism; changes mammal's metal
CC state or physical state by influencing biorhythm, circadian rhythms,
CC depression, tendency for violence, tolerance for pain, reproductive
CC capabilities, hormonal or endocrine levels, appetite, libido, memory, or
CC stress; increases or decreases storage capabilities, fat content, lipid,
CC protein, carbohydrate, vitamins, minerals, cofactors or other nutritional
CC components. This sequence encodes a novel human musculoskeletal system
CC antigen. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC ftp.segdata.uspo.gov/sequence.html?DocID=20020147140
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SQ Sequence 7739 BP; 1963 A; 1731 C; 1890 G; 2155 T; 0 U; 0 Other;
Query Match 9.24; Score 146.8; DB 8; Length 7739;
Best Local Similarity 77.54; Pred. No. 2.4e-21;
Matches 217; Conservative 0; Mismatches 57; Indels 6; Gaps 3;
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QY 121 GCTTAGTGGCTCATCCCTGGTGTCCAGACTACTAGGAGGACAGATGAGA---CTGCT 176
DB 5511 GTGTAGTGACACATACCTGTGTGTCGAGCTAGTTGGAGAGCCAGGACGATCGCTT 5452
QY 177 TGTCCAGAGAGTCAAGACTGCACTGAGTGAAGCCAGCCACTGATTCAGAGCTGG 236
DB 5451 GAGCCAGAGAGTCAAGAGTCAAGTGAAGTGAATCTTGCA-CTGACATCCAGAGCTGG 5393
QY 237 CAACAAAAGAGACCTGTCTCAAAAAATTAATTA 276

DB 5392 CAACAGACTGAGACCTGTCTCAAAAAACAAAAACAAAA 5353
RESULT 13
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ID ADJ30562 standard; DNA: 7739 BP.
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XX ADJ30562;
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XX 20-MAY-2004 (first entry)
XX
XX Human musculoskeletal system-associated genomic DNA - SEQ ID 3189.
XX
XX musculoskeletal system; cytosolic; osteopathic; cancer; osteoporosis;
KW gene therapy; vaccine; human; ds.
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XX Homo sapiens.
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XX US2004009488-A1.
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XX 15-JAN-2004.
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XX 13-SEP-2002; 2002US-00242515.
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XX 31-JAN-2000; 2000US-0179065P.
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XX 04-FEB-2000; 2000US-0180628P.
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PR 12-SEP-2000; 2000US-0231968P.
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PR 17-NOV-2000; 2000US-0249207P.
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PR 17-NOV-2000; 2000US-0249300P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764877.

XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Barash SC;
PI
XX WPI; 2004-090458/09.
XX
PT New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g., cancer of
PT musculoskeletal tissues or osteoporosis.
XX
PS Disclosure; SEQ ID NO 3189; 289pp; English.
XX
CC The invention relates to a novel isolated musculoskeletal system-
CC associated nucleic acid molecule. The nucleic acid of the invention
CC demonstrates cytoskeletal and osteopathic activities and may be useful for
CC preparing a medicament for preventing, treating or ameliorating a medical
CC condition such as cancer of the musculoskeletal tissues or osteoporosis,
CC possibly via gene therapy or vaccine production. The current sequence is
CC that of the human musculoskeletal system-associated genomic DNA of the
CC invention. The current sequence is not shown within the specification per
CC se but is available on the USPTO web-site
CC http://seqdata.uspto.gov/sequence.html?DocID=20040009488.
XX
SQ Sequence 7739 BP; 1963 A; 1731 C; 1890 G; 2155 T; 0 U; 0 Other;
Query Match 9.2%; Score 146.8; DB 12; Length 7739;
Best Local Similarity 77.5%; Pred. No. 2.4e-21;
Matches 217; Conservative 0; Mismatches 57; Indels 6; Gaps 3;

QY 2 CCTGTATTTCAGTACTGTAGAGTCCGAGCTAGAGGACTGCTTAGCGCCAGAGTTCA 61
DB 5631 CCTATATCCCAACACTTGGAGGCCGAGGTGGAGATGCTTGATCCAGTAGTTCA
QY 62 AGAGCAGCCTGAGCAACACAGGAGGA-CCTGTCACTCAAGAATAATAATTAGCCAG 120
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QY 121 GCTTAGTGCTCATCCCTGTGTGCCAGTACTAGGAGGCAGAAAGTAGGA---CTGCT 176
DB 5511 GTGTAAGTGCAATACCTGTGTGCCAGTAGTTGGAGGCCAGGACGAGAGATCCCTT 5452
QY 177 TGTCCAGAGAGTCAAGACTGCAAGTGAAGTCAACCAAGCACTGATTCAGCCCTGG 236
DB 5451 GAGCCAGAGAGTCAAGAGCTGCAATGATGCAATCTTGCA-CTGCATCCAGCCCTGG 5393
QY 237 CAACAAAAAGAGACCTGTCTCAAAAAATAATTAATAATA 276
DB 5392 CAACAGACTGAGACCTGTCTCAAAAAACAAAAACAAAA 5353

RESULT 14
AAD58279
ID AAD58279 standard; DNA; 226475 BP.
XX AAD58279;
AC
XX 20-NOV-2003 (first entry)
DT
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Tue Jun 6 12:04:07 2006

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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(Without alignments)
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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	303	18.9	314	1	AA903751 064605.8
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4	146.8	9.2	1033	3	BM556801 AGENCOURT
5	146.4	9.1	315	1	AI961957 wt4094.x
6	146.4	9.1	592	4	BX486310 DKFZP686B
7	145.2	9.1	554	11	AO784105 HS 3250.A
8	143.8	9.0	675	11	AO313572 RRC11-10
9	143.6	9.0	444	11	AQ088791 HS 3002.A
10	143.6	9.0	721	8	CR773238 DKFZP470D
11	143.4	8.9	417	11	AQ215619 HS 3217.B
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13	143.4	8.9	551	4	BX487140 DKFZP686G
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15	142.6	8.9	746	14	AG014790 Homo sapi
16	142	8.9	916	8	CR980253 CR980253
17	141.8	8.8	444	7	BE349022 ht48a11.x
18	141.8	8.8	641	3	BM555373 AGENCOURT
19	141.8	8.8	809	12	BZ603262 WHAARF45TF

C 20	141.8	8.8	1792	6	CR602256	CR602256 full-length
C 21	141.8	8.8	1941	6	CR616604	CR616604 full-length
C 22	141.4	8.8	751	12	BZ606730	BZ606730 WHAARF11TR
C 23	141.2	8.8	483	10	W45205	W45205 zc24f10.x1
C 24	141.2	8.8	558	11	AQ480483	AQ480483 RBC1-11-2
C 25	141	8.8	408	7	BE138484	BE138484 xr75h02.x
C 26	141	8.8	749	14	AG014791	AG014791 Homo sapi
C 27	141	8.8	1295	2	BG432839	BG432839 602496047
C 28	140.8	8.8	374	4	BX954311	BX954311 DKFZP781A
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C 31	140.6	8.8	400	11	AQ007744	AQ007744 CTT-HSP-2
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C 33	140.2	8.7	647	7	BB883545	BB883545 BB883545
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C 37	139.8	8.7	606	13	CZ458897	CZ458897 MCF75111
C 38	139.8	8.7	705	14	AG013775	AG013775 Homo sapi
C 39	139.8	8.7	723	14	DX360777	DX360777 MGO.CH25
C 40	139.6	8.7	547	9	DA315473	DA315473 DA315473
C 41	139.6	8.7	821	13	CZ449889	CZ449889 MCF730G23
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C 44	139.2	8.7	510	7	AW949355	AW949355 EST361425
C 45	139.2	8.7	556	3	BU664577	BU664577 cl11b11.

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
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NIH-MGC <http://mgc.nci.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
DNA Sequencing by: Incyte Genomics, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM10737 row: O column: 03
High quality sequence stop: 666.
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/db_xref="taxon:9606"
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/clone_lib="NIH MGC 97"
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(gcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTNN-3', size-selected for average
insert size 2.2 kb and normalized to ROP 5. This is a

FEATURES

source

ORIGIN

primary library enriched for full-length clones and constructed using the Cap-trapper method (Carroll, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC library."

Query Match 37.0%; Score 593.2; DB 2; Length 941;
Best Local Similarity 95.3%; Pred. No. 1.5e-94;
Matches 667; Conservative 0; Mismatches 23; Indels 10; Gaps 5;

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643 AGCTCAGCCGCAAAAGTAGAGAACTGCGAGAGGAGACTCAGAGTCCCAAAAAAAT 584
629 TATC---TTTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 684
583 TATCAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAG 524
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523 TCTTCT 464
741 TGGCAGATCT 800
463 TGGCAGATCT 404
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403 GCCAGAGCAATGCGCTCGCGGTCTTTCTTTCCGCTATAA-TTATCAGAGCCATCC 344
860 GCTCTGTCCT 919
343 GCTCTGTCCT 284
920 CCGGCTGACCAAGGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 979
283 CCGGCTGACCAAGGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 224
980 TCCGTTCT 1039
223 TCCGTTCT 164
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103 GACGGGTGACCAATTAAGAGCAACAGGCGCGGTCTCTGAGCGCTTTTTCAT 44
1160 CCCAGGCTGAGACAGGAGCTGAGCGCTGAGCGCGCTCTGCG 1199
43 CCCAGGCTGAGACAGGAGCTGAGCGCTGAGCGCGCTCTGCG 4

RESULT 2
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LOCUS OK64605.n1 NCI CGAP GC4 Homo sapiens cDNA IMAGE:1518728 3'
DEFINITION similar to gb:K17360_rnal HOMEDBOX PROTEIN HOX-D4 (HUMAN);, mRNA
sequence.

ACCESSION AA903751 GI:3038874
VERSION AA903751.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE
AUTHORS 1 (bases 1 to 314)
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Found distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINt at:
www.bio.lnlnl.gov/bdrp/image/image.html
Insert length: 521 Std Error: 0.00
Seq primer: -40ml3 fwd. RT from Amerisham
High quality sequence stop: 297.
Location/Qualifiers
1. 314
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1518728"
/feature_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC4"
/note="Vector: pTZ19-Pac1; 1st strand cDNA was prepared
from 3 pooled germ cell tumors, and was then primed with a
Not I - oligo (dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pTZ19 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

FEATURES

source

ORIGIN

Query Match 18.9%; Score 303; DB 1; Length 314;
Best Local Similarity 99.7%; Pred. No. 3.1e-43;
Matches 314; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

653 TTCTTTCTTCT 712
1 TTCTTTCTTCT 60
713 TTCTTTCTTCT 772
61 TTCTTTCTTCT 120
773 CTTGACTTCTGTTTTCAGGCTCTTCTGCGAGGACCAAGGCTCGAGGTTTCTTT 832
121 CTTGACTTCTGTTTTCAGGCTCTTCTGCGAGGACCAAGGCTCGAGGTTTCTTT 180
833 CCGCTATATTAATTCAGGCGCCATCCAGAGCTGTCCTCCCTCACTGTTCCCTG 892
181 CCGCTATATTAATTCAGGCGCCATCCAGAGCTGTCCTCCCTCACTGTTCCCTG 240
893 CTTCTGCTGTTGAAACACATATAGCGCGCGCTGACAGAGGTGAATGTAATATC 952
241 CTTCTGCTGTTGAAACACATATAGCGCGCG CTGACAGAGGTGAATGTAATATC 299

Db 953 AGGAAGATGACTGAA 967
Db 300 AGGAAGATGACTGAA 314

RESULT 3
CZ458737 836 bp DNA linear GSS 20-OCT-2005
LOCUS MCF746K19TF Human MCF7 breast cancer cell line library (MCF7.1)
DEFINITION Homo sapiens genomic clone MCF7_46K19, genomic survey sequence.
ACCESSION CZ458737 GI:77936089
VERSION CZ458737.1

KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 836)
Volk,S.V., Raphael,B.J., Huang,G.-Q., Murnane,J., Brehner,J.H., Bajarcowicz,K., Paris,P., Tao,Q., Kowal,D., Lapuk,A.V., Kuo,W.-L., Shagin,D.A., Shagina,I.A., Magrane,G., Gray,J.W., Jan,F.-C., de Jong,P., Pezner,P. and Collins,C.
Decoding the genomic architecture and high throughput detection of fusion transcripts in breast cancer cell lines: implications for a tumor genome project
Unpublished (2005)
JOURNAL
COMMENT UCSF Comprehensive Cancer Center
Colin Collins' lab
Contact: Volk SV
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7066
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
http://www.genomex.com
Classes: BAC ends.

FEATURES
source
Location/Qualifiers
1..836
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="MCF7_46K19"
/sex="female"
/clone_1ib="Human MCF7 breast cancer cell line library (MCF7_1)"
/note="Vector: pECRAC1; Site_1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."

ORIGIN

Query Match 9.4%; Score 150.8; DB 13; Length 836;
Best Local Similarity 73.7%; Pred. No. 2e-16;
Matches 233; Conservative 0; Mismatches 77; Indels 6; Gaps 3;

QY 1 ACCGTGAATTCAGTCTGTGAGAGTCCGAGTCAAGAGACTGTTGAGGCGAGAGTTC 60
DB 158 ACTGTAAATCCAGCACTTTGGAGGCTGAGGAGAGATCCCTTGAGTCCAGAGATT 217
QY 61 AAGAGAGCCTGTGACACACAGGAGA-CCTGTCACTACAAAGATTAATTAATGACCA 119
DB 218 GAGACAGCCTGGTCAACATAGGAGACCTGTCTCTAGAGTAATTTAAATTTAGCTG 277
QY 120 GGCTTAGTGGCTATCCCTGTGTGCTCCAGTACTAGGAGGAGGAAGTAGGA---CTGC 175
DB 278 GGCTGTGTGTGACACCTGTGTCTCCAGTACTTGGAGGCTGAAGCAGAGAAATCAT 337
QY 176 TTGTCCAGAGAGTCAAGACTGAGTGAAGCCAGCCAGCTGCATTCAGAGCTGG 235
DB 338 TGAACCAAGAGGTTAAGGCTGAGTGAAGCGGAGATTGGCCCA-CTACACTCCAGCTGG 396
QY 236 GCAACAAAAAGAGACCTGTCTCAAAAAAATAGTTAAATTAATTAATTAATTAATGTT 295
DB 397 GTGACAGAGTGAAGAACCTGTCTCAAAAAAAGAAAAAGTAATTAATTAATTAATTAAGT 456
QY 296 TAAACCTTAACCAT 311
DB 457 CAATCTCTTAATTCAT 472

RESULT 4
BMS56801/c 1033 bp mRNA linear EST 20-FEB-2002
LOCUS
DEFINITION AGNCOURT_6540722 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737964

ACCESSION 5', mRNA sequence.
VERSION BMS56801 GI:18798321
KEYWORDS BMS56801.1
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1033)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.jnl.gov
plate: L1AM12748 row: 0 column: 21
High quality sequence, scop: 606.

FEATURES
source
Location/Qualifiers
1..1033
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5737964"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 9.2%; Score 146.8; DB 3; Length 1033;
Best Local Similarity 77.5%; Pred. No. 9.7e-16;
Matches 217; Conservative 0; Mismatches 57; Indels 6; Gaps 3;

QY 2 CCTGTAAATCCAGTACTGTGAGAGTCCGAGTCAAGAGACTGTTGAGGCGAGAGTTC 61
DB 316 CTTATTAATCCACACTTTTGGAGGCTGAGGAGAGATGCTTGAATCACTAGTTCA 257
QY 62 AGAGCAGCCTGTGACACACAGGAGA-CCTGTCACTACAAAGATTAATTAATGACCA 120
DB 256 AGACAGCCTGGGCAACATAGGAGACCTGACTTACAAATTAATTTAAATTTAGCTGG 197
QY 121 GCTTAGTGGCTATCCCTGTGTGCTCCAGTACTAGGAGGAGGAAGTAGGA---CTGCT 176
DB 196 GTGTAGTGCACATACCTGTGTGCTCCAGTACTAGTTGGAGGCTCAGAGAGAGATCGCTT 137
QY 177 TTGTCCAGAGAGTCAAGACTGAGTGAAGCCAGCCAGCTGCATTCAGAGCTGG 236
DB 136 GAGCCAGAGAGTCAAGGCTGCAATAGCTGCAATCTTGCCA-CTGCATCTCAGCTGG 78
QY 237 CAACAAAAAGAGACCTGTCTCAAAAAAATAGTTAAATTA 276
DB 77 CAACAGACCGAGACCTGTCTCAAAAAACAAAAACAAAA 38

RESULT 5
A1961957/c 315 bp mRNA linear EST 09-MAR-2000
LOCUS
DEFINITION wt40904.x1 NCI CGAP Paul Homo sapiens cDNA clone IMAGE:2509974 3'
similar to contains Alu repetitive element;; mRNA sequence.
ACCESSION A1961957
VERSION A1961957.1 GI:5754659
KEYWORDS EST.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE AUTHORS	1 (bases 1 to 315) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Life Technologies catalog #: 11548-013 DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.lnl.gov/bbrp/image/image.html Insert length: 1397 Std Error: 0.00 Seq primer: -40UP from G10bo High quality sequence atp: 314.
FEATURES	Location/Qualifiers
source	1..315

Query Match	9.1%;	Score 146.4;	DB 1;	Length 315;
Best Local Similarity	74.6%;	Pred. No. 1.4e-15;		
Matches 212;	Conservative	0;	Mismatches 66;	Indels 6;
				Gaps 2;

OY	2	CCTGTAATTCAGATCTGTGAGAGTCCAGATCAGAGGACTGTTGAGCCAGAGATTCA	61
Db	284	CCTGTAATCCCATCTCACTTTGGAGAGCCAGAGCAGAAAGATTGCTTGAATCCAGAGATTGG	225
OY	62	AGAGCAGCCTTGACAAACACAGGAGAC--TGTCACTACAAAGATTAATTAATTAGCC	118
Db	224	AGACTAGGCTGTGGCAACATAGTAGAACCTCATCTCTACAAAAAATGAAACAAATTAGCC	165
OY	119	AGGCTTAGTGCGTCATCCCTGTGGTCCAGACTACTAGGAGAGCAAGAT--AGAGCTGC	175
Db	164	GGGCTGTGGTGTGCAATGCTGTAGTCCAGACTACTAGGAGAGCTGAGTGGAGAGATTGC	105
OY	176	TTGTCCACAGAGGTCAAGACTGACGTAGAGTGAAGCCAGCCACTGATTTCCAGCTGG	235
Db	104	TGACCTCGGTGTCAAGCTGCACTGAGCTGAGATCATGTGCCAATCTGCATCCAGCTTAA	45
OY	236	GCAACAAAAAGAGCCGTCTCCAAAAAATTAATTAAATA	279
Db	44	GGCACAGACCAAGACCTGTCTCAAAAAAATTAATTAATTAATA	1

RESULT 6	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
BX486310/c	592 bp mRNA	linear	EST 04-SEP-2003				
BX486310	DKEP686B08251_r1 686 (synonym: h1c3)	Homio sapiens	CDNA clone				
	DKEP686B08251_5', mRNA sequence.						
BX486310							
BX486310.1	GI:31949871						
EST.							
Homio sapiens (human)							
Homio sapiens							
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;							
Homioidae; Homio.							

TITLE	REFERENCE
JOURNAL	AUTHORS
COMMENT	
1 (bases 1 to 592)	Anorgew. M., Krieger, S., Regier, T., Rittmüller, C., Schwager, B., Mewes, H. W., Weill, B., Amdt, C., Osang, A., Fobo, G., Han, M. and Wieman, S.
EST (Anorgew. M., Krieger, S., Regier, T., Rittmüller, C., et al.)	
Unpublished (2003)	
Contact: MIPS	

FEATURES

SOURCE

```

/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="DKFZP568B08251"
/dev_stage="adult"
/lab_host="DH10B"
/clone_idb="686 (synonym: hlec3)"
/notes="vector: pTriplex2; Site_1: SfiI; Site_2: SfiIB
             cna-collection"

```

ORIGIN

Query Match	9.1%	Score 146.4;	DB 4	Length 592;
Best Local Similarity	74.3%	Pred. No. 1.2e-15;		
Matches 211; Conservative	0;	Mismatches 71;	Indels 2;	Gaps 2;

OY	I	AACCTGTAATTCAGTACTGTGAAGAGTCCGAGCTCAGAGCACTGGCTGAGGCCAAGAGTTTC	60
Db	287	ACCCTGTAATCCAGACACTTTGGAGGCTCGAGGCAGGTGATCATCTTGAGTCCAGGAGTTTC	228
OY	61	AAGAGCACCTCGACAACACACAGGAGACCT- GTCACTACAAAGAATAAATAATTAGCCA	119
Db	227	GAGACACAGCCTGGGCAACATAGTAGCACCTCATCTCTCAAAAAATAACAAAATTAGCCA	168
OY	120	GGCTTAGAGGTACTCCCTGTGGTCCACGACTACTAGAGGAGGACAGAAAGTAGAGACTGTCTGT	179
Db	167	GCTGTGGTGGGCACAGCCTGTGATGTTCTTAGCTACTCTCGGAGACTCAGGTGTGATCACTTGAG	108
OY	180	CCCAGAGAGTCAAGACTGTCACTGAGCTGAGACCCAGACCACTGTCACTTCAGCTTGGGCATA	239
Db	107	CCCCGGAGAGAGAGGTTCACAGTGAAGCTAGATCTGATCCACA - CTGCACTCCAGCCTGGCCAA	49
OY	240	CAAAAAGAGACCTGTCTCAAAAAAATAAGTTAAATTAATTAATA	283
Db	48	CAGAGTAGACCTGTCTTCABAGAAAAAAAAAAAAAAAAAAAAACA	5

RESULT 7	
AQ784105	
LOCUS	AQ784105 554 bp DNA linear GSS 03-AUG-1999
DEFINITION	HS_3250_A2_H10_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3250 Col=20 Row=O, genomic survey sequence.
ACCESSION	AQ784105
VERSION	AQ784105.1 GI:5691729
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Chordata; Craniota; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 554)
AUTHORS	Mahaitas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

REFERENCE 1 (bases 1 to 444)
AUTHORS Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GQ, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3002 row: K column: 9
Class: BAC ends
High quality sequence stop: 444.
Location/Qualifiers
1..444
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3002 Col=9 Row=K"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

ORIGIN
Query Match 9.0%; Score 143.6; DB 11; Length 444;
Best Local Similarity 70.3%; Pred. No. 4.1e-15;
Matches 222; Conservative 0; Mismatches 89; Indels 5; Gaps 2;
QY 3 CTGTAAATCCAGTACTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGCCAGAGATTCAA 62
DB 335 CTGTAAATCCAGACTTTTGAGAGGCTGAGCGGGTGGATCTCTGAGCTCAGAGATTCAA 276
QY 63 GAGACAGCTGGAGCAACAGGGAGAGCTGTCACTACAAAGATTAAATTAGCCAGGC 122
DB 275 GACTTACCTGGCTTAACATGTGTGAACCTGTCTACTAAATAATCAAAAATTAGCCAGGC 216
QY 123 TTAGTGGCTCATCCCTGTGTGCTCCAGTACTAGGAGGAGCAAGTAGA----CTGCTTG 178
DB 215 GTGTGGACATATCCCTGTATCCAGTCTTGGAGAGCTGAGGAGAGATGCTTGA 156
QY 179 TCCAGAGAGTCAAGACTGAGTGAAGTGAACCCAGCCACTGCAATTCAGGCTTGAGCA 238
DB 155 GCTTGAAGAGTGAAGTTCAGAGGAGTGAATCGTGCCA-CTGCACTCCAGCTGGGCA 97
QY 239 ACGAAAAAGAGACCTGTCTCAAAAAATTAATTAAATTAATTAATTAATTAATTAATTA 258
DB 96 ACGAGCCGACACATGTTCAAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 37
QY 299 ACCCTAAACACATCTT 314
DB 36 GGCTGAGAAAGTCTGT 21

RESULT 10
CR773238 721 bp mRNA linear EST 23-SRP-2004
LOCUS DKFZp470D2113_r1 470 (synonym: pliv1) Pongo pygmaeus cDNA clone
DEFINITION DKFZp470D2113_5, mRNA sequence.
ACCESSION CR773238
VERSION CR773238.1 GI:52616511
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 721)
AUTHORS Ottenwaelder,B., Obermaier,B., Deutschenbauer,S., Schallp,A., Mewes,H.W., Weill,B., Amid,C., Oeanger,A., Fobo,G., Han,M. and Wiemann,S.
TITLE Pongo pygmaeus mRNA (Ottenwaelder,B., Obermaier,B., Deutschenbauer,S., et al.)
JOURNAL Unpublished (2004)
PUBMED
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de, sequenced by Medigenomix (Martinried/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp470D2113) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneId=DKFZp470D2113
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

ORIGIN
Query Match 9.0%; Score 143.6; DB 8; Length 721;
Best Local Similarity 71.9%; Pred. No. 3.8e-15;
Matches 230; Conservative 0; Mismatches 84; Indels 6; Gaps 3;
QY 2 CCTGTAAATCCAGTACTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGCCAGAGTTCA 61
DB 95 CTGTAAATCCAGACTTTTGAGAGGCGCAAGGAGTGAATCACTGAGGTCAAGAGTTCA 154
QY 62 AGAGCAGCTGGAGCAACAGGGAGA-CCTGTACTTCAAAAGATTAAATTAGCCAG 120
DB 155 AGAGTACCTGGGCAACATGTGAGAGCCGTCTCTTAAATAATCAAAAATTAGCCAG 214
QY 121 GCTTATGGGTCTATCCCTGTGTGCTCCAGTACTAGGAGGAGCAAGTAGA----CTGCT 176
DB 215 GCATGTGGGTGCTACCTGTAGTCCAGTACTTGGAGGCTGAGGAGAGATCACTT 274
QY 177 TGTCCAGAGAGTCAAGACTGAGTGAAGTGAACCCAGCCACTGCAATTCAGGCTTGAG 236
DB 275 AAACCGGGGGGGCGAGAGTGGCAATGAGCTGAGACTCCGCCA-CTGCACTGAGGCTGAG 333
QY 237 CAACAAAAAGAGACCTGTCTCAAAAAATTAATTAAATTAATTAATTAATTAATTAATTA 256
DB 334 CAACAGAGTGAAGTCAAGTCTCAAAAAAATTAATTAATTAATTAATTAATTAATTA 393
QY 297 AAACCTAAACACATCTCT 316
DB 394 AAGATATTAAATTTT 413

RESULT 11
AQ215619/c 417 bp DNA linear GSS 19-SRP-1998
LOCUS AQ215619
DEFINITION HS_3217_B2_A01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3217 Col=2 Row=B, genomic survey
ACCESSION AQ215619
VERSION AQ215619
KEYWORDS GSS.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 417)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3217 row: B column: 2
Class: BAC ends
High quality sequence stop: 417.
FEATURES
source
1. .417
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3217 Col=2 Row=B"
/sex="male"
/clone_1ib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: Sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"

ORIGIN
Query Match 8.9%; Score 143.4; DB 11; Length 417;
Best Local Similarity 74.0%; Pred. No. 4.5e-15;
Matches 208; Conservative 0; Mismatches 71; Indels 2; Gaps 2;
QY 2 CCTGTATTCCAGTACTGTGAGAGTCCGAGTCAAGAGACTGCTTGAGCCAGAGTTCA 61
DB 413 CCTATATCCAGTACTGTGAGTGAAGCGGGATCACTTAGGTCAGAGATTGC 354
QY 62 AGAGCAGCTGGAACAACAAGGAGACT-GTCACTCAAGAATAAATAATTAGCCAG 120
DB 353 AGACCACTGACTGAACATGCTGAACCTCACTCTTAATAAATTCAAACTTACACAG 294
QY 121 GCTTAGTGGTCACTCCCTGTGCTCCAGCTACTAGGAGGAGAGAGTGAAGCTGCTGTC 180
DB 293 GTGTGGTGGCAATGCTGTAGTCCAGCTGCTTGGAGAGTGAAGCAATAGCTTGA 234
QY 181 CCAAGAGGTCAAGACTGAGTGAAGTGAACCAAGCACTGCACTTCAAGCTGGGCAAC 240
DB 233 CCGGGGGGCAAGGCTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 175
QY 241 AAAAAGAGACCTGCTCAAAAAAATAAGTTAAATAATAA 281
DB 174 AGAAGAGACTGTCTCAAAAAAATAAAAAA 134

RESULT 12
DB322788/c 454 bp mRNA linear EST 04-DEC-2005
LOCUS DB322788 NT2NE2 Homo sapiens cDNA clone NT2NE2000864 3', mRNA
DEFINITION sequence.
ACCESSION DB322788
VERSION DB322788.1 GI:83261293
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 454)
Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Tsutitani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kusida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Magatsuna,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isoga,T. and Sugano,S.
TITLE Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
JOURNAL Genome Res. 16 (1), 55-65 (2006)
PUBMED 16344560
COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
FEATURES
source
1. .454
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/mol_type="mRNA"
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/clone="NT2NE2000864"
/cell_type="leukocarcinoma"
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/clone_1ib="NT2NE2"
/note="Vector: pME18SF3; mRNA from NT2 neuron after the
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Best Local Similarity 73.4%; Pred. No. 4.4e-15;
Matches 212; Conservative 0; Mismatches 71; Indels 6; Gaps 2;
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DB 293 CTTGTAGTCCACAGACTTTGGAGGCGGAGTGGCGGATCGCTGAGTCAGAGATTGC 234
QY 62 AGAGCAGCTGGAACAACAAGGAGACT-GTGTCTCAAGAATAAATAATTAGCCAG 120
DB 233 AGAGCAGCTGGAACAACAAGGAGACTGCTGTCTTAATAAATAATTAGCCAG 174
QY 121 GCTTAGTGGTCACTCCCTGTGCTCCAGCTACTAGGAGGAGCAAGTAGGA-----CTGC 175
DB 173 GCATGGTGGGCAAGCTGTGTTTCACTGCTGAGGAGTGAAGCAAAATTGCT 114
QY 176 TTGTCCAGAGGTCAAGACTGAGTGAAGCCCAAGCACTGCACTTCCAGCTGG 235
DB 113 TAGAGCTGGAGGTGAGCTGAGTGGGCAAGATGTATCCCACTGCACTGACCTGG 54
QY 236 GCAACAAAAGAGACCTGTCTCAAAAAAATAAGTTAAATAATAATAA 284
DB 53 GCAACAGAGCAAGACTGTCTCAAAAAAATAAAAAA 5

RESULT 13
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LOCUS BX487140 DKEP686G22255.r1 686 (synonym: h1cc3) Homo sapiens cDNA clone
DEFINITION DKFZP686G22255 5', mRNA sequence.
ACCESSION BX487140
VERSION BX487140.1 GI:31951470
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 551)
 Bahr, A., Lauber, J., Mewes, H.W., Well, B., Amid, C., Oeanger, A., Fodor, G., Han, M., and Wiemann, S. (2003) EST (Bahr, A., Lauber, J., Mewes, H.W., Well, B., et al.) Unpublished (2003)
 CONTACT: MIPS
 MIPs

Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert.
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Small S. Wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
 No 3' sequence available.
 This clone (DKFZ66632255) is available at the RZPD in Berlin. Please contact the RZPD: Resourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 Location/Qualifiers

FEATURES
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 1..551
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 /clone="DKFZ66632255"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_11b="686 (synonym: hlc33)"
 /note="Vector: pT7-18x2; Site_1: SfilA; Site_2: SfilB; cDNA-collection"

ORIGIN

Query Match 8.9%; Score 143.4; DB 4; Length 551;
 Best Local Similarity 72.4%; Pred. No. 4.3e-15;
 Matches 228; Conservative 0; Mismatches 81; Indels 6; Gaps 3;
 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGAGCTGTTAGGCCAGAGTTC 60
 325 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGGTCAGAGTTCAGAGGAGCTC 266
 61 AAGAGCAGCTGAGAGAGAGAGAGAGAGCTGTCACATCAAAAGATTAATTAATTCACCA 119
 265 AAGAGCAGCTGAGAGAGAGAGAGAGAGCTGTCACATCAAAAGATTAATTAATTCACCA 206
 120 GGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 175
 205 GGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 146
 176 TTGTTCCAGAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAG 235
 145 TGAACCCAGAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAG 87
 236 GCAACAAAAGAGAGTGTGCTCAAAATAAATTAATTAATTAATTAATTAATTAATTAATTAAT 255
 86 GTAACAGAGAGAGAGTGTGCTCAAAATAAATTAATTAATTAATTAATTAATTAATTAATTA 27
 296 TAAACCTTAACACA 310
 26 GAAATAATAATAATA 12

RESULT 14
 BC029972 2821 bp mRNA linear HTC 28-JUL-2005
 LOCUS
 DEFINITION Homo sapiens clusterin (complement lysin inhibitor, SP-40, 40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J), mRNA (cDNA clone IMAGE:4939961).
 BC029972
 ACCESSION BC029972.1 GI:20455818
 VERSION
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 2821)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, K.H., Scheffer, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Mak, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L., Stappleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ueding, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullan, S.J., Bosak, S.A., McKernan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huylk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butler, A., Schein, J.E., Jones, S.J., Skalske, U., Small, D.E., Scherf, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Mammalian Gene Collection Program Team
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

CONSTRM
 TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 CONSTRM
 TITLE
 JOURNAL
 2 (bases 1 to 2821)

NIH MGC Project
 Direct Submission
 Submitted (06-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 CDNA Library Preparation: Life Technologies, Inc. (LNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
 Center code: BCM-HGSC
 Web site: http://www.hgsc.bcm.tmc.edu/cdna/
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Huylk, S.W., Louis, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
 Series: IRAC Plate: 42 Row: h Column: 7
 This clone has the following problem: no 5' EST match.
 Location/Qualifiers

FEATURES
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 /db_xref="taxon:9606"
 /clone="IMAGE:4939961"
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 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 8.9%; Score 142.8; DB 6; Length 2821;
 Best Local Similarity 71.4%; Pred. No. 4.2e-15;
 Matches 230; Conservative 0; Mismatches 87; Indels 5; Gaps 3;
 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGAGTCTGTTAGGCCAGAGTTC 61
 1686 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGAGTCTGTTAGGCCAGAGTTC 1745

QY 62 AGAGCAGCCTTGACAAACACAGGAGAG-CCTGTCACTACAAAGAAATTAATTAATGCTCAG 120
DB 1746 AGACCAAGCCTGGGCAACACAGCAAGATTCCCTCTCTCAAAAAAATACAAAAATCAGTCAG 1805
QY 121 GCTTAGTGGCTCATCCCTGTGGTCCGAGCTACTAGGAGGACAGAAAT---AGGACTGCTT 177
DB 1806 GTGTGTGGGACACACTGTGTAGTCCAGCTATTACAGAGGCTGAGGGAGGAGTTCCCT 1865
QY 178 GTCCAGAGAGGTCAAGAGCTGAGTGAAGACCCAGCCACTGCAATTCAGGCTGAGG 237
DB 1866 GAGCCCTGAAGTGAAGGCTGAGAGCTGATGATCAGCCCA-CTGCACTCAGGCTGGGT 1924
QY 238 AACAAAAAGAGACCTGTCTCAAAAAATTAAGTTAAATTAATTAATTAATTAATTAATTA 297
DB 1925 GACAGAGTGAAGCTGTCTCTTAAAAAATATATATATATATATATATATATATATATAT 1984
QY 298 AACCTTAACACATCTTCTTT 319
DB 1985 AAAAATCAATAATTAATTAATTT 2006

RESULT 15

AG014790

LOCUS AG014790 746 bp DNA linear GSS 16-FEB-2005

DEFINITION Homo sapiens genomic DNA, 21q region, clone: 762015N19, genomic

survey sequence.

ACCESSION AG014790 AG006505

VERSION AG014790.1 GI:3650008

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominiidae; Homo.

REFERENCE 1 Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Homo sapiens genomic DNA, chromosome 21q

Published Only in Database (1998)

2 (bases 1 to 746)

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Direct Submission

Submitted (23-SEP-1998) Masahira Hattori, RIKEN Genomic Sciences

Center, RIKEN Yokohama Institute, Yokohama Research Promotion

Division, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa,

230-0045, Japan (E-mail:hattori@gscl.riken.jp, Tel:01-45-503-9111,

Fax:01-45-503-9113)

On Feb 6, 1999 this sequence version replaced gi:2992383.

COMMENT AG006505: Submitted (27-Mar-1998).

Location/Qualifiers

1..746

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="21"

/map="21q"

/clone="762015N19"

ORIGIN

Query Match 8.9%; Score 142.6; DB 14; Length 746;

Best Local Similarity 73.8%; Pred. No. 5.6e-15;

Matches 220; Conservative 0; Mismatches 72; Indels 6; Gaps 3;

QY 2 CCTGTATTCCAGTACTGTGAGAGTCCGAGGTCCAGAGACTGCTTGAGGCCAGAGTTCA 61
DB 44 CCTGTATTCCAGACTTTTGGAGGTGAGGACGCAAAATGGCTTGAGGCCAGAGTTG 103
QY 62 AGAGCAGCCTTGACAAACACAGGAGAG-CCTGTCACTACAAAGAAATTAATTAATTAATTAATTA 120
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QY 121 GCTTAGTGGCTCATCCCTGTGGTCCGAGCTACTAGGAGGACAGAAATGAGACTGCTTGT- 179
DB 164 GCATTAATGGAATGCTGTAGTCTCAGCTACTGGGAGGCTGAGGTGGAGGCTTCTT 223

QY 180 ---CCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCCAGCTGCAATTCAGCCTGGG 236
DB 224 GAGCCAGAGAGGCCAAGGCTGAGTGAAGTGAAGTCAAGCCA-CTGTACTCAGCCTGGG 282
QY 237 CAACAAAAAGAGACCTGTCTCAAAAAATTAAGTTAAATTAATTAATTAATTAATTAATTA 294
DB 283 TGACAGAGCCAGACCTGTCTCAAAAAAANGTAAATTAATTAATTAATTAATTAATTAATTA 340

Search completed: June 6, 2006, 00:08:54
Job time : 11104.1 secs

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[illegible]

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Db	1403	CCGTGTGTGCAGTTCTCATTTGTTCTTCCCCCGAACACGGGGGGCTGTAAACCAATGG	1462
Qy	1441	AACGAGAGCCGGGTGGGAGAGGCCAGTCCCAGCCTTGACGAGACCAGCCGCGCTCGCT	1500
Db	1463	AACGAGAGCCGGGTGGGAGAGGCCAGTCCCAGCCTTGACGAGACCAGCCGCGCTCGCT	1522
Qy	1501	CGCAGAGAGGTGTGGTAGTTTGGCCACGCTAGGGGGGCTGGGCCAATAAAGAAGAAATGC	1560
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Qy	1561	ACTTAAGACACGGCCCCGCTGGACGCTTGTAAACACGCTCT 1603	
Db	1583	ACTTAAGACACGGCCCCGCTGGACGCTTGTAAACACGCTCT 1624	
 RESULT 2 US-09-949-016-14689 ; Sequence 14689, Application US/09949016 ; Patent No. 6812339 ; GENERAL INFORMATION: ; APPLICANT: VENTER, J. Craig et al. ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF ; FILE REFERENCE: C1001307 ; CURRENT APPLICATION NUMBER: US/09/949,016 ; CURRENT FILING DATE: 2000-04-14 ; PRIOR APPLICATION NUMBER: 60/241,755 ; PRIOR FILING DATE: 2000-10-20 ; PRIOR APPLICATION NUMBER: 60/237,768 ; PRIOR FILING DATE: 2000-10-03 ; PRIOR APPLICATION NUMBER: 60/231,498 ; PRIOR FILING DATE: 2000-09-08 ; NUMBER OF SEQ ID NOS: 207012 ; SOFTWARE: FASTSEQ For Windows Version 4.0 ; SEQ ID NO 14689 ; LENGTH: 39754 ; TYPE: DNA ; ORGANISM: Human ; FEATURE: ; NAME/KEY: misc_feature ; LOCATION: (1)...(39754) ; OTHER INFORMATION: n = A,T,C or G US-09-949-016-14689			
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Qy	1	ACCTGTAATTCACAGTACTGTGAGTCCGAGGTCAGAGAGCTGCTTGAAGGCCAGAGTTC	60
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Qy	61	AAGACAGCCTGGACAACAACAGGAGACCTGTCACTACAAGAATTAATTAATTAGCCAG	120
Db	27998	AAGACAGCCTGGACAACAATAGGAGACCTGTCACTACAAGAATTAATTAATTAGCCAG	28057
Qy	121	GCTTAGTGGCTATCCCTGTGTGCTCCAGTACTTAGGAGAGCCAGAACTAGGACTGTTTGC	180
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Qy	181	CCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCCACTGATTCAGAGCTGGGCAAC	240
Db	28118	CCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCCACTGATTCAGAGCTGGGCAAC	28177
Qy	241	AAAAAGAACCCCTGTCTCAAAAATAAGTTAATTAATTAATTAATTAATTAATTAATTAAC	300
Db	28178	AAAAAGAACCCCTGTCTCAAAAATAAGTTAATTAATTAATTAATTAATTAATTAATTAAC	28237
Qy	301	CCTAAGACATCTCTTTTCAAAGAGACTTCTTAAGAGCTTCAAGAGCTTCAAGCTGCGTCTGTTG	360

Db 28238 CTTAAACACATCTTCTTTTCAAGAGACTTTCTTAAGACCTTCATCTGCTCTCTG 28297
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Db 28298 ATCTCCACTTCCCTTTTTCAGCGTCAACCTTTAAAGTCTCTTTTGCAGAGATATA 28357
QY 421 AGTATATAGTTTCTGAAATCCAGATCTTCTCCCTGTTTGAACAGCAGGAGCAATTTT 480
Db 28358 AGTATATAGTTTCTGAAATCCAGATCTTCTCCCTGTTTGAACAGCAGGAGCAATTTT 28417
QY 481 GGTCTGAGGCTTTGATCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 28418 GGTCTGAGGCTTTGATCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 28477
QY 541 AGCCTCTCCGGAATGACAGCAGCAGAGCTGAGCCGCAAAAGCTAGAGACCTGGGGA 600
Db 28478 AGCCTCTCCGGAATGACAGCAGCAGAGCTGAGCCGCAAAAGCTAGAGACCTGGGGA 28537
QY 601 GGGAGACTCAAGTGCACAAAAAACTTTATCTTTTCTTTTCTTTTCTTTTCTTTCT 660
Db 28538 GGGAGACTCAAGTGCACAAAAAACTTTATCTTTTCTTTTCTTTTCTTTTCTTTCT 28597
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Db 28598 TTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 28657
QY 721 TTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780
Db 28658 TTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 28717
QY 781 TCTGTTTCCAGCGTCTTCTGCGCAGACCAATGCGCTGGGCTGTTTCTTCCGCTATA 840
Db 28718 TCTGTTTCCAGCGTCTTCTGCGCAGACCAATGCGCTGGGCTGTTTCTTCCGCTATA 28777
QY 841 ATTATCCAGGCCCATCCAGCTCTGATCCCTCAGCTGTTCCCTGAGTCCCTTCTGCT 900
Db 28778 ATTATCCAGGCCCATCCAGCTCTGATCCCTCAGCTGTTCCCTGAGTCCCTTCTGCT 28837
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QY 1141 TCCGAGCGCTTTTCTATCCAGGCTGAGACAGGAGCTGAGCTGAGCCCGCTGAGC 1200
Db 29078 TCCGAGCGCTTTTCTATCCAGGCTGAGACAGGAGCTGAGCTGAGCCCGCTGAGC 29137
QY 1201 TTGTCACTGCGGAGCGGCGCTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
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QY 1261 GGGTGTCTCCGCGCGCGCGGAGCTTTAGTGTCTTGTCTTAAACGCAAGCGCTCC 1320
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Db 29258 ACCGAGGAGAGAGGCGGAAACCCAGCGAGGCGCAAGGCGTGTGTGTGTGTGTGTGTGT 29317
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Db 29318 CTTGTGCTCAGTTCTGATTTGTTCTTCTTCCCGCAACAGCGGCGCTGTAAACCAATCG 29377
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Db 29378 ACAGCAGGCGGCTGCGAGGCGCCAGTCCCGCTTGCAGAGGCGCAGCGCGCTGCT 29437
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Db 29438 CGCAGAGGCTGAGTATTGCCCCAGGCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 29497
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Db 29498 ACTTAAGACAGCGCGCGCTGAGCGC-TGTTAGAAACCGTCT 29539

RESULT 3

US-09-949-016-165996/c
; Sequence 165996, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 165996
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-165996

Query Match 9.6%; Score 153.4; DB 3; Length 601;
Best Local Similarity 68.8%; Pred. No. 4,4e-28;
Matches 225; Conservative 1; Mismatches 97; Indels 4; Gaps 1;

QY 2 CTTGTAATTCAGTAATCTGAGAGTCCGAGCTCAGAGAGCTGTTGAGCGCAGAGTTCA 61
Db 489 CTTGTAATTCAGTAATCTGAGAGTCCGAGCTCAGAGAGCTGTTGAGCGCAGAGTTTCG 430
QY 62 AGAGCAGCGCTGAGCAACACAGAGAGCTGTCTACTAACAAGATTAATTAATTAATTAATTA 121
Db 429 AGAGCAGCGCTGAGCAACACAGAGAGCTGTCTACTAACAAGATTAATTAATTAATTAATTA 370
QY 122 CTTAGTGTCTATCTCTGT 179
Db 369 CATGTGTGTGTCTCTGT 310
QY 180 -CCAGAGAGTGAAGACAGT 237
Db 309 AACCGAGGAGT 250
QY 238 AACCAAAAAGAGCCCTGTCTCAAAAAAATAGTTAATTAATTAATTAATTAATTAATTAATTA 297
Db 249 AACGAGT 190
QY 298 AACCTTAACACATCTTTTTCAAA 324
Db 189 AACCTGAAGT 163

RESULT 4
US-09-949-016-16419
; Sequence 16419, Application US/09949016
; Patent No. 6812339


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; SOFTWARE: FASTSQ for Windows Version 4.0.
; SEQ ID NO 17540
; LENGTH: 99370
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17540

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Query Match	9.2%	Score 147.2;	DB 3;	Length 99370;
Best Local Similarity	73.5%;	Pred. No. 1.3e-25;		
Matches 216;	Conservative 0;	Mismatches 73;	Indels 5;	Gaps 2;

OY	3	CTGTAATTCACAGTACTGTGAGAGTCGCAAGGTACAGAGGACTGTGTTGAGGCGAGAGATTCAA	62
Db	66673	CTGTATTTCCAAACACTTTGGAGGCCAAGGTGGCAGGATCACTAATAGTCCAGAGATTCAA	66732
OY	63	GAGCAGCCTTGAGCAACAACAGGAGAG-CTGTCACTACAAAGATTAATAATTATGGCAGG	121
Db	66733	GACAAAGCTTGACAAACAATGCGAAAACCTCTCTCTCAATAAATAATACAAAAATTATGGCAGG	66792
OY	122	CTTATGTGGCTATCCCTGTGGTCCCACTCTACTAGGGAGGAGAGTAGAG- ---CTGCTT	177
Db	66793	CATGTGGCTTATGCTCTGTGTGCCAAGTACTCAGAGAGGCTGAGAGTGGAGAGATCACTTG	66852
OY	178	GTCCCAAGAGGTCAAGACTGCAGTGAAGTGAAGCCAGCCACTGCATTTCCAGCTGGGC	237
Db	66853	AACCAGAGAACAGAGGTTGCAAGTGAAGTCAATGATCATGCCACTGCAGCTCTAGCCTGGGG	66912
OY	238	AAACAAAAAGAGACCTGTCTCAAAAAATAAGTTAAATTAATTAATTAATTAATAAT	291
Db	66913	AACGAGCAGAACCTCTGTCTCAAAAAATAAAAAAATAAATAAATAAATAAATAAATAAAT	66966

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Job time : 414.645 Secs

Search completed: June 5, 2006, 22:39:46
Job time : 414.645 Secs

Oy	771	GGCCCTGACCTTCGTGTTCCAGGCGCTCTGACAGAGACATGACGGTGGCGCTGTTTTCT	830
Db	121	TGCCTGACCTTCGTGTTCCAGGCGCTCTCTGCAAGACCATGCGCTCGG -GTGTTTTCT	179
Oy	831	TTCCGCTATTAATTATCCAGGCCCATCCAGCTTGCTGCTCCCTCAGCTGTTCCCTGGCAGT	890
Db	180	TTCCCGCTTAATTATTCACGAGGCCCATCCAGCTTGCTGCTCCCTCAGCTGTTCCCTGGCAGT	239
Oy	891	CCCTCTGCTGGTGA AAAACA CATATGAGGCGCGGCGCTGACAGGGGTGAAGTGA GTGATA	950
Db	240	CCCTCTGCTGGTGA AAAACA CATATGAGGCGCGGCGCTGACAGGGGTGAAGTGA GTGATA	299
Oy	951	TCAGGAAGATGACGTAGCAAGCTCTTTGGGACCTCGTTTCTCATTTGTAATGAGAGTTAT	1010
Db	300	TCAGGAAGATGACGTAGCAAGCTCTTTGGGACCTCGTTTCTCATTTGTAATGAGAGTTAT	359
Oy	1011	ACCAAGCTTTCTTCTACCTCCCAACAGCAGTGTTGTTGCTCCGGCCAGAGAGGCCCAATTGTT	1070
Db	360	ACCAAGCTTTCTTCTACCTCCCAACAGCAGTGTTGTTGCTCCGGCCAGAGAGGCCCAATTGTT	419
Oy	1071	GAGCTTTACGCGATAGTTAACCCCAACAGAGAGGGTTCAGCAATTAAAGCGAACCAGGC	1130
Db	420	GAGCTTTACGCGRTAGTTAACCCCAACAGAGAGGGTTCAGCAATTAAAGCGAACCAGGC	479
Oy	1131	CCGAGTCATCTTCTGACGCGCTTTTCTCATCCCAAGGCGTGAACAGGACCTGACCTGAGCC	1190
Db	480	CCGAGTCATCTTCTGACGCGCTTTTCTCATCCCAAGGCGTGAACAGGACCTGACCTGAGCC	539
Oy	1191	GAGGCTGAGCTGTGTCACGCGGG 1213	
Db	540	CAGGCTTGCTGTGTCACGCGGG 562	

```

RESULT 2
/ Sequence 566754, Application US/09925065A
/ Publication NO. US20050228172A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 566754
/ LENGTH: 562
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-566754

```

	Query Match	34.3%	Score 550.6;	DB 5,	Length 562;
	Best Local Similarity	99.6%;	Pred. No.7.1e-129;		
	Matches 561;	Conservative 1;	Mismatches 0;	Indels 1;	Gaps 1;
Oy	651 TTTCTTCTTCCTCCTTCCTTCGTGCTTCCTTCCTCCTCCTCCTTCCT	710			
Dd	1 TTTCTTCTTCCTCCTTCCTTCGTGCTTCCTTCCTCCTCCTCCTTCCT	60			
Oy	711 CTTTCTCTCTTCCTTCCTTTTTCTCAATGGCAAGATCTCTCATGGCAAAATATC	770			

Db	6	CTTCCGCTGCTTTCTTTCTTTTTCCTACAAATGGCAAGATCCTCCATGGCGAAATATAC	120
OY	771	TGCTTTGACTTTCTGTTTCCAGCGCTCTTTCGCCAGACCAATGGCTGGGGTGTTTTCT	830
Db	121	TGCCTTAACCTTCTGTTCACGCGCTCTTTCGCAAGAACAAAGCGCTGG-GTGTTTTCT	179
OY	831	TTCCGCTAATATTATCCAGGCCCATCCAGCTCTGTGACCCCTCAGCTTTCCCTGGCAGT	890
Db	180	TTCCGCTATATTATCCAGGCCCATCCAGCTCTGTGACCCCTCAGCTTTCCCTGGCAGT	239
OY	891	CCCTTCTGTGTGTAAAAACACATATGGCGCCGACTTGACCAAGGTTGAATGTGTGATA	950
Db	240	CCCTTCTGTGTGTAAAAACACATATGGCGCCGACTTGACCAAGGTTGAATGTGTGATA	299
OY	951	TCAGAGAAATGACTGAAAGCTTTGGGAGCTCCGTTTCTCATTTGTAAATGGAAGTTAAT	1010
Db	300	TCAGAGAAATGACTGAAAGCTTTGGGAGCTCCGTTTCTCATTTGTAAATGGAAGTTAAT	359
OY	1011	ACGAGCCTTCTTACTCCCCAAACGACGCTGTGTTCGCGCCAGAGGCGCCCAATTGTT	1070
Db	360	ACGAGCCTTCTTACTCCCCAAACGACGCTGTGTTCGCGCCAGAGGCGCCCAATTGTT	419
OY	1071	GGCTGTTCAGGCATCACTTAACCCCAAGGACGGGTGAGCCAAATTAAAGCGAACCAAGGC	1130
Db	420	GGCTGTTCAGGCATCACTTAACCCCAAGGACGGGTGAGCCAAATTAAAGCGAACCAAGGC	479
OY	1131	CCGGTCACTCTCTGAAGCCTTTTCTCATCCCAAGGCTGGAACAGGACAGCTGGAGCC	1190
Db	480	CCGGTCACTCTCTGAAGCCTTTTCTCATCCCAAGGCTGGAACAGGACAGCTGGAGCC	539
OY	1191	CGGCTTCGCTTGTCAAGTGGG	1213
Db	540	CGGCTTCGCTTGTCAAGTGGG	562

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RESULT 3
US-10-301-480-268288/c
; Sequence 268288, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OR INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 268288
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-268288

```

Query Match	33.6%	Score 538.6	DB 12	Length 561
Best Local Similarity	99.5%	Pred. No. 7.9e-126		
Matches	560	Conservative 1	Mismatches 0	Indels 2
			Gaps 2	
Qy	877	TGTTCCCTGGAGAGTCCCTTCTGTGCTGTGTAACAATATGCGCGCCCTGACCAAGGTG	936	
Db	561	TGTTCCCTGGAGAGTCCCTTCTGTGCTGTGTAACAATATGCGCGCGCTGACCAAGGTG	502	
Qy	937	TAAGTGTGAATATCAGGAAGATGACTGAAACGTCCTTGGGACATCCCTTCTCATTTGTA	996	
Db	501	TAAGTGTGAATATCAGGAAGATGACTGAAACGTCCTTGGGACATCCCTTCTCATTTGTA	442	
Qy	997	AAATGGAGTTAAATACGAGCCTCTTCTACACCCCAAAACGACGCTGTTGTGCCGGCCAG	1056	
Db	441	AAATGGAGTTAAATACGAGCCTCTTCTACACCCCAAAACGACGCTGTTGTGCCGGCCAG	382	

QY	1057	AGGAGCCCAATTGGTTGGCTGTTCACGCATCAGTTACCCACAGACGGGGTCAGCCAAATTA	1118
Dd	381	AGGG-CCAAATTGTTGGCTGTTCACGCR(C)CACTGTAACCCCAAGAGACGGGGTCAGCCAAATTA	323
QY	1117	AAGCGAAACAGGCCCCGGGTCCATCTCTGACGCGCTTTTCTCATCCAGAGGGCTGACAGGC	1176
Dd	322	AAGCGAAACAGGCCCCGGGTCCATCTCTGACGCGCTTTTCTCATCCAGAGGGCTGACAGGC	263
QY	1177	AGCTGGCCTGGAGCCCGGGCTCTGGCTTTGTCACGTGGGGGGGGCCGGCCGCTTGTGTGTCTG	1238
Dd	262	AGCTGGCCTGGAG-CCGGCTCTGGCTTTGTCACGTGGGGGGGGCCGGCCGCTTGTGTGTCTG	204
QY	1237	TGTGTAGAGAGGCTGAGTCAAGCTGGGGTCTCCCGCCCCCGCGGGGGCTTTTAGTGTCCCT	1298
Dd	203	TGTGTAGAGAGGCTGAGTCAAGCTGGGGTGTCTCCCGCCCCCGCGGGGGCTTTTAGTGTCCCT	144
QY	1297	GGTCCCTTAAACGCGCAGGCGGCTCCACCGAGGAGAAAGGCGGGAACCCAGCGCGAGCCCA	1356
Dd	143	GGTCCCTTAAACGCGCAGGCGGCTCCACCGAGGAGAAAGGCGGGAACCCAGCGCGAGCCCA	84
QY	1357	CGGCTGTGTGTGGGTGGCGGGGCAACTGTGTGTGCAAGTTCTGAATTGGTTCTTCCCCCGGA	1416
Dd	83	CGGCTGTGTGTGGGTGGCGGGGCAACTGTGTGTGCAAGTTCTGAATTGGTTCTTCCCCCGGA	24
QY	1417	CAACCGGCGGCTGTAAACCAATC	1439
Dd	23	CAACCGGCGGCTGTAAACCAATC	1

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RESULT 4
US-10-301-480-881697/C
Sequence: 881697, Application US/10301480
Publication No. US2005057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,655
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 881697
LENGTH: 561
TYPE: DNA
ORGANISM: Homo sapien
US-10-301-480-881697

```

Query Match	33.6%	Score 538.6	DB 12	Length 561
Best Local Similarity	99.5%	Pred. No. 7.9e-126		
Matches 560	Conservative 1	Mismatches 0	Indels 2	Gaps 2

Oy	937	TAAGTGTGTAATATCAGAGAAGATGACTGAAAGCTCTTGGGAGCTCCGTTCCCTCATTTGTA	996
Db	501	TAAGTGTGTAATATCAGAGAAGATGACTGAAAGCTCTTGGGAGCTCCGTTCCCTCATTTGTA	442
Oy	997	AAATGAGAGTTAATACAGACCTCTTCTTACTTCCCAACGCAAGTGTTTGTGCCGGGCAG	1056
Db	441	AAATGAGAGTTAATACAGACCTCTTCTTACTTCCCAACGCAAGTGTTTGTGCCGGGCAG	382
Oy	1057	AGGGCCCAATGTTGGCTGTTCACGACATCAGTTACCCCAAGAGAGCGGGTCAGGCCAATTTA	1116
Db	381	AGGG-CCAAATGTTGGCTGTTCACGACATCAGTTACCCCAAGAGAGCGGGTCAGGCCAATTTA	323

Oy	1117	AAGCGAAACAGAGCCCGATCCATCTCCGTAGAGCTTTTTCATATCCAGAGGCTGGACAAGGC	1176
Dd	322	AAGCGAAACAGAGCCCGATCCATCTCCGTAGAGCTTTTTCATATCCAGAGGCTGGACAAGGC	263
Oy	1177	AGCTGAGCTGGGCCCCGAGCTCTGCTTGTGACAGTGCAGGAGGCGAGCCGATTGCTTGTCTG	1238
Dd	262	AGCTGAGCTGGG - CGAGCTCTGCTTGTGACAGTGCAGGAGGCGAGCCGATTGCTTGTCTG	204
Oy	1237	TGTGTAGAGAGCTGAGGTCAAGCTGGGTGTCTCCGCCCCGCGGAGGCTTTTAGTGTCTCT	1296
Dd	203	TGTGTAGAGAGCTGAGGTCAAGCTGGGTGTCTCCGCCCCGCGGAGGCTTTTAGTGTCTCT	144
Oy	1297	GGTCTCCCTAAACGCCAGAGCCGCTCCACCGGGGGANAAGCGGAAACCCAGCGGAAGCCCA	1356
Dd	143	GGTCTCCCTAAACGCCAGAGCCGCTCCACCGGGGGANAAGCGGAAACCCAGCGGAAGCCCA	84
Oy	1357	CGGCTGTTTGCAGTTGCGGGGCAACGTGTGCTCAGTTTGATTTGTTGTTCTTCCCCGA	1416
Dd	83	CGGCTGTTTGCAGTTGCGGGGCAACGTGTGCTCAGTTTGATTTGTTTCTTCCCCGA	24
Oy	1417	CAACGCGAGGCTGTAAACCAATC	1439
Dd	23	CAACGCGAGGCTGTAAACCAATC	1

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RESULT 5
US-09-925-065A-177131/c
; Sequence 177131, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177131
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-177131

```

Query Match	33.2%	Score	531.6;	DB	4;	length	554;
Best Local Similarity	99.5%	Pred. No.	4.7e-124;				
Matches	553;	Conservative	1;	Mismatches	0;	Indels	2;
						Gaps	2;

Oy	937	TAACTGTGTGAATATCAGAAAGATGACTGAACGTCCTTTGGAGCTCCGTTTCTCATTTGTA	996
Db	554	TGTTCCCTGGCAGTCCCTTCTGCTGTGTGAAAAACAATATGGACGCGCATGACAGAGGTG	936
Oy	877	TGTTCCCTGGCAGTCCCTTCTGCTGTGTGAAAAACAATATGGACGCGCATGACAGAGGTG	936
Db	554	TGTTCCCTGGCAGTCCCTTCTGCTGTGTGAAAAACAATATGGACGCGCATGACAGAGGTG	995
Oy	937	TAACTGTGTGAATATCAGAAAGATGACTGAACGTCCTTTGGAGCTCCGTTTCTCATTTGTA	996
Db	494	TAACTGTGTGAATATCAGAAAGATGACTGAACGTCCTTTGGAGCTCCGTTTCTCATTTGTA	435
Oy	997	AAATGAGAGTTAAATACAGCTCTTTCTATCTCCCAAACGACGTTTGTGTCCGGCCAG	1056
Db	434	AAATGAGAGTTAAATACAGCTCTTTCTATCTCCCAAACGACGTTTGTGTCCGGCCAG	375
Oy	1057	AGGGCCCAATTTGTGGCTGTTCACGACATGTTATCCCCACAGGACGGGTACGCCAATTA	1116
Db	374	AGGG-CCAAATTTGTGGCTGTTCACGACATGTTATCCCCACAGGACGGGTACGCCAATTA	316

QY 1117 AAGGCGAACCAAGGCCGCTGCATCTCTGACGCGCTTTTCTCATCCAGAGGCTGAGACAGC 1176
DB 315 AAGGCGAACCAAGGCCGCTGCATCTCTGACGCGCTTTTCTCATCCAGAGGCTGAGACAGC 256
QY 1177 AGCTGGCCCTGGAGCCCGGCTCTGCTTGTCACTGTCGCGAGGAGCCGAGCCGCTTGTCTG 1236
DB 255 AGCTGGCCCTGGAG-CCGAGCTCTGCTTGTCACTGTCGCGAGGAGCCGAGCCGCTTGTCTG 197
QY 1237 TGTGTAGAGAGCGTGAAGTCAAGCTGAGTGTCTCCGAGCCGAGGAGCTTTAGTGTCTCT 1296
DB 196 TGTGTAGAGAGCGTGAAGTCAAGCTGAGTGTCTCCGAGCCGAGGAGCTTTAGTGTCTCT 137
QY 1297 GGTCCCTTAAAGCGCAGAGCGCTCTCAACCGAGGAGAGAAAGCGCGAACCCAGCCGAGCCAA 1356
DB 136 GGTCCCTTAAAGCGCAGAGCGCTCTCAACCGAGGAGAGAAAGCGCGAACCCAGCCGAGCCAA 77
QY 1357 CGGCTGTGTGCGGTTGCGGAGCCGAGCGCTGCTGAGTGTCTGATTTGGTTCTTCCCCCGA 1416
DB 76 CGGCTGTGTGCGGTTGCGGAGCCGAGCGCTGCTGAGTGTCTGATTTGGTTCTTCCCCCGA 17
QY 1417 CAACGCGAGCGGCTGTA 1432
DB 16 CAACGCGAGCGGCTGTA 1

RESULT 6

US-09-925-065A-177131/c
Sequence 177131, Application US/09925065A
Publication No. US2005028172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827, 135
CURRENT APPLICATION NUMBER: US/09/925, 065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243, 096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289, 846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 177131
LENGTH: 554
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-177131

Query Match 33.2%; Score 531.6; DB 5; Length 554;
Best Local Similarity 99.5%; Pred. No. 4,7e-124;
Matches 553; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

QY 877 TGTTCCTGCGAGTCCCTTCTGCTGTGAAACAACATATGCGCGCGGCTGACCAAGGTG 936
DB 554 TGTTCCTGCGAGTCCCTTCTGCTGTGAAACAACATATGCGCGCGGCTGACCAAGGTG 495
QY 937 TAAGTGTGATATATGAGAAATGACTGAAGCTTTGGAGACTCGCTTCTCATTTGTA 996
DB 494 TAAGTGTGATATATGAGAAATGACTGAAGCTTTGGAGACTCGCTTCTCATTTGTA 435
QY 997 AAATGAGGTTAATACAGGCTTCTTACTCTCCCAACGACAGTGTGTTGCTCCGAGCAG 1056
DB 434 AAATGAGGTTAATACAGGCTTCTTACTCTCCCAACGACAGTGTGTTGCTCCGAGCAG 375
QY 1057 AGGAGCCCAATTGTTGCTGTTACAGCATGATTACCCCAAGAGAGGCTCAGCAATTA 1116

DB 374 AGGG-CCAAATTGTGAGCTTTACAGGCTCAAGTTACCCCAAGAGAGGCTCAGCAATTA 316
QY 1117 AAGGCGAACCAAGGCCCGGTCATCTCTGACGCGCTTTTCTCATCCAGAGGCTGAGACAGC 1176
DB 315 AAGGCGAACCAAGGCCCGGTCATCTCTGACGCGCTTTTCTCATCCAGAGGCTGAGACAGC 256
QY 1177 AGCTGGCCCTGGAGCCCGGCTCTGCTTGTCACTGTCGCGAGGAGCCGAGCCGCTTGTCTG 1236
DB 255 AGCTGGCCCTGGAG-CCGAGCTCTGCTTGTCACTGTCGCGAGGAGCCGAGCCGCTTGTCTG 197
QY 1237 TGTGTAGAGAGCGTGAAGTCAAGCTGAGTGTCTCCGAGCCGAGGAGCTTTAGTGTCTCT 1296
DB 196 TGTGTAGAGAGCGTGAAGTCAAGCTGAGTGTCTCCGAGCCGAGGAGCTTTAGTGTCTCT 137
QY 1297 GGTCCCTTAAAGCGCAGAGCGCTCTCAACCGAGGAGAGAAAGCGCGAACCCAGCCGAGCCAA 1356
DB 136 GGTCCCTTAAAGCGCAGAGCGCTCTCAACCGAGGAGAGAAAGCGCGAACCCAGCCGAGCCAA 77
QY 1357 CGGCTGTGTGCGGTTGCGGAGCCGAGCGCTGCTGAGTGTCTGATTTGGTTCTTCCCCCGA 1416
DB 76 CGGCTGTGTGCGGTTGCGGAGCCGAGCGCTGCTGAGTGTCTGATTTGGTTCTTCCCCCGA 17
QY 1417 CAACGCGAGCGGCTGTA 1432
DB 16 CAACGCGAGCGGCTGTA 1

RESULT 7

US-10-197-019-1
Sequence 1, Application US/10197019
Publication No. US2003020784A1
GENERAL INFORMATION:
APPLICANT: Chew, Anne
APPLICANT: Denton, R. Rex
APPLICANT: Gilson, Christopher Raleigh
APPLICANT: Mandabalan, Krishnan
APPLICANT: Parks, Katie E.
TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
FILE REFERENCE: MMH-0042US
CURRENT APPLICATION NUMBER: US/10/197, 019
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: PCT/US01/02485
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 9314
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (1283)..(1283)
OTHER INFORMATION: PS1: polymorphic base cytosine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (1714)..(1714)
OTHER INFORMATION: PS2: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (2051)..(2051)
OTHER INFORMATION: PS3: polymorphic base thymine or cytosine
FEATURE:
NAME/KEY: allele
LOCATION: (2124)..(2124)
OTHER INFORMATION: PS4: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (2287)..(2287)
OTHER INFORMATION: PS5: polymorphic base cytosine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (2408)..(2408)
OTHER INFORMATION: PS6: polymorphic base adenine or guanine

1	FEATURE:		
2	NAME/KEY:	allele	
3	LOCATION:	(4768) .. (4768)	
4	OTHER INFORMATION:	PS7:	polymorphic base adenine or guanine
5	FEATURE:		
6	NAME/KEY:	allele	
7	LOCATION:	(4785) .. (4785)	
8	OTHER INFORMATION:	PS8:	polymorphic base guanine or adenine
9	FEATURE:		
10	NAME/KEY:	allele	
11	LOCATION:	(4813) .. (4813)	
12	OTHER INFORMATION:	PS9:	polymorphic base thymine or cytosine
13	FEATURE:		
14	NAME/KEY:	allele	
15	LOCATION:	(4882) .. (4882)	
16	OTHER INFORMATION:	PS10:	polymorphic base adenine or cytosine
17	FEATURE:		
18	NAME/KEY:	allele	
19	LOCATION:	(4976) .. (4976)	
20	OTHER INFORMATION:	PS11:	polymorphic base thymine or adenine
21	FEATURE:		
22	NAME/KEY:	allele	
23	LOCATION:	(5820) .. (5820)	
24	OTHER INFORMATION:	PS13:	polymorphic base thymine or guanine
25	FEATURE:		
26	NAME/KEY:	allele	
27	LOCATION:	(6536) .. (6536)	
28	OTHER INFORMATION:	PS14:	polymorphic base thymine or adenine
29	FEATURE:		
30	NAME/KEY:	allele	
31	LOCATION:	(6607) .. (6607)	
32	OTHER INFORMATION:	PS15:	polymorphic base guanine or adenine
33	FEATURE:		
34	NAME/KEY:	allele	
35	LOCATION:	(6617) .. (6617)	
36	OTHER INFORMATION:	PS16:	polymorphic base cytosine or thymine
37	FEATURE:		
38	NAME/KEY:	allele	
39	LOCATION:	(6872) .. (6872)	
40	OTHER INFORMATION:	PS17:	polymorphic base cytosine or guanine
41	FEATURE:		
42	NAME/KEY:	allele	
43	LOCATION:	(6966) .. (6966)	
44	OTHER INFORMATION:	PS18:	polymorphic base guanine or adenine
45	FEATURE:		
46	NAME/KEY:	allele	
47	LOCATION:	(7036) .. (7036)	
48	OTHER INFORMATION:	PS19:	polymorphic base cytosine or thymine
49	FEATURE:		
50	NAME/KEY:	allele	
51	LOCATION:	(7086) .. (7086)	
52	OTHER INFORMATION:	PS20:	polymorphic base adenine or guanine
53	FEATURE:		
54	NAME/KEY:	allele	
55	LOCATION:	(8100) .. (8100)	
56	OTHER INFORMATION:	PS21:	polymorphic base cytosine or thymine
57	FEATURE:		
58	NAME/KEY:	allele	
59	LOCATION:	(8221) .. (8221)	
60	OTHER INFORMATION:	PS22:	polymorphic base guanine or adenine
61	FEATURE:		
62	NAME/KEY:	allele	
63	LOCATION:	(8677) .. (8677)	
64	OTHER INFORMATION:	PS23:	polymorphic base thymine or adenine
65	PS-10-197-019-1		

Query Match	27.1%	Score 433.8;	DB 7;	Length 9314;
Best Local Similarity	97.9%	Pred. No. 1.1e-98;		
Matches 461; Conservative	0;	Mismatches 7;	Indels 3;	Gaps 2;

QY	1133	GGTCAATCTCTGAAGCCCTTTTCTCATCCAGGGCTGAAAGGACGCTGACCTGGGCGC	1192
Db	1	GGTCAATCTCTGAAGCCCTTTTCTCATCCAGGGCTGAAAGGACGCTGACCTGGGCGC	60
QY	1193	GCTCTGCCTTGTCAAGTGCAGGAGGCGCGGCCGCTTGTCTGTGTGTGAAGAGCTGAG	1252
Db	61	GCTCTGCCTTGTCAAGTGCAGGAGGCGCGGCCGCTTGTCTGTGTGTGAAGAGCTGAG	120
QY	1253	GTCAGCGTGGGTGTCTCCGGCCCGCGCGGGGCTTTAGTGTCCCTGTGCTTAAACGCGCAG	1312
Db	121	GTCAGCGTGGGTGTCTCCGGCCCGCGCGGGGCTTTAGTGTCTCCGTGCTTAAACGCGCAG	180
QY	1313	GCCGCTCCACCGGAGGAGAAAGGCGCGCAGACCCAGACCCAAAGCTGTGTGCGTTG	1372
Db	181	GCCGCTCCACCGGAGGAGAAAGGCGCGCAGACCCAGACCCAAAGCTGTGTGCGTTG	240
QY	1373	CCGGGCAACCTGTGTGTGCAAGTCTGTATTGTGTTCTTCCCCCGAACACGGGCGGCTGTGA	1432
Db	241	CCGGGCAACCTGTGTGTGCAAGTCTGTATTGTGTTCTTCCCCCGAACACGGGCGGCTGTGA	300
QY	1433	ACCAATCGACAGCGAGGCGCGGTGCGAGAGGCCCAAGTCCGCCCTGTGACGAGACGACGCGC	1492
Db	301	ACCAATCGACAGCGAGGCGCGGTGCGAGAGGCCCAAGTCCGCCCTGTGACGAGACGACGCGC	360
QY	1493	CGCTTCGCTCGCAGAGAGGGTGGGTGAATTGTGCCACGCTGAGGGGGGCTGGGCCCTAAAGA	1552
Db	361	CGCTTCGCTCGCAGAGAGGGTGGGTGAATTGTGCCACGCTGA-GGGGGCTGGGCCCTAAAGA	419
QY	1553	GGAAGTCACTTAAAGACAGCGCCCGCGCTGACGCTGTGTGAAGAACGCTCTCT	1603
Db	420	GGAAGTCACTTAAAGACAGCGCCCG--TGAAGCTGTGTGAAGAACGCTCTCT	468

```

RESULT 8
US-10-719-993-6827/C
: Sequence: 6827, Application US/10719993
: Publication No. US20040265849A1
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele et al.
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C0001496
: CURRENT APPLICATION NUMBER: US/10/719,993
: CURRENT FILING DATE: 2003-11-24
: NUMBER OF SEQ ID NOS: 55342
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6827
: LENGTH: 160556
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (1)_(160556)
: OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-719-993-6827

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Query Match	9.8%	Score 157.8	DB 9	Length 160556
Best Local Similarity	68.3%	Pred. No. 4,5e-28		
Matches 233	Conservative 1	Mismatches 103	Indels 4	Gaps 1
QY	2	CCTGTATTCCTAGTACTGTGAGAGTCCGAGGTCAGAGGACTGTGGCCAGGAGTTCA	61	
Db	30072	CTGTATCTCTACACCTTTGGGAGGCGAAGGCGAGTGATTCGTAGTCCAGGAGTTG	30013	
QY	62	AGAGCAGCCTTGACAACACAGGAGACCTGTCTACTAACAAGATAATTAATTGACGAG	121	
Db	30012	AGACGAGCCTTGACAACATGTGACACCTGTCTCTAATAAATAACAATAATTAGCCAGG	29953	
QY	122	CTTAGAGGCTCATCCCTGTGGTCCGACGATCTAGGGAGGACAGATGAGGAGG-----CTGCTT	177	
Db	29952	YGTGATTGTGCGCGCCTGTATGTCCACGACTACTTGGAGGCTGAGCGACGAGATCATCTTG	29893	

QY 178 GTCCAGAGGCTGACAGTGTGAGCTGAGACCCAGCCACTGCTTCCAGCTGGGC 237
DB 29892 AACCCAGAGGCTGAGGTTACAGTACCTGAGCTGACCCACTGACCTCCAGCTGGGT 29833
QY 238 AACCAAAAGAGCCCTGCTCAAAAATAGTTAAATTAATTAATTAATTAATTAAT 297
DB 29832 GACAGAGTACACTGTCTCAAAAATTAATTAATTAATTAATTAATTAATTAAT 29773
QY 298 AACCTTAACACATCTTCTTTTCAAGAAGAGACTTCTTAAG 338
DB 29772 AATGCTAGAGAACACTTGTATGACAAAATGTGTACTTAAG 29732
RESULT 9
US-10-723-860-2320/c
Sequence 2320, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
PRIOR FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2320
LENGTH: 135005
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-860-2320
Query Match 9.5%; Score 152; DB 9; Length 135005;
Best Local Similarity 80.0%; Pred. No. 1.2e-26;
Matches 216; Conservative 0; Mismatches 50; Indels 4; Gaps 3;
QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGGACTGCTTGAAGGCCAGAGTTC 60
DB 84820 ATCTGTAATCTGACACTTTGGAGGAGAGGTAGAGAGATCTTGAAGGCCAGAGTTC 84761
QY 61 AAGAGAGCCTGGAACAACAAGAGAGAG--CCTGTCACTACAAAGATTAATTAATTAAGCC 118
DB 84760 AAGACTATCTGGGCAACATAGTGAAGACCCCTGTCTCTACAAAATTAATTAATTAAGTC 84701
QY 119 AGGCTTAGTGGCTCATCCTGTGTGCTCCAGCTACTAGAGGAGGAGAAATTAATTAATTA 178
DB 84700 GGGTATGTGTGGACATGCTGTGTAGTCCAGCTACTCAGAGGCTGAGTGAATTCCTTG 84641
QY 179 -TCCAGAGAGGTCAGAGCTGAGTGTGAGCCAGCCAGCTGATTCAGCTGGGC 237
DB 84640 AGCTCAGAGAGTGAAGGCGGAGGAGTGAAGAGAGTCCA-CTGTACTCAACTGGGC 84582
QY 238 AACAAAAAGAGACCTGTCTCAAAAATTA 267
DB 84581 AACGAAACAAGACCTGTCTCAAAAATTA 84552
RESULT 10
US-10-756-149-1719/c
Sequence 1719, Application US/10756149
Publication No. US20050181375A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12

QY 178 GTCCAGAGGCTGACAGTGTGAGCTGAGACCCAGCCACTGCTTCCAGCTGGGC 237
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DB 29832 GACAGAGTACACTGTCTCAAAAATTAATTAATTAATTAATTAATTAATTAAT 29773
QY 298 AACCTTAACACATCTTCTTTTCAAGAAGAGACTTCTTAAG 338
DB 29772 AATGCTAGAGAACACTTGTATGACAAAATGTGTACTTAAG 29732
RESULT 9
US-10-723-860-2320/c
Sequence 2320, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
PRIOR FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2320
LENGTH: 135005
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-860-2320
Query Match 9.5%; Score 152; DB 10; Length 135005;
Best Local Similarity 80.0%; Pred. No. 1.2e-26;
Matches 216; Conservative 0; Mismatches 50; Indels 4; Gaps 3;
QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGGACTGCTTGAAGGCCAGAGTTC 60
DB 84820 ATCTGTAATCTGACACTTTGGAGGAGAGGTAGAGAGATCTTGAAGGCCAGAGTTC 84761
QY 61 AAGAGAGCCTGGAACAACAAGAGAGAG--CCTGTCACTACAAAGATTAATTAATTAAGCC 118
DB 84760 AAGACTATCTGGGCAACATAGTGAAGACCCCTGTCTCTACAAAATTAATTAATTAAGTC 84701
QY 119 AGGCTTAGTGGCTCATCCTGTGTGCTCCAGCTACTAGAGGAGGAGAAATTAATTAATTA 178
DB 84700 GGGTATGTGTGGACATGCTGTGTAGTCCAGCTACTCAGAGGCTGAGTGAATTCCTTG 84641
QY 179 -TCCAGAGAGGTCAGAGCTGAGTGTGAGCCAGCCAGCTGATTCAGCTGGGC 237
DB 84640 AGCTCAGAGAGTGAAGGCGGAGGAGTGAAGAGAGTCCA-CTGTACTCAACTGGGC 84582
QY 238 AACAAAAAGAGACCTGTCTCAAAAATTA 267
DB 84581 AACGAAACAAGACCTGTCTCAAAAATTA 84552
RESULT 11
US-09-925-065A-822292/c
Sequence 822292, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 822292
LENGTH: 558
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-822292
Query Match 9.4%; Score 150.6; DB 4; Length 558;
Best Local Similarity 74.1%; Pred. No. 2e-27;
Matches 217; Conservative 1; Mismatches 70; Indels 5; Gaps 2;
QY 2 CCTGTATTCCTACTGTGAGAGTCCGAGGTCAGAGGACTGCTTGAAGGCCAGAGTTC 61
DB 345 CCTGTATTCCTACTGTGAGAGTCCGAGGTCAGAGGACTGCTTGAAGGCCAGAGTTC 286
QY 62 AGAGAGCCTGGGCAACAAGAGGAGCCTGTCTACTCAAAAGATTAATTAATTAATTAAGCCAG 121
DB 285 AGAGAGCCTGGGCAACAAGAGGAGCCTGTCTACTCAAAAGATTAATTAATTAATTAAGCCAG 226

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Oy      122  CTATATGGGCTATATCCCTGGTGGTCCAGACTATGGGAGGAGAAAGTAGAGACTGTTGT - 179
Db      225  TGTGGTGGTGCATGCCCTTGAATGCCAGCTATCTTGGAGGGCTGAGGCAGGGGGGGTTGCTTG 166
Oy      180  --CCGAGGAGGTCAAGACTGCAGTAGTGAAGAGCCAGCCAGCTGCATTCAGACTGGGC 237
Db      165  AACCTGGGAGGGTGGAGGTTGCAGTAGGCCAAGATCAAGTGA - CTGGCCTTCAGGCTGGGG 107
Oy      238  AACAAAAAGAGACCCCTGTCTCAAAAATAATGAATTAATTAATATAAAAA 290
Db      106  AACTAATGAGACTCTGTCTCAAAAAAATAAAAAAAGATATAAAAATTTAAA 54

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RESULT 12
US-09-925-065A-839930
Sequence 839930, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.13
CURRENT APPLICATION NUMBER: US/09/925, 065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243, 096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289, 846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 839930
LENGTH: 558
TYPE: DNA
ORGANISM: Homo sapiens
US-925-065A-839930

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	Query Match	Similarity	7.4%	Score 150.6	DB 4	Length 558
	Best Local	Similarity	94.1%	Pred. No. 2e-27		
	Matches	217	Conservative	1	Mismatches	70
					Indels	5
					Gaps	2
OY	2	CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAGAGGACGTGCTTGAGGCCAGAGATTCA	61			
Db	215	CCTGTAATTCAGGACCTTTGGGAGGCCAAGGACGGTGGATTACTTGAGGTGAGGATTCA	274			
OY	62	AGAGCAGCGCTGGAACAACAAGGAGACCTGTGCATCAACAAGATTTAAATTAGCCAGG	121			
Db	275	AGACGAGCTGGCCAAACAACGGTGAACCCGCTCTCTAATAAATAATACAAATTTAGCCAGG	334			
OY	122	CTTAGTGCTCATCCCTGTGGTCCCACTACTAGGAGGACGAAGTAGAGACTGCTGTG--	179			
Db	335	TGTGGTGGTGAATGCTGTGATGCCAGGTACTCTGGGAGCTGAGGACAGGGGGTGGCTTG	394			
OY	180	--CCAGAGGTCACAAGCTGCAGTGAAGCTGAGACCAACCACTGTCATTTCAGCCTGGGC	237			
Db	395	AACCTGGGAGGTGGAGGTTTGACAGTGAAGCAAGATACAGTCA--CTGCCCTCCAGCCTGGGG	453			
OY	238	AACAAAAAGAACCTGTCTCAAAAATAATAGTTAAATTAAATTAATATATATAA	290			
Db	454	AACATAAGTGAAGCTCTGTCTCAAAAAAAAAAAAAAAAAAAGATTAAATAATATAA	506			

RESULT 13
US-09-925-065A-822292/c
; Sequence 822292, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:

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1  APPLICANT: Wang, David G.
2  TITLE OF INVENTION: Identification and Mapping of Single
3  TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
4  FILE REFERENCE: 108827.135
5  CURRENT APPLICATION NUMBER: US/09/925,065A
6  CURRENT FILING DATE: 2001-08-09
7  PRIOR APPLICATION NUMBER: US 60/243,096
8  PRIOR FILING DATE: 2000-10-24
9  PRIOR APPLICATION NUMBER: US 60/252,147
10 PRIOR FILING DATE: 2000-11-20
11 PRIOR APPLICATION NUMBER: US 60/250,092
12 PRIOR FILING DATE: 2000-11-30
13 PRIOR APPLICATION NUMBER: US 60/261,766
14 PRIOR FILING DATE: 2001-01-16
15 PRIOR APPLICATION NUMBER: US 60/289,846
16 PRIOR FILING DATE: 2001-05-09
17 NUMBER OF SEQ ID NOS: 957086
18 SOFTWARE: FastSeq for Windows Version 4.0
19 SEQ ID NO 822292
20 LENGTH: 558
21 TYPE: DNA
22 ORGANISM: Homo sapiens
23 US-09-925-065A-822292

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Query Match	9.4%;	Score 150.67;	DB 5;	Length 558;
Best Local Similarity	74.1%;	Pred. No. 2e-17;		
Matches	217;	Conservative	1;	Mismatches 70; Indels 5; Gaps 2.
QY	2	CCTGTAATTCAGACTGTGAGAGTCCGAGGTCAGAGACCTGCTTTGAGGCCAGAGTTCA	61	
Db	345	CCTGTAAATCCAGACATTTTGGGAGGCCAAGGCAAGTGATTAATTGAGGTCAAGAGTTCA	286	
QY	62	AGAGCAGCCTTGACAAACAGAGGAGACCTGTCACTACAAAGATTAATTAATTGACCAGG	121	
Db	285	AGACCAAGCTGTGCCAAACACGGTGAATCCCGTCTACTAAATAATACAAAAATTAGCCAGG	226	
QY	122	CTTAGTGGCTATCCCTGTGGTCCCAAGTAACTAAGGAGGCAAGATGAGACTGCTGT--	179	
Db	225	TGTGTGGTGTATCCCTGTAGTCCCACTAATTTGGAGGCTGAGGCAAGGGAGTGTCTTG	166	
QY	180	--CCAGAGAGTCAAGACTGCAGTGAGCTGAGACCCAGCCACTGATCTTCAGCCTGGGC	237	
Db	165	AACTGGGAGGTGAGGTTGTCAGTGAAGCAAGATCAAGYCA-CTGCCCTTCAGCCTGGGG	107	
QY	238	AACAAAAAGAGACCTGTCTCAAAAAATTAAGTTAAATTAATTAATTAATTAATAA	290	
Db	106	AACTAAGAGACTGTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATAA	54	

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RESULT 14
US/09-925-065A-839930
Sequence 839930, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Map-
ping of Invention: Nucleotide Polymorph-
ic File REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925, 065/
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: RASEQ for Windows Version 4.0
SEQ ID NO 839930

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LENGTH: 558
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-839930

Query Match 9.4%; Score 150.6; DB 5; Length 558;
Best Local Similarity 74.1%; Pred. No. 2e-27;
Matches 217; Conservative 1; Mismatches 70; Indels 5; Gaps 2;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCCAGAGACTGCTTGTAGGCGCAGAGTTCA 61
DB 215 CCTGTAATCCAGACCTTTGGAGGCCAAGGCGAGGTGATTTACTTTAGGTGAGAGTTCA 274
QY 62 AGAGCAGCTTGACAAACAGGAGACCTGTCTCACTAAGAAATTAATTAATTAGCCAG 121
DB 275 AGAGCAGCTTGACAAACAGGTAACCCGTCTCTAATAAATAAATAAATTAGCCAG 334
QY 122 CTTAGTGCTCATCCCTGTGTGTCCAGCTACTAGGAGGCAAGTAGAGCTGCTTGT-- 179
DB 335 TGTGTGTGTGCTAGCTGTGTGTCTCCAGCTACTTGTGAGGCGAGGCGGTGCTTG 394
QY 180 --CCGAGAGGTGACAGCTGAGTGTGAGCCAGCCAGCCTGATTCAGCTGAGC 237
DB 395 AACCTGGAGGTGAGAGGTGAGAGCCAGATCAAGTCA--CTGCCCTTCAGCTGAGG 453
QY 238 AACAAAAAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 290
DB 454 AACTAAGTGAGCTGTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 506

RESULT 15
US-10-017-161-1909
Sequence 1909, Application US/10017161
Publication No. US20030143668A1

GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1909
LENGTH: 23579
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: source
LOCATION: (1)..(23579)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(292)
FEATURE:
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LOCATION: (7942)..(8265)
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LOCATION: (23298)..(23379)
US-10-017-161-1909

Query Match 9.4%; Score 150.4; DB 7; Length 23579;
Best Local Similarity 72.4%; Pred. No. 1.3e-26;
Matches 223; Conservative 0; Mismatches 81; Indels 4; Gaps 2;

QY 2 CCTGTAATTCAGTACTGTGAGAGTCCGAGGTCCAGAGCTGCTGAGGCCAGAGTTCA 61
DB 14855 CCTATAGCCAGACCTTTGGAGGTGAGGTGCTCATCACTTAGGCGCAGAGGTTTG 14914

QY 62 AGAGCAGCTTGACAAACAGGAGACCTGTCTACCTACAAAGAAATTAATTAATTAGCCAG 121
DB 14915 AGAGCAGCATGGCCAAACATGTGAACCCGTCTTAATAAATAATTAATTAAGCCAG 14974
QY 122 CTTAGTGCTCATCCCTGTGTGTCCAGCTACTAGGAGGCGC--AGAAATGAGACTGCTTG 178
DB 14975 CTTAGTGCTCATCCCTTAATTCAGCTACTTTGGAGGCTGAGGAGAAATTCGCTTG 15034
QY 179 TCCAGAGGTCAAGACTGAGTGTGAGCCAGCCAGCCTGATTCAGCTGAGGCA 238
DB 15035 AACCGGAGGCGAGGTTGCACTGAGCTGAGATTGCGCA--TTGCACCTCGGCTGAGCA 15093
QY 239 ACAAAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTAATTAATTAATTA 298
DB 15094 ACGAGCAAGCTGTCTTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 15153
QY 299 ACCCTAAA 306
DB 15154 AAAATAAA 15161

Search completed: June 6, 2006, 00:21:03
Job time : 3191.86 secs

Publication No. US20060105381A1
GENERAL INFORMATION:
APPLICANT: Eilipais Bioherapeutics Corporation
APPLICANT: Peltekova, Vanya D
APPLICANT: Siminovitich, Katherine A
APPLICANT: St George-Hyslop, Peter H
APPLICANT: Rubin, Laurence A
APPLICANT: Peltekova, Vanya D
APPLICANT: Mincle, Richard F
TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSOCIATED WITH INFLAMMATORY BOWEL DISORDERS
FILE REFERENCE: ELP-020
CURRENT APPLICATION NUMBER: US/11/318,813
CURRENT FILING DATE: 2005-12-27
PRIOR APPLICATION NUMBER: US/10/327,188
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 60/362,700
PRIOR FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 60/343,338
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/427,529
PRIOR FILING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: 60/362,717
PRIOR FILING DATE: 2002-03-08
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 42
LENGTH: 54550
TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION: n can be a or t or g or c
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NAME/KEY: misc_feature
LOCATION: (4809)..(4809)
OTHER INFORMATION: n can be a or t or g or c

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39 LOCATION: (9403)..(9403)
40 OTHER_INFORMATION: n can be a or t or g or c
41 FEATURE:
42 NAME/KEY: misc_feature
43 LOCATION: (9598)..(9598)
44 OTHER_INFORMATION: n can be a or t or g or c
45 FEATURE:
46 NAME/KEY: misc_feature
47 LOCATION: (10245)..(10245)
48 OTHER_INFORMATION: n can be a or t or g or c
49 FEATURE:
50 NAME/KEY: misc_feature
51 LOCATION: (10817)..(10817)
52 OTHER_INFORMATION: n can be a or t or g or c
53 FEATURE:

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	Query Match	8.5%	Score 136.8	DB 7	Length 54550
	Best Local Similarity	69.5%	Pred. No. 6,2e-15		
	Matches 228	Conservative 0	Mismatches 94	Indels 6	Gaps 3
QY	2	CCTGTAAATTCAGTACTGTGTAGAGTCCGAGGTACAGAGACTGTGTAGAGCCACAGAGTTCA	61		
Db	46202	CATGTAAATCCAGACACTTTGTGANNAGGCCAAGGTAGTGTGATCACTGAGGCCACAGAGTTCA	46261		
QY	62	AGACACACCTGGACCAACACAGGAGA--CTGTACATCAAAAGAAATTAATTAACCG	120		
Db	46262	AGACACACCTGGACCAACAGTGTGAACCCGTCTCTCACTAAATTAATTAATTAACCG	46321		
QY	121	GCTTAGTGGCTCATCCCTGTGTGTCCACACTACTAGGAGGACAGATGAGACTGCTTGT-	179		
Db	46322	GTGTGCTGGCAGGAGCTGTAAATCCCGGTACTCTGAGGCTGAGTAGAGAAATTTGCTT	46381		
QY	180	---CCAGAGAGTCAAAAGCTGTGACGTAGCTGAGAACCCAGGCACCTGTGACCTGGG	236		
Db	46382	GAACCCAGAGAGGACAGAGGTGTGACATGTGTCAAGTTTGACCA--CTGCATCTTCAACCTGGG	46440		

[illegible]

```

RESULT 3
US-11-293-697-1292
; Sequence 1292, Application US/11293697
; Publication No. US20060105376A1
GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1292
; LENGTH: 2252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1292

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	Query Match	8.4%;	Score 134.6;	DB 7;	Length 2252;
	Best Local Similarity	72.1%;	Pred. No. 1.2e-14;	Mismatches 204;	Conservative 0;
				Mismatches 74;	Indels 5;
				Gaps 2;	
Qy	2 CCTGTAAATTCACGACTGTGTAGAGTCCGAGTCAAGAGAATCTTTGAGGCCAGAGTTCA				61
Db	1691 CCTGTAAATCCAGACATTGGGATTTGGAGGTGGCGGATCATTGAGGTCCAGAGTTCA				1950
Qy	62 AGAGCAGCCTTGACAACACAGGAGACCTGTCACTACAAAAGATTAATAATTAGCCAGG				121
Db	1951 AGACCAGCTGGGCCAACATGGTATAAACCCTCTCTAACAATAACAAAGATTAGCTGG				2010
Qy	122 CTTNATGGCTCATCCCTGTGTGTTCCAGCTACTAGGAGGCAAGATGGA---CTGCTT				177
Db	2011 TGTGTGGCACGGGCTGTGTAATCCGACCCCCTTGGAAGGCCAAGGCAGGAATATGCTTC				2070
Qy	178 GTCCACGAGGTCAAAGCTGCAGTGAAGCTGAGCCAGCCACTGTCATTCCAGCTGGGC				237
Db	2071 AACACTGGAAGGTGAGGTTGCAGTAGMACTGAGATTGGCCA-CTGCACTCAGCCTGGGC				2129
Qy	238 AACAACAAAAAGAGACCTGTCTCAAAAAAATAAGTTAAATAATAA 280				
Db	2130 AATGAGGCAAGACCTGTCTCAAAAAAATAATAATAATAATAA 2172				

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RESULT 4
US-11-293-697-441/c
; Sequence 441, Application US//11293697
; Publication No. US20060105376A1
;
GENERAL INFORMATION:
;
APPLICANT: HELIX RESEARCH INSTITUTE
;
TITLE OF INVENTION: Novel full length cDNA
;
FILE REFERENCE: H1-A0106
;
CURRENT APPLICATION NUMBER: US//11/293,697
;
CURRENT FILING DATE: 2005-12-05
;
PRIOR APPLICATION NUMBER: US//10/108,260
;
PRIOR FILING DATE: 2002-03-28
;
NUMBER OF SEQ ID NOS: 5458
;
SOFTWARE: PatentIn Ver. 2.1
;
SEQ ID NO 441
;
LENGTH: 2374
;
TYPE: DNA
;
ORGANISM: Homo sapiens
;

```

US-11-293-697-441

Query Match 8.2%; Score 132; DB 7; Length 2374;

Best Local Similarity 72.4%; Pred. No. 3.3e-14;

Matches 213; Conservative 0; Mismatches 75; Indels 6; Gaps 3;

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGTGAGGCCAGAGTTTC 60
|||
DB 2139 ACCTAATATCCCGACCTTTGGAGGCGCGAGCTGGGGGATTCCTTGACCTCAGAGTTTC 2080
|||
QY 61 AAGAGAGCCTGGACAACAACAGGAGA-CCTGTCACTACAAGATTAATTAATTAGCCA 119
|||
DB 2079 GAGACAGCCTGCCCAACATGTGAACCTGTCTTACTTAATAAATACAAAAGTAGCCA 2020
|||
QY 120 GGGTATGAGCTCATCTGTGTGTCCAGCTACTAGAGAGCGAAGTAGA----CTGC 175
|||
DB 2019 GGGATGTGTGTGATGCTGTATCTCTGTACTTGGAGAGCTGAGAGCGAAGATCACT 1960
|||
QY 176 TTGTCCAGAGAGTCAAGACTGCAAGTGAAGTGAAGCCAGCCCTGTCATTCCAGCTTG 235
|||
DB 1959 TGAACCTGGAGGCGGAGGTTGCTGTGAGCTGAGATTGTGGCA-CTGCACCTCCAGCTTG 1901
|||
QY 236 GCAACAAAAGAGACCCCTGTCTCAAAAAATTAAGTTAATTAATTAATTAATA 289
|||
DB 1900 GTGACAGAGTGAGACTGTCTGTCTCAAAAAAAGAAAAAAGAAAAAAGAAA 1847
|||

RESULT 5

US-11-293-697-723/C

Sequence 723, Application US/11293697

Publication No. US20060105376A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: Novel full length cDNA

FILE REFERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/11/293,697

CURRENT FILING DATE: 2005-12-05

PRIOR APPLICATION NUMBER: US/10/108,260

PRIOR FILING DATE: 2002-03-28

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 723

LENGTH: 3226

TYPE: DNA

ORGANISM: Homo sapiens

US-11-293-697-723

Query Match 8.1%; Score 130.2; DB 7; Length 3226;

Best Local Similarity 71.7%; Pred. No. 6.6e-14;

Matches 213; Conservative 0; Mismatches 78; Indels 6; Gaps 3;

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGTGAGGCCAGAGTTTC 60
|||
DB 2780 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTGGGCTGTATCACTGAGTCAAGAGTTTC 2721
|||
QY 61 AAGAGAGCCTGGACAACAACAGGAGA-CCTGTCACTACAAGATTAATTAATTAGCCA 119
|||
DB 2720 AAGACAGCCTGGACAACAAGTGAACCTGTCTTACTTAATAAATTAAGAAATTAGCTG 2661
|||
QY 120 GGGTATGAGCTCATCTGTGTGTCCAGCTACTAGAGAGCGAAGTAGA----CTGC 175
|||
DB 2660 GGTGGGTGTGAGAGTGTCTGTATGCTCCAGCTACTCAGAGAGTTGAGGCGAAGATGCT 2601
|||
QY 176 TTGTCCAGAGAGTCAAGACTGCAAGTGAAGTGAAGCCAGCCCTGTCATTCCAGCTTG 235
|||
DB 2600 TGAACCTGGAGGTTGAGGTTGAGTGAAGTGAAGATGAGATGCCCA-CTGCACCTCCAGCTTG 2542
|||
QY 236 GCAACAAAAGAGACCCCTGTCTCAAAAAATTAAGTTAATTAATTAATTAATA 292
|||
DB 2541 GCAACGAGAGTGAAGTGTCTGTCTTAATAAATAAATAAATAAATAAATAAATAAATA 2485
|||

RESULT 6

US-10-511-937-453/C

Sequence 453, Application US/10511937

Publication No. US20060088836A1

GENERAL INFORMATION:

APPLICANT: EXPRESSION DIAGNOSTICS, INC.

APPLICANT: Mohlenguth, Jay

APPLICANT: Fry, Kirk

APPLICANT: Woodward, Robert

APPLICANT: Ly, Ngoc

APPLICANT: Prentice, James

APPLICANT: Morris, Macdonald

APPLICANT: Rosenberg, Steven

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

FILE REFERENCE: 506612000104

CURRENT APPLICATION NUMBER: US/10/511,937

CURRENT FILING DATE: 2004-10-19

PRIOR APPLICATION NUMBER: PCT/US2003/012946

PRIOR FILING DATE: 2003-04-24

PRIOR APPLICATION NUMBER: US 10/131,831

PRIOR FILING DATE: 2002-04-24

PRIOR APPLICATION NUMBER: US 10/325,899

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 3117

SOFTWARE: PatentIn version 3.2

SEQ ID NO 453

LENGTH: 4156

TYPE: DNA

ORGANISM: Homo sapiens

US-10-511-937-453

Query Match

8.1%; Score 129.8; DB 6; Length 4156;

Best Local Similarity 70.0%; Pred. No. 7.7e-14;

Matches 219; Conservative 0; Mismatches 87; Indels 7; Gaps 3;

QY 1 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGTGAGGCCAGAGTTTC 60
|||
DB 2891 ACCTGTAATTCAGTACTGTGAGAGTCCGAGTGGGCTGTATCACTTGCAGTCAAGAGTTTC 2832
|||
QY 61 AAGAGAGCCTGGACAACAACAGGAGACC---TGTCCTACAAGATTAATTAATTAGC 117
|||
DB 2831 TAGACAGCCTGGACAACAAGTGAACCCCATCTTACTTAATAAACAACAAAATTTAGC 2772
|||
QY 118 CAGCTTAAGTGTCTATCTCTGTGTGTCCAGTACTAGGAGGCAAGATAGG---ACTG 174
|||
DB 2771 CGGGCATGTGTGTGATGCTGCTGTATCTCAGCTACTGAGAGGCTGAGGTGAAGATCG 2712
|||
QY 175 CTGTCCAGAGAGTCAAGACTGCAAGTGAAGTGAAGCCAGCAGCTGCACTTCAGCTG 234
|||
DB 2711 CTGACCCGAGAGGCGAGGCTGCAAGTGAAGCCGAGATTTGCCA-CTGCACCTCAGCTG 2653
|||
QY 235 GCAACAAAAGAGACCCCTGTCTCAAAAAATTAAGTTAATTAATTAATTAATA 294
|||
DB 2652 GCAACGAGAGAGACTCTCTCTCAAAAAAAGAAAAAAGAAAAAAGAAAAAGA 2593
|||
QY 295 TTAACCTTAAC 307
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DB 2592 AAAAAATCAATC 2580
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RESULT 7

US-10-505-928-433/C

Sequence 433, Application US/10505928

Publication No. US20060088532A1

GENERAL INFORMATION:

APPLICANT: Ludwig Institute for Cancer Research et al.

TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

FILE REFERENCE: 28967/39178

CURRENT APPLICATION NUMBER: US/10/505,928

CURRENT FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: US 60/363,019

PRIOR FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 866


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/ SEQ ID NO 1324
/ LENGTH: 2682
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-293-697-1324

Query Match      8.1%; Score 129.4; DB 7; Length 2682;
Best Local Similarity 71.1%; Pred. No. 8.8e-14;
Matches 214; Conservative 0; Mismatches 81; Indels 6; Gaps 3;

QY      2 CCTGTAAATCCAGTACTGTGAGAGTCCGAGGTCAGAGGACCTGTGAGGCCAGAGTTCA 61
DB      2090 CCTGTAAATCCAGCATTGTTGAGAGGCCAAGTGGTGATCACTTGAAGTCAGAGATTGG 2149
QY      62 AGAGCAGCCTGGAACAACAGAGGAGA-CCTGTCACTACAAAGATTAATTAATTAGCCAG 120
DB      2150 AGAGCAGCCTGCGCAACATGTTGAAACCCCGTCTTACTTAAATTAATTAATTAAGCCAG 2209
QY      121 GCTTAATGGCTCATCTCCTGTGCTCCAGCTACTAGAGGAGCAGAAAGTAGACTGCTTGT- 179
DB      2210 GTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2269
QY      180 ---CCAGAGAGTCAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 236
DB      2270 GAACCTGGAGAGGCGAGGCTTGCAGTGAAGCCAGACTGTGCCA-CTGTACTCCAGCCTGGG 2328
QY      237 CAACAAGAGAGAGCCTGTCTCAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 296
DB      2329 TGACAGAGGAGAGCGCTGTCTCAAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 2388
QY      297 A 297
DB      2389 A 2389

RESULT 11
US-11-318-813-42/c
/ Sequence 42, Application US/11318813
/ Publication No. US20060105381A1
/ GENERAL INFORMATION:
/ APPLICANT: Ellipsis Biotherapeutics Corporation
/ APPLICANT: Peltekova, Yanya D
/ APPLICANT: Stimovitch, Katherine A
/ APPLICANT: St George-Hyslop, Peter H
/ APPLICANT: Rubin, Laurence A
/ APPLICANT: Peltekova, Yanya D
/ APPLICANT: Winkle, Richard F
/ TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSOCIAT
/ TITLE OF INVENTION: INFLAMMATORY BOWEL DISORDERS
/ FILER REFERENCE: ELP-020
/ CURRENT APPLICATION NUMBER: US/11/318,813
/ CURRENT FILING DATE: 2005-12-27
/ PRIOR APPLICATION NUMBER: US/10/327,188
/ PRIOR FILING DATE: 2002-12-20
/ PRIOR APPLICATION NUMBER: 60/362,700
/ PRIOR FILING DATE: 2002-03-08
/ PRIOR APPLICATION NUMBER: 60/343,338
/ PRIOR FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 60/427,529
/ PRIOR FILING DATE: 2002-11-19
/ PRIOR APPLICATION NUMBER: 60/362,717
/ PRIOR FILING DATE: 2002-03-08
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 42
/ LENGTH: 54550
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (351)..(351)
/ OTHER INFORMATION: n can be a or t or g or c
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OTHER INFORMATION: n can be a or t or g or c
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OTHER INFORMATION: n can be a or t or g or c
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LOCATION: (5207)..(5207)
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LOCATION: (6668)..(6668)
OTHER INFORMATION: n can be a or t or g or c
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NAME/KEY: misc feature
LOCATION: (8656)..(8656)
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OTHER INFORMATION: n can be a or t or g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (9403)..(9403)
OTHER INFORMATION: n can be a or t or g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (9598)..(9598)
OTHER INFORMATION: n can be a or t or g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (10245)..(10245)
OTHER INFORMATION: n can be a or t or g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (10817)..(10817)
OTHER INFORMATION: n can be a or t or g or c
FEATURE:
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Query Match 8.0%; Score 128.6; DB 7; Length 54550;
Best Local Similarity 72.5%; Pred. No. 1,4e-13;
Matches 208; Conservative 0; Mismatches 74; Indels 5; Gaps 3;

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QY 1 ACCTGTAATCCAGTACTGTGAGAGTCCGAGGTCAGAGGACTGTTAGGCGCAGAGTTTC 60
|||||
DB 16700 ACCGTGTAATCCAGCACTTGGAGGCGGCGGGGTCACTGAGGTCAGAGAGTTTC 16641

QY 61 AAGAGCAGCCTGGAACAACAGGAGAG-CCTGTCACTACAAGAAATTAATTAGGCA 119
|||||
DB 16640 AAGACAGCCTGGGTAACAGTGTAACCTGTCTTACTTAATAATTAATTAGGCTG 16581

QY 120 GGCTTAGTGCTCATCTCTGTGTGTCGCCAGCTACTAGGAGGAGCAAGTAGGA--CTGCT 176
|||||
DB 16580 GGACAGGTGCAAGTGTCTTAACTCCAGCTAATTGGGAACCTGAGCAGAGAGAGTTGCT 16521

QY 177 TGTCCAGAGGTCAGAGTGCAGTGAAGTGAAGCCAGCCACTGATTCAGAGCTGGG 236
|||||
DB 16520 TGAGCCTGAGGTGAGGTGTCAGTGAATCAGATCACACA-CTGCACTTCAGAGCTGGG 16462

QY 237 CAACAAAAGAGACCCCTGTCAAAAATAAGTTAATAATAATA 283
|||||
DB 16461 CAACAAAAGAGACTCATCTCAACACAACAACAACAACAATA 16415
```

RESULT 12
US-11-293-697-1206/c
Sequence 1206, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1206
LENGTH: 3097
TYPE: DNA
ORGANISM: Homo sapiens
US-11-293-697-1206

Query Match 8.0%; Score 128.2; DB 7; Length 3097;
Best Local Similarity 72.5%; Pred. No. 1,4e-13;
Matches 208; Conservative 0; Mismatches 73; Indels 6; Gaps 3;

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QY 2 CCTGTATTCACGACTGTGAGAGTCCGAGGTCAGAGGACTGCTGAGGCGCAGAGTTCA 61
|||||
DB 2323 CCTGTATTCACGACTGTTGGAGGCCAAGGTGGCAGATCATCTTGGGCGCAGAGTTCA 2264

QY 62 AGAGCAGCCTGGAACAACAGGAGAG-CCTGTCACTACAAGAAATTAATTAGCCAG 120
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Query Match	7.9%	Score 127.2	DB 7	Length 2140
Best Local Similarity	70.5%	Pred. No. 2e-13		
Matches 213, Conservative	0	Mismatches 83	Indels 6	Gaps 3

OY	2	CCTGAAATTCAGATCTGTGAGAGTCCGAGGCTCAGAGACCTGTGAGGCCAGGATCTCA	61
Db	1834	CCTGAAATCCAGACTTTTGGAGGCTGAGCGGGCGAATTTCATGAGGCCAGAAATTGG	1775
OY	62	AGAGCAGCCTGGACAACA CAGGAGA - CCTGTCACTACAAAGAAATTAATTAATGACCG	120
Db	1774	AGACCAAGCCTGGCCAACATGTTGAACCTGTCTTACTAAACATACAAAATTTAGTGG	1715
OY	121	GCTTAGTGATCATCCCTGTGTGTCCAGCTACTAGGAGGAGAAATGATGACTGCTGT -	179
Db	1714	GCATGTGTGGACATGCTCTGTATCCAGCTATTCTGGAGGCTGAGGACAAGAAATTTGCTT	1655
OY	180	---CCAGAGAGTCAAGA CTGAGCTGAGACCCAGGCCACTGTCAATTCAGCTGGG	236
Db	1654	GAACCTCCAGAGAGGTGAGGTTGACAGTGAACCAAGATCATGSCA - CTACACTCCAGCTGGG	1586
OY	237	CAACAAAAGAAGACCTGTCTCAAAAATTAAGTTAAATTAATTAATTAATTAATTAATGTT	296
Db	1595	AGACAGAAAGAGATCTCCTCTGTAAACAAACAGAAAATCATTTAGAGAGAAAAATGAT	1536
OY	297	AA 298	
Db	1535	AA 1534	

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OM nucleic - nucleic search, using sw model

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Perfect score: 2270
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2238.8	98.6	39754	3	US-09-949-016-14689
2	2022.8	89.1	11808	3	US-09-949-016-15281
3	485	21.4	736	2	US-08-846-012A-1
4	485	21.4	736	2	US-09-100-297-1
5	170.4	7.5	601	3	US-09-949-016-176561
6	170.4	7.5	35493	3	US-09-949-016-15780
7	168.4	7.4	37292	3	US-09-949-016-15382
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17	163.8	7.2	601	3	US-09-949-016-63328
18	163	7.2	32594	3	US-09-949-016-12219
19	163	7.2	32658	3	US-09-949-016-15242
20	162.6	7.2	29171	3	US-09-949-016-12283
21	162.6	7.2	29171	3	US-09-949-016-13509
22	162.2	7.1	119981	3	US-09-949-016-11844
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24	161.8	7.1	601	3	US-09-949-016-16596

25	161.6	7.1	601	3	US-09-949-016-56159	Sequence 56159, A
26	161.6	7.1	94133	3	US-09-949-016-11901	Sequence 11901, A
27	161.6	7.1	94133	3	US-09-949-016-12713	Sequence 12713, A
28	161.6	7.1	94135	3	US-09-949-016-15934	Sequence 15934, A
29	161.6	7.1	94135	3	US-09-949-016-15935	Sequence 15935, A
30	161.6	7.1	94135	3	US-09-949-016-15936	Sequence 15936, A
31	161.6	7.1	94135	3	US-09-949-016-15937	Sequence 15937, A
32	161.4	7.1	17607	3	US-09-949-016-15968	Sequence 15968, A
33	161.2	7.1	56737	3	US-09-782-378A-17	Sequence 17, Appl
34	161	7.1	601	3	US-09-949-016-28523	Sequence 28523, A
35	161	7.1	601	3	US-09-949-016-60956	Sequence 60956, A
36	161	7.1	601	3	US-09-949-016-150302	Sequence 150302, A
37	160.8	7.1	52821	3	US-09-949-016-11857	Sequence 11857, A
38	160.8	7.1	52824	3	US-09-949-016-12116	Sequence 12116, A
39	160.6	7.1	8133	3	US-09-659-791A-10	Sequence 10, Appl
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43	160.4	7.1	55130	3	US-09-949-016-11850	Sequence 11850, A
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45	160	7.0	152583	3	US-09-949-016-17390	Sequence 17390, A

ALIGNMENTS

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RESULT 1
US-09-949-016-14689
; Sequence 14689, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01037
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14689
; LENGTH: 39754
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (39754)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14689
;
; Query Match          98.6%; Score 2238.8; DB 3; Length 39754;
; Best Local Similarity 99.8%; Pred. No. 0;
; Matches 2262; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
;
; 5 GATCGCCCGGCTCAGCTCCCAAGTCGTGAGTTGAGAGCGTGAAGCCTCACTCGG 64
; |||||
; 27669 GATCGCCCGGCTCAGCTCCCAAGTCGTGAGTTGAGAGCGTGAAGCCTCACTCGG 27748
; |||||
; 65 CTACAAGTTTCAAAATACATTTCATGATCCCATACATTCCTCAGTTTGTCCACAGGA 124
; |||||
; 27749 CTACAAGTTTCAAAATACATTTCATGATCCCATACATTCCTCAGTTTGTCCACAGGA 27807
; |||||
; 125 CATCTTATGACTTGAAGAGCTGTAAATAATCCAAAGGTGACAGCGTTGTATGTCTATAG 184
; |||||
; 27808 CATCTTATGACTTGAAGAGCTGTAAATAATCCAAAGGTGACAGCGTTGTATGTCTATAG 27867
; |||||
; 185 GATGCTGAGATTCGCCCGCCCAAGTGAAGATTTGAAGAAATTTCTTGAAGCCAGCGAC 244
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Db 27868 GATTGCTAGATCTGCCCCACCCCTGAAAAGATTTAAGAAATTTCTTGAGGCGAGCAC 27927
QY 245 AGTGCTCAACCTGTAAATTCAGTACTGTGAGATGCCAGAGTCAGAGACTGTCTTGAGG 304
Db 27928 AGTGCTCAACCTGTAAATTCAGTACTGTGAGATGCCAGAGACTGTCTTGAGG 27987
QY 305 CCAGAGGTTCAAGAGAGGCTGGACAACACAGGGAGACCTGTCACTACAAAGAAATAA 364
Db 27988 CCAGAGGTTCAAGAGAGGCTGGACAACATAGGGAGACCTGTCACTACAAAGAAATAA 28047
QY 365 AATTAGCCAGGCTTAAGTGTCTATCCCTGTGTGTCAGGCTACTAGGAGGAGAGAGTAG 424
Db 28048 AATTAGCCAGGCTTAAGTGTCTATCCCTGTGTGTCAGGCTACTAGGAGGAGAGAGTAG 28107
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Db 28108 ACTGCTTGTCCAGAGAGTCAAGACTGCAAGTGAAGTGAAGCCAGCCACTGTGATTCAG 28167
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Db 28168 CCTGGGCAACAAAAGAGACCTGTCTCAAAAATAAGTTAAATAATAATAATAA 28227
QY 545 TAGTTAAACCTTAAACACATCTTCTTTTCAAGAGAGACTTCTTAAGAGACTTCATG 604
Db 28228 TAGTTAAACCTTAAACACATCTTCTTTTCAAGAGAGACTTCTTAAGAGACTTCATG 28287
QY 605 CGTCTGTGTATCTCCACTTCCCTTTTTCAGGCTCCACACTTTTAACAGTCTTTTGCC 664
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QY 1145 CCTTCTGTGTGAGAAACATATAGGCGCGGCTGACCAAGGCTGTAATGTGTGATA 1204
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QY 1325 GGCTGTTCACGCATGATTAACCCCAACAGAGAGGAGTCAAGCAATTAAGAGCCGACAGGC 1384
Db 29008 GGCTGTTCACGCATGATTAACCCCAACAGAGAGGAGTCAAGCAATTAAGAGCCGACAGGC 29067
QY 1385 CCGGTTCATCTCTGACGCTTTTCTTCTATCCAGAGGCTGAGACAGGAGCTGAGCTGAGGC 1444
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QY 1445 CGGCTTGTCTTGTCAAGTGTGCGGAGGCGGAGGCTGCTTGTCTGTGTGTGTGTGTGT 1504
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QY 1565 AGGCGCTCCACCGGAGGAGAGAGGCGGAGACCCAGCCAGCCAGCCAGCTGTGTGTGT 1624
Db 29248 AGGCGCTCCACCGGAGGAGAGAGGCGGAGACCCAGCCAGCCAGCCAGCTGTGTGTGT 29307
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Db 29368 TAAACCAATGAGACAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCG 29427
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RESULT 2
US-09-949-016-15281
; Sequence 15281: Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 15281
LENGTH: 11808
TYPE: DNA
ORGANISM: Human
US-09-949-016-15281

Query Match 89.1%; Score 2022.8; DB 3; Length 11808;
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 2; Indels 1; Gaps 1;

Matches 2035; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 233 GAGGCGAGGACAGTGGCTCAACCTGTATTCAGTACTGTGAGAGTCCGAGGTCAAG 292
DB 1 GAGGCGAGGACAGTGGCTCAACCTGTATTCAGTACTGTGAGAGTCCGAGGTCAAG 60
QY 293 GACTGCTTGAAGCCAGAGATTCAAGAGAGCTTGAGCAACAAGAGAGAGCTGTCTAC 352
DB 61 GACTGCTTGAAGCCAGAGATTCAAGAGAGCTTGAGCAACAAGAGAGAGCTGTCTAC 120
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DB 181 GGCAGAGTAGAGTCTTGTCCAGAGAGTCAAGAGTCAAGTCAAGTCAAGTCAAGTCA 240
QY 473 CCTGATTCCAGCTGGGCAACAAAGAGAGCCCTGTCTCAAAAATTAAGTTAATAAT 532
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DB 1619 GTCTGTGCTGGAAGGCAAGAGGTGTGATGATGATGATGATGATGATGATGATGATG 1679
QY 1913 TTGCTATCTTCAAGAGAGTGTGGCGCGCGGAGAGAGTGTAGAGCAGAGCGGGAGTGA 1972
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QY 2033 GAGTGAAGAAAGTCAAGAGAGAACTTAGCGGGGCGGTCTCCCGGAAAGCGGCTGC 2092
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QY	2153	CCCGGGCCCCCGCCGAGGCTTAAAGCGCGCCGCGCTGCGGAGACCCCACTGGGAA	2212
Db	1920	CCCGGGCCCCCGCCGAGGCTTAAAGCGCGCCGCGCTGCGGAGACCCCACTGGGAA	1979
QY	2213	GCCCAGCTGCGGCGCGCTTTGGGATTGACGTTCACGCTCGCCGGCTGTGCGAGCGG	2270
Db	1980	GCCCACTGCGGCGCGCTTTGGGATTGACGTTCACGCTCGCCGGCTGTGCGAGCGG	2037

RESULT 3

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US-08-846-012A-1
Sequence 1, Application US/08846012A
Patent No. 5807740
GENERAL INFORMATION:
APPLICANT: AMARAL, M. Catherine.
APPLICANT: CHEN, Jin-Long
TITLE OF INVENTION: Regulators of UCP2 Gene Expression
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,012A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 736 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-846-012A-1

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Query Match	21.4%	Score 485;	DB 2;	Length 736;
Best Local Similarity	99.6%;	Pred. No. 3.5e-100;		
Matches 507;	Conservative 0;	Mismatches 0;	Indels 2;	Gaps 2;

QY	1782	GGGATGGGTAAGTTTGGCCAGCGTGAAGGGGGCGCTGGGGCCATTAAGAAGAAAGTGCACCTTAAG	1822
Db	1	GGGTGGGTAGTTTGGCCAGCGTGAAGGGGGCGCTGGGGCCATTAAGAAGAAAGTGCACCTTAAG	60
QY	1822	ACACGGCCCCCGCTGGAACGCTTGTTAAGAAACGCTCCGGCTGGGAAGCCAAAGAGTGTGTG	1882
Db	61	ACACGGCCCCCGCTGGAACG - TGTTAAGAAACGCTCCGGCTGGGAAGCCAAAGAGTGTGTG	119
QY	1882	ACTGACAAGACTTGTTTCTTGGCGGTCACTCTTGGCATCTTCACAGAAGTTGGCGGCCG	1941
Db	120	ACTGACAAGACTTGTTTCTTGGCGGTCACTCTTGGCATCTTCACAGAAGTTGGCGGCCG	179
QY	1942	AGAGAGTGTGAGGCGAAGCGCGGGGAGTGGCAAGGAGTGAACCATCTTCGGGCAACGAAAGA	2001
Db	180	AGAGAGTGTGAGGCGAAGCGCGGGGAGTGGCAAGGAGTGAACCATCTTCGGGCAACGAAAGA	239

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Db	240	GTAAACCGGGGATGGAGCGACCGAAACGGAGATGGAGAAAGTCATGAGAGAAACCTA	299
QY	2062	GGCGGGGCGGTCCCGCGGAAAGCGAGCTGCTCCAGAGTCTCCGACCCAAATGAGAGCT	2121
Db	300	GGCGGGGCGGTCCCGCGGAAAGCGAGCTGCTCCAGAGTCTCCGACCCAAATGAGAG-T	358
QY	2122	GGCAGGCCCCGGCCCCCGCCGACGCCCCCGGGCCCCCGCCCGAGGCTTAAACCG	2181
Db	359	GGCAGGCCCCGGCCCCCGCCGACGCCCCCGGGCCCCCGCCCGAGGCTTAAACCG	418
QY	2182	CGCGCGCGCTCGCGCGGAGCCCACTGCGAAGCCCACTGCGCGCGCTTGGATTGACT	2241
Db	419	CGCGCGCGCGTGGCGGAGCCCACTGCGAAGCCCACTGCGCGCGCTTGGATTGACT	478
QY	2242	GTCCACGCTGCGCGGCTCTGTCGACGCG	2270
Db	479	GTCCACGCTGCGCGGCTCTGTCGACGCG	507

RESULT 4

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US-09-100-297-1
: Sequence 1, Application US/09100297
: Patent No. 5849514
: GENERAL INFORMATION:
: APPLICANT: AMARAL, M. Catherine.
: APPLICANT: CHEN, Jin-Long
: TITLE OF INVENTION: Regulators of UCP2 Gene Expression
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
: STREET: 268 BUSH STREET, SUITE 3200
: CITY: SAN FRANCISCO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/100,297
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/846,012
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: OSMAN, RICHARD A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: T97-003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 343-4341
: TELEFAX: (415) 343-4342
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 736 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
US-09-100-297-1

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Query Match	21.4%	Score 485;	DB 2;	Length 736;
Best Local Similarity	99.6%	Pred. No. 3.5e-100;		
Matches 507; Conservative	0;	Mismatches	0;	Indels 2; Gaps 2;

Oy 1762 GGGTGGGTGATTTCGCCAGCGTAGGGGGGGCTGGGCCCATAAAAGAGGAAGTGCATTAAg 1821
 Db 1 GGGTGGGTGATTTCGCCAGCGTAGGGGGGGCTGGGCCCATAAAAGAGGAAGTGCATTAAg 60


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RESULT 7
US-09-949-016-15382/c
; Sequence 15382, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15382
; LENGTH: 37292
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(37292)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15382

Query Match          7.4%; Score 168.4; DB 3; Length 37292;
Best Local Similarity 63.2%; Pred. No. 5.2e-28;
Matches 345; Conservative 0; Mismatches 186; Indels 15; Gaps 5;

QY      5 GATTCGCCCGCTCAACCTTCCCAAAAGTCTGGATTGCGAGGTGAGCCACCTCACTTGG 64
DB      31797 GATTCGCCCGCTCGGCTCCCAAAAGTCTGGATTGCGAGGTGAGCCACCTCGG 31738
QY      65 CTACAGATTTTCAAAATATCATTTATCTAGTACCATACTTCCAGTTTGTTCACAGGA 124
DB      31737 C-----CCTAGACATAGGGGTTTCAATTCACAGCTTCCCGATGTTTGGGGGGT 31685
QY      125 CATCTTATGACTTGTAGCAAGCTGTAAATCCAAAGGGTGACGCTTTGTATGTCTAAG 184
DB      31684 TGCCTCAGAGGGCTGTCACTGGGGAAAGATGTAGAAATGATC-TCAGTCCCCCTTTC 31626
QY      185 GATGTCTAGATCTGCCCAACCTCGTAAAGAAATTTAAGAAATTTCTTGAAGCCAGGCAC 244
DB      31625 AAGTCCCTTCTATCTGGCTTCCCTATTTAGCACTTCTAAG--TCTTCAGGCTGGGCGT 31568
QY      245 AGTGGCTCACACCTGTAAATTCAGTACTGTAGAGTCCGAGGTCAAGGACTGCTTGAGG 304
DB      31567 GGTGGCTCATGCTTATATTCAGCAGCTTTGGAGGCTGAGGTGAGAAATTTGCTTGAG 31508
QY      305 CCAGAGATTCAAGAGCAGCTGTGACAAACAGAGGAGACCTGTCTACTACAAAGATTAATA 364
DB      31507 CCTGAGATTTCAGACAGCAGCTGGGCAACATTAAGAGACCTGTCTCTACAAAATTAATAA 31448
QY      365 AATTAGCCAGGCTTATGTGCTATCCCTGTGTCCAGCTACTAGGAGGAGGAGCAAGTAGG 424
DB      31447 AATGAGCCAGGATGTGTGTGCTGTGTGCTGTGCTCCAGCAACTCAGAGGCTGAGGTGG 31388
QY      425 A-----CTGCTTGTCCAGAGAGTCAAGACTGAGTGAAGCCAGCCACTTGCTATT 480
DB      31387 AGGACCGATTCAAGCTCGGAGGTAGAGGCTGAGTGGCCATGATTTGTGCCA-CTGCACT 31329
QY      481 CCAGCTGGGCAACAAAAGAGACCTGTCTCAAAAATTAAGTTAATAATAATAATAATA 540
DB      31328 CCAGCTGGGCAACAAAAGAGACCTGTCTCAAAAATTAAGTTAATAATAATAACTGAT 31269
QY      541 AAAATA 546
DB      31268 AAAATA 31263
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RESULT 8
US-09-949-016-16674/c
; Sequence 16674, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16674
; LENGTH: 126237
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16674

Query Match          7.4%; Score 167.4; DB 3; Length 126237;
Best Local Similarity 70.1%; Pred. No. 1.4e-27;
Matches 253; Conservative 0; Mismatches 106; Indels 2; Gaps 2;

QY      178 TCTATAGATTGCTCAGATCTGCCCCCAACCTGAAAGATTTTAAAGAAATTTCTGAGGC 237
DB      21667 TCTTTGAGAGATCAGGGGTGACCAAGCTATTATTCCTATTAAAGTAACATAGGC 21608
QY      238 CAGGCACAGTGGCTCAACCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTG 297
DB      21607 CAGGTGAGTGGCTCAACCTGTAAATTCAGCACTTTGGAGGCCAAGGCAGAGAGATCA 21548
QY      298 CTGAGGCGCAGAGTCAAGAGCAGCTGGAGCAACAGAGGAGA-CCTGTCACTCAAAAG 356
DB      21547 CATTGAGCCCGGAGTTTGACAGCTGGGCAACAGAGGAGCCCACTCTTCAAAAC 21488
QY      357 AATAAATAAATTAGCAGGCTTATGTGCTCATCCCTGTGTCCAGCTACTAGGAGAGCA 416
DB      21487 AAACAATAAATTAGCTGGCAGATGATGATGATGATGATGATGATGATGATGATGATG 21428
QY      417 GAATGAGACTGCTGTGCTCCAGAGGTCAAGACTGCAAGTGAAGTCAAGCCCACTG 476
DB      21427 GAGCAGAGACTGCTTGAAGCCCGAGGTCAAGACTGCTGTGAGCTGTGCTGCA-CTG 21369
QY      477 CATTCAAGCTGGGCAACAAAAGAGCCGTCTCAAAAATTAAGTTAATAATAATA 536
DB      21368 CACTACAGCTGGGTGACAGATGAGACCTGTCTTGGAAAAAACCACCAAC 21309
QY      537 A 537
DB      21308 A 21308

RESULT 9
US-09-949-016-16675/c
; Sequence 16675, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16675
LENGTH: 126237
TYPE: DNA
ORGANISM: Human
US-09-949-016-16675

Query Match
Best Local Similarity 7.4%; Score 167.4; DB 3; length 126237;
Matches 253; Conservative 0; Mismatches 106; Indels 2; Gaps 2;

QY 178 TCTATAGATTGCTCAGATCTGCCCCACCTGAAAGATTAAAGATTCTTGAGGC 237
DB 21667 TCCTTTGGAAGCATCAGGGTGACCAAGCTATTATTCCTATTAAAAAGTAACTAGGC 21608
QY 238 CAGGCACAGTGGCTCACAACCTGTATTTCAGTACTGTGAGAGTCCGAGTCAAGAGACTG 297
DB 21607 CAGGTGAGTGGCTCACAACCTGTATTTCAGTACTGTGAGAGTCCGAGTCAAGAGACTG 21548
QY 298 CTGAGGCCAGAGATTCAAGAGAGCTGAGCAACACAGAGGAGA-CCTGTCACTACAAAG 356
DB 21547 CATAGCCCGGAGATTGAGACCAAGTCTGGGCAACACAGGAGACCCCATCTTACAAAC 21488
QY 357 AATAAATAATTAATCCAGGCTTAAGTGTGCTATCCCTGTGTCCAGCTACTAGGAGGCA 416
DB 21487 AAAAATAAATTAATCTGGGCTATGATGATGCTGTGTGTCCAGCTATGTGGGAGCT 21428
QY 417 GAATAGACTGCTTTGCCAGAGGTCAACACTGCACTGAGTGAAGCCACCACTG 476
DB 21427 GAGCAGAGTCTGTGAGCTCGGAGGTCAAGACTGCTGTGAGTGAAGTGAAGTGAAGTGA 21369
QY 477 CATCCAGCTGGGCAACAAAAGAGACCTGTCTCAAAAATAAGTTAATAATAATAAT 536
DB 21368 CACTACAGCTGGGTGACAGAGTGAAGACCTGTCTGTGAAAAAACAACCAACCAAC 21309
QY 537 A 537
DB 21308 A 21308

RESULT 10
US-09-949-016-14788
Sequence 14788, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14788
LENGTH: 16230
TYPE: DNA
ORGANISM: Human
US-09-949-016-14788

Query Match
Best Local Similarity 7.4%; Score 167; DB 3; length 16230;
Matches 254; Conservative 0; Mismatches 85; Indels 6; Gaps 3;

QY 213 AGAATTTAAGGAATTTCTGAGCCAGGACAGTGGCTCACACCTGTATTTCCAGTACT 272
DB 11027 AGAATTTAAGGAATTTCTGATTAACCTGGCAGGACAGTGGCTCACACCTGTATTTCCAGTACT 11086
QY 273 GTGAGATCCGAGGTCAAGAGACTGCTTGAGCCAGGAGTTCAAGAGAGCCTGGAGAC 332
DB 11087 TTGGAGGCCAGGACAGAGAGATCACTTGACACTAGAGTTTGAGATAGCCTGGAGAC 11146
QY 333 ACAGGAGA-CCTGTCACTACAAAGAAATAATAATTAGCCAGGCTTAGTGGCTATCC 391
DB 11147 ATGTGAGACCCCTGTCTACAGAAAATTTAAATTTAGCCACTTGTGTGCTCATGCC 11206
QY 392 TGTGTCTCCAGCTACTGAGGAGCAGAAAGTGA-CTGCTTGTCCAGAGAGTCAAG 447
DB 11207 TGTGTCTCCAGCTACTGAGGAGGCTGAAGTGGAGATCACTTGAAGCCAGAGAGTCAAG 11266
QY 448 ACTGAGTGAAGTGAAGCCAGGACCTGATTCAGACCTGGGCAACAAAAGAGACCT 507
DB 11267 GCTGAGTGAAGTGTGATGACCA-CTGCACTTCCAGCTTGGGTGAGACAGACAGACCT 11325
QY 508 GTCTCAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 552
DB 11326 GTTCAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 11370

RESULT 11
US-09-949-016-12816
Sequence 12816, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12816
LENGTH: 99370
TYPE: DNA
ORGANISM: Human
US-09-949-016-12816

Query Match
Best Local Similarity 7.3%; Score 165.2; DB 3; length 99370;
Matches 240; Conservative 0; Mismatches 83; Indels 5; Gaps 2;

QY 223 AGAATTTCTGAGGCCAGGACAGTGGCTCAACCTGTATTTCCAGTACTGTGAGTCC 282
DB 66639 ATAATTTGACAGGCCAGGTGACAGTGGCTCACAAGTATTTCCAACTTTGGAGGCC 66698
QY 283 GAGGTGAGAGTCTGTTGAGGCCAGGAGTTCAAGAGAGCCTGGAGCAACAGAGAGA- 341
DB 66699 AAGGTGAGAGATCACTTAAGTCCAGAGAGTTCAAGAGAGCCTGGAGCAACAGAGAGA 66758
QY 342 CTTGTCACTACAAAGAAATAATAATTAGCCAGGCTTAGTGGCTCATCCCTGTGCTCCA 401
DB 66759 CTTGTCTCTCAATAATAATAATAATAATTAGCCAGGAGTGTGCTTAGCTGTGCTCCA 66818
QY 402 GCTACTAGGAGGAGAGAGTGA-CTGCTTGTCCAGAGAGTCAAGAGTCAAGAGTGA 457
DB 66819 GCTACTAGGAGGAGTGTGAGAGATCACTTGAACCCAGAGAGAGAGAGTGA 66878
QY 458 GCTGAGACCCAGCAGCTGATTCAGCCTGGGCAACAAAAGAGACCTGTCTCAAAA 517
DB 66879 GCTGAGATCATGCCACTGCACTGTAGCTTGGGGAACAGAGCAAGACCTGTCTCAAAA 66938

Qy 518 ATAGTAAATAATAATAATAAT 545
Db 66939 AAAAAAAAAAACCAACCCCAAT 66966

RESULT 12

US-09-949-016-17540
; Sequence 17540, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 17540
; LENGTH: 99370
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17540

Query Match

Best Local Similarity 7.3%; Score 165.2; DB 3; Length 99370;
Matches 240; Conservative 0; Mismatches 83; Indels 5; Gaps 2;

Qy 223 AGAATTTCTTGGAGCCAGGACAGTGGCTCAGACCTGTAATTCAGTCTGTGAGATCC 282
Db 66639 AATATTTGACAGGCGAGGTGAGTGGCTCAGACCTGTAATTCAGTCTGTGAGAGGCC 66698
Qy 283 GAGGTCAAGGAGCTGTTGAGGCCAGAGATTCAAGAGAGCCTGAGCAACACAGGAGAG- 341
Db 66699 AAGGTGGAGGATCATCATAGTCCAGAGATTCAAGAGAGCCTGAGCAACACAGGAGAGC 66758
Qy 342 CCTGCTACTACAAAGATTAATAATTAGCCAGGCTTAAGTGGCTCATCCCTGTGTCCTCA 401
Db 66739 CCTGCTCTACAAATAATACAAATAATTAGCCAGGAGTGTGCTTATGCTGTGTCCTCA 66818
Qy 402 GCTACTAGGAGGAGCAAGATGAGA---CTGCTTGTCCAGAGAGTCAAGACTGAGTGA 457
Db 66819 GCTACTCAGAGAGGTGAGGTGAGGATGATCACTTGAACCCAGAGAGAGGTTGAGTGA 66878
Qy 458 GGTGAGACCCAGCCAGCTGCTGATTCAGAGCTTGGGCAACAAAAGAGACCTGTCTCAAAA 517
Db 66879 GGTGAGATCATGCTCCAGCTCTAGCTTGGGGAACAGAGCAACCTGTCTCAAAA 66938
Qy 518 ATAGTAAATAATAATAATAATAAT 545
Db 66939 AAAAAAAAAAACCAACCCCAAT 66966

RESULT 13

US-09-949-016-27232/c
; Sequence 27232, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 27232
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-27232

Query Match

Best Local Similarity 7.2%; Score 164.2; DB 3; Length 601;
Matches 330; Conservative 1; Mismatches 214; Indels 8; Gaps 3;

Qy 6 ATTCGCCGCTCAGCTTCCCAAGTGTGGATTGACAGGGTGAAGCCACTCAGCTGAC 65
Db 588 ATTCGCTGCTCAGCTCAGCAAGTGTGACATTAACAGGACAGGACCTGTCAGAGC 529
Qy 66 TACAAAT---TTTCAAAATACATTTATAGTACCCATACATCTCCAGTTGTCCACAG 122
Db 528 CCTCATGACTTTTAAAAAACAATTAAAGAAATGAACCTTGTAAATAGTAAAAATG 469
Qy 123 GACATCTATGACTTGACCAAGCTGCTAAATATCCAAAGGTGACAGCTTGTATGTAT 182
Db 468 GACGAATTTTGAATTAATATGATTCATTAATTAAGAACAGTATTTGATGATGTAT 409
Qy 183 AGGATTGCTCAGATCTGCCCCCAGCCCTGAAGAAATTTAAGAAATTTCTTGAAGCCAGGC 242
Db 408 TCAATAGTATTTCTTACCATATGAAATTAATTTTAAATTTATTTATTTCTGCCCAGGC 349
Qy 243 ACAGTGGCTCACCTGTATATTCAGTACTGTGAGAGTCCAGAGTCAAGAGCTGCTTGA 302
Db 348 ACGGTGCTCATGCTGTAAATCCAGCACTTGAGGAGCCAGAGGAGTGAATCACTTGA 289
Qy 303 GGCAGGATTCAGAGAGCCTGAGCAACACAGAGAGACCTGTACTACAAAGATTA 362
Db 288 GGTCAAGATTCAGAGAGCCTGTATCAACATGAACAAACCCATCTACTAATAATATC 229
Qy 363 TAAATTAAGCAGCTTATGCTCATCCCTGTGTGCTCCAGTACTAGGAGGAGAGTA 422
Db 228 AAAATTAAGCGGGGCTGTGTGAGCATGTCTGTAAATCCAGTACTTGGAGGCTGAGGCA 169
Qy 423 GGA---CTGCTTGTCCAGAGGCTCAAGCTGAGTGAAGTGAAGCCAGCA---CTGC 477
Db 168 GGAAGATGCTTGAACCGGGAGGCGAGGTTGAGTGAAGTGAAGTGAAGTGAAGTGA 109
Qy 478 ATTCAGCCTGGGCAACAAAGAGACCTGTCTCAAAAATAAGTTAAATAATAATA 537
Db 108 ACTCAGCCTGGGCAACAGAGCAAGAACTCCATCTCAAAAAATAATAATAATAATA 49
Qy 538 ATAAATAATGTTT 550
Db 48 TTCTGAATATATGT 36

RESULT 14

US-09-949-016-160756/c
; Sequence 160756, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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OM nucleic - nucleic search, using sw model

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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:

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- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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- 7: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	846.8	37.3	9314	6	US-10-197-019-1 Sequence 1, Appl1
2	550.6	24.3	562	4	US-09-925-065A-566754 Sequence 566754
3	531.6	23.4	554	4	US-09-925-065A-177131 Sequence 177131
4	447.4	19.7	1161	6	US-10-265-689-27 Sequence 27, Appl1
5	364.2	16.0	5283	6	US-10-311-455-1865 Sequence 1865, Ap
6	312.4	13.8	5283	6	US-10-311-455-1866 Sequence 1866, Ap
7	188.4	8.3	44348	7	US-10-301-832-11 Sequence 11, Appl
8	175	7.7	160556	8	US-10-719-993-6827 Sequence 6827, Ap
9	172.8	7.6	11172	3	US-09-764-878-231 Sequence 231, App
10	172.8	7.6	11172	5	US-10-079-854-231 Sequence 231, App
11	168	7.4	563	4	US-09-925-065A-770821 Sequence 770821, Ap
12	167.2	7.4	135005	8	US-10-723-860-2320 Sequence 2320, Ap
13	167.2	7.4	135005	9	US-10-756-149-1719 Sequence 1719, Ap
14	166.8	7.3	3030	5	US-10-027-632-115210 Sequence 115210, Ap
15	166.8	7.3	3030	5	US-10-027-632-115211 Sequence 115211, Ap
16	166.8	7.3	3030	5	US-10-027-632-115210 Sequence 115210, Ap
17	166.8	7.3	3030	6	US-10-027-632-115211 Sequence 115211, Ap
18	166.6	7.3	52242	7	US-10-052-482-172 Sequence 172, App
19	166	7.3	1614	4	US-09-925-065A-551304 Sequence 551304, A
20	165.6	7.3	1187	4	US-09-925-065A-71294 Sequence 71294, A
21	165.6	7.3	1187	4	US-09-925-065A-71295 Sequence 71295, A
22	164	7.2	1369	5	US-10-027-632-86881 Sequence 86881, A
23	164	7.2	1369	5	US-10-027-632-178961 Sequence 178961, A

ALIGNMENTS

24	164	7.2	1369	6	US-10-027-632-86881 Sequence 86881, A
25	164	7.2	1369	6	US-10-027-632-178961 Sequence 178961, A
26	164	7.2	186510	6	US-10-043-715-1 Sequence 1, Appl1
27	163.4	7.2	558	4	US-09-925-065A-822292 Sequence 822292, A
28	163.4	7.2	558	4	US-09-925-065A-839930 Sequence 839930, A
29	163.2	7.2	561515	8	US-10-741-600-5682 Sequence 5682, Ap
30	163.2	7.2	561515	8	US-10-741-600-17730 Sequence 17730, A
31	162.6	7.2	81099	5	US-10-087-192-1756 Sequence 1756, Ap
32	161.8	7.1	109906	5	US-10-235-192A-31 Sequence 31, Appl
33	161.4	7.1	383432	9	US-10-737-082-34 Sequence 34, Appl
34	161.4	7.1	383432	9	US-10-765-790-34 Sequence 34, Appl
35	161.2	7.1	56737	3	US-09-782-378A-17 Sequence 17, Appl
36	160.8	7.1	60815	5	US-10-087-132-52 Sequence 52, Appl
37	160.6	7.1	599	4	US-09-925-065A-875725 Sequence 875725, A
38	160.6	7.1	599	4	US-09-925-065A-905153 Sequence 905153, A
39	160.6	7.1	7739	6	US-09-764-877-3189 Sequence 3189, Ap
40	160.6	7.1	7739	6	US-10-242-515-3189 Sequence 3189, Ap
41	160.6	7.1	8133	7	US-10-380-124-10 Sequence 10, Appl
42	160.4	7.1	87467	7	US-10-741-600-5634 Sequence 5634, Ap
43	160.4	7.1	87467	8	US-10-741-600-17624 Sequence 17624, A
44	160.4	7.1	136436	9	US-10-756-149-3773 Sequence 3773, Ap
45	160.2	7.1	492	5	US-10-027-632-84916 Sequence 84916, A

RESULT 1
US-10-197-019-1
Sequence 1, Application US/10197019
Publication No. US20030207284A1

GENERAL INFORMATION:
APPLICANT: Chew, Anne

APPLICANT: Denton, R. Rex
APPLICANT: Gilson, Christopher Raleigh

APPLICANT: Nandabalan, Krishnan

APPLICANT: Parks, Katie E.
TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE

FILE REFERENCE: MMH-004205
CURRENT APPLICATION NUMBER: US/10/197,019

CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: PCT/US01/02485

PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 116

SOFTWARE: PatentIn version 3.1
SEQ ID NO 1

LENGTH: 9314
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: allele
LOCATION: (1283)..
OTHER INFORMATION: P81: polymorphic base cytosine or guanine

NAME/KEY: allele
LOCATION: (1714)..
OTHER INFORMATION: P82: polymorphic base cytosine or thymine

NAME/KEY: allele
LOCATION: (2051)..
OTHER INFORMATION: P83: polymorphic base thymine or cytosine

NAME/KEY: allele
LOCATION: (2124)..
OTHER INFORMATION: P84: polymorphic base cytosine or thymine

NAME/KEY: allele
LOCATION: (2287)..
OTHER INFORMATION: P85: polymorphic base cytosine or guanine

NAME/KEY: allele
LOCATION: (2408)..
OTHER INFORMATION: P86: polymorphic base adenine or guanine

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1 FEATURE:
2 NAME/KEY: allele
3 LOCATION: (4768)..(4768)
4 OTHER INFORMATION: PS7: polymorphic base adenine or guanine
5 FEATURE:
6 NAME/KEY: allele
7 LOCATION: (4785)..(4785)
8 OTHER INFORMATION: PS8: polymorphic base guanine or adenine
9 FEATURE:
10 NAME/KEY: allele
11 LOCATION: (4813)..(4813)
12 OTHER INFORMATION: PS9: polymorphic base thymine or cytosine
13 FEATURE:
14 NAME/KEY: allele
15 LOCATION: (4882)..(4882)
16 OTHER INFORMATION: PS10: polymorphic base adenine or cytosine
17 FEATURE:
18 NAME/KEY: allele
19 LOCATION: (4976)..(4976)
20 OTHER INFORMATION: PS11: polymorphic base thymine or adenine
21 FEATURE:
22 NAME/KEY: allele
23 LOCATION: (5600)..(5600)
24 OTHER INFORMATION: PS12: polymorphic base cytosine or thymine
25 FEATURE:
26 NAME/KEY: allele
27 LOCATION: (5820)..(5820)
28 OTHER INFORMATION: PS13: polymorphic base thymine or guanine
29 FEATURE:
30 NAME/KEY: allele
31 LOCATION: (6536)..(6536)
32 OTHER INFORMATION: PS14: polymorphic base thymine or adenine
33 FEATURE:
34 NAME/KEY: allele
35 LOCATION: (6607)..(6607)
36 OTHER INFORMATION: PS15: polymorphic base guanine or adenine
37 FEATURE:
38 NAME/KEY: allele
39 LOCATION: (6617)..(6617)
40 OTHER INFORMATION: PS16: polymorphic base cytosine or thymine
41 FEATURE:
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43 LOCATION: (6872)..(6872)
44 OTHER INFORMATION: PS17: polymorphic base cytosine or guanine
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47 LOCATION: (6966)..(6966)
48 OTHER INFORMATION: PS18: polymorphic base guanine or adenine
49 FEATURE:
50 NAME/KEY: allele
51 LOCATION: (7036)..(7036)
52 OTHER INFORMATION: PS19: polymorphic base cytosine or thymine
53 FEATURE:
54 NAME/KEY: allele
55 LOCATION: (7086)..(7086)
56 OTHER INFORMATION: PS20: polymorphic base adenine or guanine
57 FEATURE:
58 NAME/KEY: allele
59 LOCATION: (8100)..(8100)
60 OTHER INFORMATION: PS21: polymorphic base cytosine or thymine
61 FEATURE:
62 NAME/KEY: allele
63 LOCATION: (8221)..(8221)
64 OTHER INFORMATION: PS22: polymorphic base guanine or adenine
65 FEATURE:
66 NAME/KEY: allele
67 LOCATION: (8677)..(8677)
68 OTHER INFORMATION: PS23: polymorphic base thymine or adenine
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Query Match	37.3%	Score 846.8;	DB 6;	Length 9314;
Best Local Similarity	98.9%	Pred. No. 2e-204;		
Matches 874; Conservative	0;	Mismatches 7;	Indels 3;	Gaps 2;

[illegible]

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RESULT 2
US-09-925-065A-566754
; Sequence 566754, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08

```



```
APPLICANT: RICOIER, DANIEL
APPLICANT: BOULLAUD, FREDERIC
TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
FILE REFERENCE: 1579-376
CURRENT APPLICATION NUMBER: US/10/265,689
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: US/09/353,645
PRIOR FILING DATE: 1999-07-15
PRIOR APPLICATION NUMBER: PCT/US97/06864
PRIOR FILING DATE: 1997-04-22
PRIOR APPLICATION NUMBER: 60/034,960
PRIOR FILING DATE: 1997-01-15
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 1161
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: "n" bases may be a, t, c, g, modified or unknown
US-10-265-689-27
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Query Match      19.7%; Score 447.4; DB 6; Length 1161;
Best Local Similarity 94.9%; Pred. No. 3.9e-103;
Matches 516; Conservative 0; Mismatches 22; Indels 6; Gaps 5;

QY 1733 AGAGCGACCCGCGCTCGCTCGAGAGAGGTGGTATTGTCACAGCT--AGGGGGG 1790
DB 2 AAGAACCCAGCGCGCTTGTGTCAGAGGTTGTTATTTGCCAGGGGTAAAGGGGG 61
QY 1791 CTGGGCGCATTAAGAGAGAGTGTC-ACCTTAAGACACAGCGCCCGCTGAGCGCTTTGTTAGA 1849
DB 62 CTGGGCGCATTAAGAGAGAGTGTC-ACCTTAAGACACAGCGCCCGCTGAGCGCTTTGTTAGA 121
QY 1850 ACCGTCCT-GGCTGGAGAGCGCAAGAGTGTGTGACTGCAACAAGCTTTGTTCT-GGCGGT 1907
DB 122 ACCCTTCCTGGTGGGAGAGCAAGAGTGTGTGACTGCAACAAGATTGTTCTGGGCGGT 181
QY 1908 CAGTCTTGTCATCTTCACAGAGGTGGCGCGCCGAGAGAGTGTGAGAGCGAGAGCGGGGAG 1967
DB 182 CAGTCTTGTCATCTTCACAGAGGTGGCGCGCCGAGAGAGTGTGAGAGCGAGAGCGGGGAG 241
QY 1968 TGGCAAGAGAGTGACCATCTCGGGGAAAGAGAGTAAACGCGGTGATGGAGCGACAG- 2026
DB 242 TGGCAAGAGAGTGACCATCTCGGGGAAAGAGAGTAAACGCGGTGATGGAGCGACAG- 301
QY 2027 AAACGGAGTGAGAAAGTCAATGAGAGAAACCTTAGCGCGGGCGTCCCGCGGAAAGGC 2086
DB 302 AAACGGAGTGAGAAAGTCAATGAGAGAAACCTTAGCGCGGGCGTCCCGCGGAAAGGC 361
QY 2087 GGCTGCTCAGAGGTCTCCGACCCAGTAGTAGAGCTGGAGGCGCGCGCCCGCGCCGACAG 2146
DB 362 GGCTGCTCAGAGGTCTCCGACCCAGTAGTAGAGCTGGAGGCGCGCGCCCGCGCCGACAG 421
QY 2147 CCCCAACCCCGGCGCCCGCGCGCTTAAGCCGCGCGCGCGCTGCGCGAGCCCAAC 2206
DB 422 CCCCAACCCCGGCGCCCGCGCGCTTAAGCCGCGCGCGCGCTGCGCGAGCCCAAC 481
QY 2207 TGGGAAGCCAGCTGCGCGCGCTTGGAGTTGACTGTCCACGCTGCGCGCGCTGTCGCA 2266
DB 482 TGGGAAGCCAGCTGCGCGCGCTTGGAGTTGACTGTCCACGCTGCGCGCGCTGTCGCA 541
QY 2267 CGCG 2270
DB 542 CGCG 545
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RESULT 5
US-10-311-455-1865
Sequence 1865, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
```

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APPLICANT: PIERPENROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1865
LENGTH: 5283
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1865
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Query Match      16.0%; Score 364.2; DB 6; Length 5283;
Best Local Similarity 77.4%; Pred. No. 1.3e-81;
Matches 467; Conservative 0; Mismatches 133; Indels 3; Gaps 2;

QY 1668 CGACAAACCGCGCGGTGTAAACCAATCGACAGAGCCGTCGCGAGGCCCAAGTCCCGC 1727
DB 2 CGATACCCGCGCGGTGTAAATTAATCAATCGATAGAGAGTGTGCGCAAGTATTAGTTTGT 61
QY 1728 CCGCAGAGAGCGAGCGCGCTCGCTCGAGAGAGGTGGTATTGTCACAGCGCTAGAGG 1787
DB 62 TTTGTAGAGAGTAAAGAGAGAGTGTGCTGCTGAGAGAGGTGGTATTGTTAGGCTA-GG 120
QY 1788 GGGCTGGGCCCATTAAGAGAGAGTGTCACTTAAGACACAGCGCCCGCTGAGCGCTTGTAG 1847
DB 121 GGGTGGGTATTAAAGAGAGAGTGTATTAAAGATAGCGTTTAA--TGAACGTGTAG 178
QY 1848 AACCGTCTGCTGTGGAGAGCAAGAGTGTGTGACTGGAACAAGCTTTGTTCTGGCGGT 1907
DB 179 AATGTGTTGTGTGGAGAGTAAAGAGTGTGTGATTAAGATTGTTGTTGTTGTTGTTGTTG 238
QY 1908 CAGTCTTGTCATCTTCACAGAGTGTGGCGCGCCGAGAGAGTGTGAGAGAGCGGGAG 1967
DB 239 TAGTTTGTATTTTAAAGAGTGTGGCGGTTTGAAGAGTGTGAGAGAGCGGGAG 298
QY 1968 TGGCAAGAGAGTGACCATCTCGGGGAAAGAGAGTAAACGCGGTGATGGAGCGACAG- 2027
DB 239 TGGTAAGAGAGTGAATTAATTCGGGGAGCAAGAGTAAACGCGGTGATGGAGCGACAG- 358
QY 2028 AACGGAGTGAGAAAGTCAATGAGAGAAACCTTAGCGCGGGCGTCCCGCGGAAAGGC 2087
DB 359 AACGGAGTGAGAAAGTCAATGAGAGAAATTTTAAGCGGGGCGGTTTTCGCGAAAGGC 418
QY 2088 GCTGCTCAGAGGTCTCCGACCCAGTAGTAGAGCTGGAGGCGCGCGCCCGCGCCGACAG 2147
DB 419 GTTGTTTAAGGTTTTCGATTTAAGTAGAGTGTGATGAGTTGCGGTTTTCGTTGAGGT 478
QY 2148 CCCACCCCGGCGCCCGCGCGCTTAAGCCGCGCGCGCGCTGCGCGAGCCCACT 2207
DB 479 TTTAATTTGCGGTTTGTGTTTTCGAGGTTTAAGTGTGCGTGTCTTTGCGGAGTTTAT 538
QY 2208 GCGAAGCCAGCTGCGCGCGCTTGGAGTTGACTGTCCACGCTGCGCGCGCTGTCGCA 2267
DB 539 GCGAAGTTAGTGTGCGCGGTTTGGAGTGAATGTTTAAAGTTTAAAGTTTAAAGTTTAA 598
QY 2268 GCG 2270
DB 599 GCG 601
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RESULT 6
US-10-311-455-1866/c
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Db 8510 AGGATAAATTATAGATATAGTATATATAGATTTTCTGTGTACTATAGAGACGTT 8451
Qy 181 ATAGATTGCTAGATCTGCCCCCACCCTGAAAGATTTTAAAGAAATTTCTTGAAGCCAG 240
Db 8450 TCCCTCAGACAAAGATGATATAAATTTGGGTTTTCTTTTAAAGATAGGACCTGCGAG 8391
Qy 241 GCACAGTGGCTCAGACCTGTATATTCAGACTGTGAGAGTCCGAGAGTCAAGACCTGCTT 300
Db 8390 GCACAGTGGCTCAGACCTGTATATTCAGACTGTGAGAGTCCGAGAGTGGGTGAGACCT 8331
Qy 301 GAGGACAGAGTTCAGAGCAGCCTGACCAACAGAGGAGA-CCTGTCACTCAAAAGAT 359
Db 8330 GAGGTCAAGAGTTCAGAGCAGCCTGACCAATATGTATAAACCACATCTTACTATAAAT 8271
Qy 360 AAATTAATTAAGCAGGCTTATGTGCTCATCCTGTGTGCCAGTACTAGAGGACAGAA 419
Db 8270 ACAAATAATTAAGCAGGCTGCGGTGGCTACCTGTATGTCCAGTACTAGAGGCTGAG 8211
Qy 420 GTAGAGCTGCTTGTCCAGAGAGTGA-AGACTGCACTAGAGTGAACCCAGCCTGCA 478
Db 8210 ACAGATTTGCTTGAACCGGAAAGCAGAGTTTACAGTTCAGATTTGTGCTGCTGAC 8151
Qy 479 TTCCAGCTGGGCAAAAGAGAGACCTGTCTCAAAAAATTAATTAATTAATTAATTA 538
Db 8150 TCCAGCTAGGTGTGAGACAGAGTGAAGTCTTCTCAAAAAATTAATTAATTAATTAATTA 8091
Qy 539 TAAAAATGTTAAACCTTAACACATCTTCTTTT 574
Db 8090 AAAAAAGTAGGACCATGACTTATATATTTGT 8055

RESULT 11

US-09-925-065A-770821/c
; Sequence 770821, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770821
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-770821

Query Match 7.4%; Score 168; DB 4; Length 563;
Best Local Similarity 74.6%; Pred. No. 4.1e-32;
Matches 252; Conservative 0; Mismatches 80; Indels 6; Gaps 3;

Qy 218 TTAAGAGATTTCTTGAAGCCAGGACAGTGGCTCAGACCTGTATATTCAGTACTGTAG 277
Db 493 TTCAAGCATATCTTGAAGCCAGGACAGTGGCTCAGACCTGTATATTCAGTACTGTAG 434
Qy 278 AGTCCAGAGTCAAGAGACTGCTTGAAGCCAGGAGTTCAGAGCAGCCTGAGCAACACAGG 337
Db 433 AGGTCAAGGTGGGTGATCCTTGAAGCCAGGAGTTCAGAGCAGCCTGAGCAACATGAT 374
Qy 338 GAGACCTGTCACTAACAAGATTAATTAATTAAGCAGGCTTATGTGCTCATCCCTGTGT 397

Db 373 GAAACTGTCTCTATTTAAAAATACAAAAATTAAGCCGGCATGTGGGCAATGCTGTAT 314
Qy 398 CCCAGCTACTAGGAGGAGAGAGTGAAGTCTGTGT-----CCAGAGAGTCAAGACTCA 453
Db 313 CCCAGCTACTAGGAGGAGTGAAGTCTGTGTGTGAATTCCTTAACCCAGAGAGGAGGTTGCA 254
Qy 454 GTAGAGTGAAGCCAGCAGCCTGCAATTCAGCCTGGGCAAAAAAGAGACCTGTCTC 512
Db 253 GTGAGCTGAGATTGGCCA-TTGCAACAAGCCTGGGTGAGAGCAAGACTGTCTCA 195
Qy 513 AAAAAATAGTTAATAATTAATTAATTAATTAATTTT 550
Db 194 AAAAAAATAATTAATTAATTAATTAATTAATTTCTCT 157

RESULT 12

US-10-723-860-2320/c
; Sequence 2320, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2320
; LENGTH: 135005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2320

Query Match 7.4%; Score 167.2; DB 8; Length 135005;
Best Local Similarity 80.3%; Pred. No. 9.3e-31;
Matches 233; Conservative 0; Mismatches 53; Indels 4; Gaps 3;

Qy 235 GGCAGGACAGTGGCTTCAACCTGTATATTCAGTACTGTGAGTCCGAGTCAAGAGA 294
Db 84840 GGCCTGACACAGTGGCTTCAACCTGTATATTCAGTACTGTGAGTCCGAGTCAAGAGA 84781
Qy 295 CTGCTTGAAGCCAGAGTTCAGAGCAGCCTGGCAACACAGGAGA--CCTGTCACTAC 352
Db 84780 TTGCTTGAAGCCAGAGTTCAGAGCAGCCTGGCAACATAGTAGAGCCCTGTCTTAC 84721
Qy 353 AAGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 412
Db 84720 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 84661
Qy 413 GGCAGAGTGAAGTCTGCTTGC-TCCAGAGGTCAAGACTGAGTGAAGTGAAGCCAGCC 471
Db 84660 GGCTGAGGTGAAGTCTGCTTGCAGAGAGGTGAGAGGCGGAGTGAAGTGAAGTGAAGTCC 84601
Qy 472 ACCGTCAATTCAGGCTGGGCAAAAAAGAGACCTGTCTCAAAAAATTA 521
Db 84600 A-CTGTACTCAACCTGGCAAGAAAGAGACCTGTCTCAAAAAAAA 84552

RESULT 13
US-10-756-149-1719/c
; Sequence 1719, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS &
; METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER


```
; Sequence 1866, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecting
; TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1866
; LENGTH: 5283
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1866

Query Match      13.8%; Score 312.4; DB 6; Length 5283;
Best Local Similarity 72.0%; Pred. No. 2e-68;
Matches 435; Conservative 0; Mismatches 166; Indels 3; Gaps 2;

OY 1667 CGACAAAGGGGGGCTGTAAACCATCGACAGCGGCGCGGTGGAGGCCCCCACTCCCG 1726
DB 5283 CGACAAAGCGACGACTTAACCAATCAACAGCAACGAAACCGATCGGAAACCCCAATCCCG 5224
OY 1727 CCTGCGAGAGCGACGCGCGCGCTGCTGCGAGAGGGTGGGTATTTGCCAGCGTAGG 1786
DB 5223 CCTGCGAGAGCGACGCGCGCGCTGCTGCGAGAGGGTGGGTATTTGCCAGCGTAGG-A 5165
OY 1787 GGGGCTGGGCCCCATTAAGAGAGAGTCACTTAAGACACGCGCCCGCTGACGCTTTGTTA 1846
DB 5164 AAAACTAAACCCATTAACCACTTAACCACTTAACCACTTAACCACTTAACCACTTA 5107
OY 1847 GAAACCGGCTGCGCGGGAAGCAAGAGTGTGACGACGACCAACTTTGTTCTGGGGG 1906
DB 5106 AAAACCGGCTGCGCGGGAAGCAAGAGTGTGACGACGACCAACTTTGTTCTGGGGG 5047
OY 1907 TCACTCTTGCATCTCTCAAGAGGTTGGCGCGCGAGAGTGTGAGGAGAGCGGGGA 1966
DB 5046 TCACTCTTGCATCTCTCAAGAGGTTGGCGCGCGAGAGTGTGAGGAGAGCGGGGA 4987
OY 1967 GTGCGAAGGAGTGCATCTCTGGGGAAGCAAGAGTAAACGCGGTGATGGAGCGCAGG 2026
DB 4986 ATAAACAAATAATTAACATCTCGAATAACGAAATAATTAACGCGGTGATTAACGCGCAG 4927
OY 2027 AAAGGAGGTGGAATAATCAATGAGAGAACCTTAAGGCGGGGCGTCCCCCGGAAAGC 2086
DB 4926 AAAGGAGGTGGAATAATCAATGAGAGAACCTTAAGGCGGGGCGTCCCCCGGAAAGC 4867
OY 2087 GGCTGCTCCAGGCTCTCCGACCCCAAGTAGAGTGCAGAGCGCGCGCGCGCTGCGGAGCGCAC 2146
DB 4866 GACTACTCTCAAAATCTCTCGACCCCAATTAAGAGTGCAGAGCGCGCGCGCGCTGCGGAGCGCAC 4807
OY 2147 CCCCCACCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2206
DB 4806 CCCCCACCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4747
OY 2207 TGCGAAGCGCGAGCTCGCGCGCGCTTGAGATTGACTGTCAGAGTGCAGCGCGCGCGCTGCGG 2266
DB 4746 TACGAAACCAACTACGCGCGCGCTTAATAATTAATCAATCAATCAATCAATCAATCA 4687
OY 2267 CGCG 2270
DB 4686 CGCG 4683
```

```
RESULT 7
US-10-301-832-11/c
; Sequence 11, Application US/10301832
; Publication No. US20040102390A1
; GENERAL INFORMATION:
; APPLICANT: Susan W. Freier
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF NOTCH3 EXPRESSION
; FILE REFERENCE: RTS-0414
; CURRENT APPLICATION NUMBER: US/10/301,832
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 155
; SEQ ID NO 11
; LENGTH: 44348
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-301-832-11

Query Match      8.3%; Score 188.4; DB 7; Length 44348;
Best Local Similarity 63.7%; Pred. No. 2.2e-36;
Matches 354; Conservative 0; Mismatches 191; Indels 11; Gaps 4;

OY 5 GATCTGCCCGCTCAGCCTCCCAAGTGTGGATTGCGAGCGTGAAGCCACTCACTCG 64
DB 12725 GATCTGCCCGCTCAGCCTCCCAAGTGTGGATTGCGAGCGTGAAGCCACTCACTCG 12666
OY 65 CTACAGTTTCAAAATATACATTA---TCTAGTACCATTAATCTCCAGTTGCCACA 121
DB 12665 CTTGTTGTTTATTAACCTTAACAGATTATTAAGTCTGTTTATTAATCAATTATTA 12606
OY 122 GGAATCTTAATGACTGTGCAAGCTGTAAATAATCAAGGCTGCAAGCTTGTATCTA 181
DB 12605 TGAAGACTATTAACATATACAGAAAGTTGACATTAATACCAACCACTAGATTCAAC 12546
OY 182 TAGAATGCTCAGATCTGCCCCCAGCTGAAAGAT---TTAAGAAATTTCTTGAGCC 238
DB 12545 TATGTTAGCTTAATCTACCAATCTCTTTCTTAACCATTTAAATAATGACAGACC 12486
OY 239 AGGCAAGTGGCTACACCTGTATTCAGTACTGTAGAGTCCGAGGTGAGAGACTGC 298
DB 12485 GGGCAAGTGGCTACACCTGTATTCAGTACTGTAGAGTCCGAGGTGAGAGACTGC 12426
OY 299 TTGAGGCGAGGTTCAAGAGCAGCTGACCAACAGAGGAGACCTGTCACTAATAAGAA 358
DB 12425 TTGAGGCGAGGTTCAAGAGCAGCTGAGCAATATAGTAGACCCGCTCTTACAAAAA 12366
OY 359 TAAATTAATTAAGCAGGCTTAGTGCTATCTCTGTGGTCCAGCTACTAGGAGGCGA 418
DB 12365 TACAAACCTTAAGCGGCGCATAGTGCGCACCGCTGTATCCCACTACTTGGGGAATGA 12306
OY 419 AGTAGA-----CTGCTGTGCTCCAGAGGTGCAAGCTCAGTAGACTAGAACCCGACCC 474
DB 12305 GGTGGAGAGTCACTTAGCCAGAGAGTCAAGGCTCAGTAGACTAGAACCCGACCC 12247
OY 475 TGCAATTCAGGCTGGGCAACAAAAAGAGACCTGTCTCAAAAAATTAATTAATAA 534
DB 12246 TGTAATCTCAGCTGGGAGCAAAAGTAGAGCTGTCTCAAAAAATTAATAATAA 12187
OY 535 ATAAATTAATTAATGTTT 550
DB 12186 CAACATCCACATATTT 12171

RESULT 8
US-10-719-993-6827/c
; Sequence 6827, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARBIL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
```


TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 6827
LENGTH: 160556
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(160556)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-719-993-6627

Query Match
Best Local Similarity 7.7%; Score 175; DB 8; Length 160556;
Matches 258; Conservative 2; Mismatches 117; Indels 4; Gaps 1;

216 ATTTAAGAGATTCTTGAGGCGCAGAGCTGCTCAGACCTGTATTCAGTACTGTG 275
30112 ATTCAAAATAACATATCTCAGCCGGGTGAGTGCTCAVGCCTGTATCTTGACACTTTG 30053
276 AGAGTCGAGCTCAGAGAGCTGTTGAGCGCCAGAGTTCAAGAGCAGCTTGACAAACA 335
30052 GGAAGCGCAAGCAGAGTGATTCGTAGAGTCAGAGATTGAGACCGCTGGCCAAACAG 29993
336 GGGAGACTGTCTCACTCAAAAGATTAATAATTAGCCAGGCTTATGTGCTCATCCCTGTG 395
29992 GTGACACCTGTCTCTACTATAAAATACAAAATTAGCCAGGCTGTGTCGCCGCTGTA 29933
396 GTCCCGCTACTAGAGGCGAGAGTAAGA---CTGCTGTGCCAGAGGTCAAGACTG 451
29932 GTCCCGCTACTAGAGGCGAGAGTAAGA---CTGCTGTGCCAGAGGTCAAGACTG 29873
452 CAGTAGCTGAGACCCAGCCACTGCTTCCAGCTGCGCAACAAAAGAGACCTGTCT 511
29872 CAGTAGCTGAGATTGGACACCTGCACTCCAGCCCTGGGTGACAGAGTCACTGTCT 29813
512 CAAAAAATAGTTAATAATAATAATAATAATAAGTTTAAACCTTAAACACATCTTCT 571
29812 CAAAAAATAGTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 29753
572 TTTCAAGAGAGACTTCTTAG 592
29752 TGACAAAATGTGTTACTAAG 29732

RESULT 9
US-09-764-878-231/c
Sequence 231, Application US/09764878
Patent No. US20020090615A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA121
CURRENT APPLICATION NUMBER: US/09/764,878
CURRENT FILING DATE: 2001-01-17
Prior Application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 428
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 231
LENGTH: 11172
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-878-231

Query Match
Best Local Similarity 7.6%; Score 172.8; DB 3; Length 11172;
Matches 337; Conservative 0; Mismatches 237; Indels 2; Gaps 2;

1 AACGATCTGCCCGCTCAGCCTCCCAAGTGTGGATTGACGGCTGAGCCACCTCAG 60

8630 AAGTATCCGCTGCTTGGCTCCCAAGTGTAGATTACAGCAGTACCGCAG 8571
61 CTGGCTACAGATTTCAAAATATCATTTATCTAGTACCATATCTTCCAGTTTCCAC 120
8570 CTGGCTCCCTCCCAAGTGTAGATTACAGTACCATATCTTCCAGTTTCCAC 8511
121 AGGACATCTTATGATTAGCTAGCAGCTGTAATAAATCCAAAGGTGACGGTTGTATGCT 180
8510 AGGACTTAATTTATGATTATGATTATGATTATGATTATGATTATGATTATGATTATG 8451
181 ATGAGATCTCAGATCTGCTCCCGCCAGCCCTGAAAGATTTAAGAAATTTTGGAGCCAG 240
8450 TCCCTCAGACAAAGATGATTAATTAATTTGGTTTCTTTTAAAGATGAGGACTGCGAG 8391
241 GCACAGTGTCTCAGCCTGTATTTCCAGTACTCTGAGAGTCCGAGTCAAGAGATCTGCT 300
8390 GCACAGTGTCTCAGCCTGTATTTCCAGTACTCTGAGAGTCCGAGTGTGAGCAGCT 8331
301 GAGGCGAGAGTTCAAGAGCAGCTGAGCAACAGAGGAGA-CCTGTACTTCAAGAAT 359
8330 GAGGCGAGAGTTCAAGAGCAGCTGAGCAACATATGTAAACCCATCTTCTTAAAAAT 8271
360 AATTAATTTAGCAGCTTATGCTCATCCCTGTGCTCCAGTACTTACAGGAGCAGAA 419
8270 ACAAATTTAGCAGGCGGCTGCTCATCCCTGTGCTCCAGTACTTACAGGAGCAG 8211
420 GTAGAGCTGCTTGTCCAGAGAGTCA-AGACTGAGTGTAGTGAACCCAGCAGCTGCA 478
8210 ACAGATTTGCTTGAACCCGGAAGGAGGTTACAGTATGAGCTTATGCTGACCTGAC 8151
479 TTCCAGCTGAGGCAACAAAAGAGCCTGTCTCAAAAATTAATAATAATAATAATA 538
8150 TCCAGCTGAGGCAACAAAAGAGCCTGTCTCAAAAATTAATAATAATAATAATAATA 8091
539 TAAATAATGTTTAAACCTTAAACACATCTTCTTTT 574
8090 AAAAAAGATGAGGAGCAGTATGATTATTAATTTGT 8055

RESULT 10
US-10-079-854-231/c
Sequence 231, Application US/10079854
Publication No. US20030054368A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA121C1
CURRENT APPLICATION NUMBER: US/10/079,854
CURRENT FILING DATE: 2002-02-22
Prior Application data removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 428
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 231
LENGTH: 11172
TYPE: DNA
ORGANISM: Homo sapiens
US-10-079-854-231

Query Match
Best Local Similarity 7.6%; Score 172.8; DB 5; Length 11172;
Matches 337; Conservative 0; Mismatches 237; Indels 2; Gaps 2;

1 AACGATCTGCCCGCTCAGCCTCCCAAGTGTGGATTGACGGCTGAGCCACCTCAG 60
8630 AAGTATCCGCTGCTTGGCTCCCAAGTGTAGATTACAGCAGTACCGCAG 8571
61 CTGGCTACAGATTTCAAAATATCATTTATCTAGTACCATATCTTCCAGTTTCCAC 120
8570 CTGGCTCCCTCCCAAGTGTAGATTACAGTACCATATCTTCCAGTTTCCAC 8511
121 AGGACATCTTATGATTAGCTAGCAGCTGTAATAAATCCAAAGGTGACGGTTGTATGCT 180
8510 AGGACTTAATTTATGATTATGATTATGATTATGATTATGATTATGATTATGATTATG 8451
181 ATGAGATCTCAGATCTGCTCCCGCCAGCCCTGAAAGATTTAAGAAATTTTGGAGCCAG 240
8450 TCCCTCAGACAAAGATGATTAATTAATTTGGTTTCTTTTAAAGATGAGGACTGCGAG 8391
241 GCACAGTGTCTCAGCCTGTATTTCCAGTACTCTGAGAGTCCGAGTCAAGAGATCTGCT 300
8390 GCACAGTGTCTCAGCCTGTATTTCCAGTACTCTGAGAGTCCGAGTGTGAGCAGCT 8331
301 GAGGCGAGAGTTCAAGAGCAGCTGAGCAACAGAGGAGA-CCTGTACTTCAAGAAT 359
8330 GAGGCGAGAGTTCAAGAGCAGCTGAGCAACATATGTAAACCCATCTTCTTAAAAAT 8271
360 AATTAATTTAGCAGCTTATGCTCATCCCTGTGCTCCAGTACTTACAGGAGCAGAA 419
8270 ACAAATTTAGCAGGCGGCTGCTCATCCCTGTGCTCCAGTACTTACAGGAGCAG 8211
420 GTAGAGCTGCTTGTCCAGAGAGTCA-AGACTGAGTGTAGTGAACCCAGCAGCTGCA 478
8210 ACAGATTTGCTTGAACCCGGAAGGAGGTTACAGTATGAGCTTATGCTGACCTGAC 8151
479 TTCCAGCTGAGGCAACAAAAGAGCCTGTCTCAAAAATTAATAATAATAATAATA 538
8150 TCCAGCTGAGGCAACAAAAGAGCCTGTCTCAAAAATTAATAATAATAATAATAATA 8091
539 TAAATAATGTTTAAACCTTAAACACATCTTCTTTT 574
8090 AAAAAAGATGAGGAGCAGTATGATTATTAATTTGT 8055

Query Match 7.3%; Score 166.8; DB 5; Length 3030;
Best Local Similarity 61.8%; Pred.No.1.9e-31;
Matches 336; Conservative 0; Mismatches 197; Indels 11; Gaps 4;

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OY 1 AACGATCTGCCCGCTCAGCTCCCAAGTGTGGGATTCAGAGCGGTAGCCACTCAC 60
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2458 AAGCATCTTCTGCTCTCAGCTCAGCTTACCAAAATGCTGAGATTACAGGTTGATCAGACGAC 2399
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 CTGGCTACAGTTTCAAAATACATTATCTAGTACCAATCTCCAGTTTGTCCAC 120
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2398 CTGGCCCTAAATTAATTGATTTGACATTGATTATGTTTCTGAAGTGACTCCTTTCTTA 2339
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 121 AGGACATCTTATGACTTGAGCAAGCTGCTAAAATCCAAAGGTGACGCTTGTATGCT 180
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2338 GACAAAGCCACATGGATCTTCAGGTTTAAAGGTTTATATGATTAACCTTCTTAATTGT 2279
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 181 ATAGGATTGCTCAGATCTGCCCGCCCAACCCCTGAA-----AGATTTAAGGAATTTCTTGA 234
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2278 AAAGAAATGAATACAGATTCTTGAGACTTGATTTTCCAAATCATATTTAAAGCCTTGA 2219
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 235 GGCCAGGACACAGTGGCTCACACCTGTAAATCCAGTACTGTAGAGTCCGAGGTCAAGAGA 294
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2218 GGCTAGGAGAGTGGCTCATGCTTGTAAATTCAGCATTAGAGGCCAAGGTGGAAGA 2159
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 295 CTGCTTGAGGCCAGAGATTCAAGAGCAGCTGGACAACAGAGAGACC--TGTCACTA 351
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2158 TGGTTTGGGGCCAGAGATTGAGACCAGCTGGCAACCTAGTGAGACCCCGTTTCACA 2099
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 352 CAAGAATAAATAATTAAGCCAGGCTTAGTGGCTCATCCCTGTGTGCCAGCTACTAGGG 411
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2098 AAATTTTAAATTAATTAAGCTGGCAATGCTGTAAATGCTGTGTCTCAACTACTTGGG 2039
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 412 AGGCAAGATAGACTGCTTG-TCCAGAGAGTCAAGACTGCAGTGAAGTGAACCCAGC 470
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2038 AGGCAAGAGTGAATCAGCTTGAGGCCAAGATTGAGGCTGCAATGAGCTATGATCGGT 1979
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 471 CACCTGCATTCAGGCTTGCGCAACAAAAGAGACCCCTGTCTCAAAAAATTAAGTTAAATPA 530
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1978 CA-CTGCACTCCAGCTGGGCAACAGATAGATCTGTCTCAAAAAAAGAGGTCTTA 1920
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 531 ATAA 534
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1919 AAAA 1916
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: April 22, 2006, 16:00:00
Job time : 1636 secs

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QY	1025	TTGGCTTGAATCTCTGTTTTCACAGCTGCTCTTGCCAGAGACATATGGCTGGGCTGTTTTTCT	1084
Db	121	TGCTTTGAATCTCTGTTTTCACAGCTGCTCTTGCCAGAGACATATGGCTGGG-GTGTTTTTCT	179
QY	1085	TTCCGCTAATTAATTATCCAGGCCATCCAGCTCTGAGCCCCCTCAGCTGTTCCCTGGCAGT	1144
Db	180	TTCCGCTAATTAATTATCCAGGCCATCCAGCTCTGAGCCCCCTCAGCTGTTCCCTGGCAGT	239
QY	1145	CCCTTCTGCTGTGAAAACACATATGGCGCCGCGCTGACACAGGTTGAAGTGTGAATA	1204
Db	240	CCCTTCTGCTGTGAAAACACATATGGCGCCGCGCTGACACAGGTTGAAGTGTGAATA	299
QY	1205	TCAGGAAGATGACTGAACGCTTTTGAGGACTCCGTTTCTCATTTGTAATAATGGAGTTAAT	1264
Db	300	TGAGGAAGATGACTGAACGCTTTTGAGGACTCCGTTTCTCATTTGTAATAATGGAGTTAAT	359
QY	1265	ACCAGGCTTCTTTACTCCCCAAACGACGCTGTTTGTCCCGGCCAGAGGGCCCAATTGTT	1324
Db	360	ACCAGGCTTCTTTACTCCCCAAACGACGCTGTTTGTCCCGGCCAGAGGGCCCAATTGTT	419
QY	1325	GGCTGTTACAGCATCATGTTATACCCCCACAGACGGGTAGGCCAATTAAGAAGGAACCAAGC	1384
Db	420	GGCTGTTACAGCATCATGTTATACCCCCACAGACGGGTAGGCCAATTAAGAAGGAACCAAGC	479
QY	1385	CCGGTTCATCTCCTGACGCGCTTTTTCATATCCACAGGCGTGGACAGGACGCTGGCGCC	1444
Db	480	CCGGTTCATCTCCTGACGCGCTTTTTCATATCCACAGGCGTGGACAGGACGCTGGCGCC	539
QY	1445	CGGCTTCTGCTTGTACAGTGGCGG	1467
Db	540	CGGCTTCTGCTTGTACAGTGGCGG	562

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RESULT 2
US-10-301-480-268288/C
; Sequence 268288, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: mang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,655
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 268288
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-268288

```

	Query Match	23.7%	Score 538.6	DB 10	Length 561	
	Beet Local Similarity	99.5%	Pred. No. 3,9e-05			
	Matches 560	Conservative 1	Id. Matches 0	Indels 2	Gaps 2	
QY	1131	TTTTCCTCGGAGTCCCTTCTGCTGTGTA	AAAAACATATGCGCGCGCTGACGAGGTG	1190		
DB	561	TGTTCCCTGGAGTCCCTTCTGCTGTGTA	AAAAACATATGCGCGCGCTGACGAGGTG	502		
QY	1191	TAAGTGTGAATATACGAGATGACTGAA	CGTCTTTGGGACTCCGTTTCCCTCATTTGA	1256		
DB	501	TAAAGTGTGAATATACGAGATGACTGAA	CGTCTTTGGGACTCCGTTTCCCTCATTTGA	442		
QY	1251	AAATGAGGTTAATACGAGCTCTTCTTACT	CCCCAAGCAGCGTTTGTCCGGGCGAG	1310		
DB	441	AAATGAGGTTAATACGAGCTCTTCTTACT	CCCCAAGCAGCGTTTGTCCGGGCGAG	382		
QY	1311	AGGGGCAATTGTTGGCTGTTCCAGCAT	GTATACCCCAAGAGGAGTCAAGCCATTA	1370		

Db	381	AGGG-CCAAATTGTTGCGTGTTCACGCRKCAATTACCCCAAGGACGGGTGAGCCAAATT	323
Qy	1371	AAGGCGAACCAGGCGCCGGTCCATCTCCTGACGCGCTTTTCTCATCCAGGGCTGGACAGGC	1430
Db	322	AAGCGAAACCAAGGCCCGGTCATCTCTGACGCGCTTTTCTCATCCAGGGCTGGACAGGC	263
Qy	1431	AGCTGCGCTGGGCGCGGCTCTGCTTGTGTCAAGTGCAGGAGGCGCGGCCGCTTGTGTCTG	1490
Db	262	AGCTGCGCTGGG-CCGGCTCTGCTTGTGTCAAGTGCAGGAGGCGCGGCCGCTTGTGTCTG	204
Qy	1491	TGTGTAGAGAGGTGAGGTCAAGCTGGGTGCTCCCGCCGCGCGGGGCGCTTTAGTGTCCCT	1550
Db	203	TGTGTAGAGAGGTGAGGTCAAGCTGGGTGCTCCCGCCGCGGGGCGCTTTAGTGTCCCT	144
Qy	1551	GGTCTCCCTTAACGCCAGGCGCGCTCCACCGGAGGAGAAAGCGCGAAACCCCAAGCCGACCA	1610
Db	143	GGTCTCCCTTAACGCCAGGCGCGCTCCACCGGAGGAGAAAGCGCGAAACCCCAAGCCGACCA	84
Qy	1611	CGGCTGTTGTGCGTGTGCCGGGCGCACTGTGTGTGCAATTTGATTTGATTTCTTCCCCGA	1670
Db	83	CGGCTGTTGTGCGTGTGCCGGGCGCACTGTGTGTGCAATTTGATTTGATTTCTTCCCCGA	24
Qy	1671	CAAGCGGCGGCGGTGAACCAATC	1693
Db	23	CAAGCGGCGGCGGTGAACCAATC	1

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RESULT 3
US-10-301-480-881697/C
; Sequence 881697, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108627.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 881697
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-881697

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Query Match	23.7%	Score 538.6	DB 10	Length 561
Best Local Similarity	99.5%	Pred. No. 3.9e-05		
Matches 560	Conservative 1	Mismatches 0	Indels 2	Gaps 2
QY	1131	TGTTCCCTGGAGTCCCTTCTGCTGTGGAAACACATATGGCGCGGCTGACAGGGTG	1190	
DB	561	TGTTCCCTGGAGTCCCTTCTGCTGTGGAAACACATATGGCGCGGCTGACAGGGTG	502	
QY	1191	TAAGTGTGAAATACAGAAAGATGACTGAACGTCCTTTGGAGCTCCGTTCTCATTTGA	1250	
DB	501	TAAGTGTGAAATACAGAAAGATGACTGAACGTCCTTTGGAGCTCCGTTCTCATTTGA	442	
QY	1251	AAATGAGAGTTAAATACAGACCTTCTTCTACGCCCAAAAGCAGAGTTGTGCCGGCCAG	1310	
DB	441	AAATGAGAGTTAAATACAGACCTTCTTCTACGCCCAAAAGCAGAGTTGTGCCGGCCAG	382	
QY	1311	AGGCGCCATTTGTTGCTGTTACAGCATCATGTTACCCCAAGAGCGGGTCAGCCAAATTA	1370	
DB	381	AGGCGCCATTTGTTGCTGTTACAGCATCATGTTACCCCAAGAGCGGGTCAGCCAAATTA	323	
QY	1371	AAGGGAAACAGGCCCGGTCATCTCTGACGCGCTTTTCATCCCAAGGCTGACAGGC	1430	

```
Db 322 AAGGGAACACAGCCCGGCTCATCTCTGACGCTTTTCTCATCCAGGAGCTGACAGGC 263
Qy 1431 AGCTGACCTGGAGCCCGGCTCTGCTCTTGTACGCTGGGGGGGCGGCGCTTTGCTGTG 1490
Db 262 AGCTGACCTGGAG-CCGGCTCTGCTCTTGTACGCTGGGGGGGCGGCGCTTTGCTGTG 204
Qy 1491 TGTGTAGAGGCTGAGAGTACGCTGGGCTCTCCCGCGCGGGGCTTTAGTGTCTT 1550
Db 203 TGTGTAGAGGCTGAGAGTACGCTGGGCTCTCCCGCGCGGGGCTTTAGTGTCTT 144
Qy 1551 GGTCCCTAAACCCAGGCGCTCTCAACCGGGGAGAAAGCGGCAACCCAGCGAGCCCA 1610
Db 143 GGTCCCTAAACCCAGGCGCTCTCAACCGGGGAGAAAGCGGCAACCCAGCGAGCCCA 84
Qy 1611 CGGCTGTGTGCTGGTTCGGGGGCACTGTGTGCAATTCTGATTTGTTCTTCCCGCA 1670
Db 83 CGGCTGTGTGCTGGTTCGGGGGCACTGTGTGCAATTCTGATTTGTTCTTCCCGCA 24
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Db 23 CAACGGCGGCGCTGTACCAATC 1
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RESULT 4

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US-09-925-065A-177131/C
; Sequence 177131, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177131
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-177131
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Query Match 23.4%; Score 531.6; DB 6; Length 554;

Best Local Similarity 99.5%; Pred. No. 5.5e-05;

Matches 553; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

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Qy 1131 TGTTCCTGGAGCTCCCTTCTGCTGTGTAACACATATGCGCGGCTTGACAGGGTG 1190
Db 554 TGTTCCTGGAGCTCCCTTCTGCTGTGTAACACATATGCGCGGCTTGACAGGGTG 495
Qy 1191 TAAAGTGTGAATATCAGAGATGACAGTCTTTGGAGCTCCGTTTCTCTCATTTTA 1250
Db 494 TAAAGTGTGAATATCAGAGATGACAGTCTTTGGAGCTCCGTTTCTCTCATTTTA 435
Qy 1251 AAATGAGGTAAATACAGACCTTCTTCTACTCCCAAAAGCAGTGTGTGTCGCGGCGAG 1310
Db 434 AAATGAGGTAAATACAGACCTTCTTCTACTCCCAAAAGCAGTGTGTGTCGCGGCGAG 375
Qy 1311 AGGCGCCCAATTTGTGGCTGTTACGAGCATGATTACCCCAAGAGCGGGTACGCCAATTA 1370
Db 374 AGGCG-CCAAATTTGTGGCTGTTACGAGCATGATTACCCCAAGAGCGGGTACGCCAATTA 316
Qy 1371 AAGGGAACACAGCCCGGCTCATCTCTGACGCTTTTCTCATCCAGGAGCTGACAGGC 1430
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Db 315 AAGGGAACACAGCCCGGCTCATCTCTGACGCTTTTCTCATCCAGGAGCTGACAGGC 256
Qy 1431 AGCTGACCTGGAGCCCGGCTCTGCTCTTGTACGCTGGGGGGGCGGCGCTTTGCTGTG 1490
Db 255 AGCTGACCTGGAG-CCGGCTCTGCTCTTGTACGCTGGGGGGGCGGCGCTTTGCTGTG 197
Qy 1491 TGTGTAGAGGCTGAGAGTACGCTGGGCTCTCCCGCGCGGGGCTTTAGTGTCTT 1550
Db 196 TGTGTAGAGGCTGAGAGTACGCTGGGCTCTCCCGCGCGGGGCTTTAGTGTCTT 137
Qy 1551 GGTCCCTAAACCCAGGCGCTCTCAACCGGGGAGAAAGCGGCAACCCAGCGAGCCCA 1610
Db 136 GGTCCCTAAACCCAGGCGCTCTCAACCGGGGAGAAAGCGGCAACCCAGCGAGCCCA 77
Qy 1611 CGGCTGTGTGCTGGTTCGGGGGCACTGTGTGCAATTCTGATTTGTTCTTCCCGCA 1670
Db 76 CGGCTGTGTGCTGGTTCGGGGGCACTGTGTGCAATTCTGATTTGTTCTTCCCGCA 17
Qy 1671 CAACGGCGGCGCTGTGA 1686
Db 16 CAACGGCGGCGCTGTGA 1
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RESULT 5

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US-09-925-065A-770821/C
; Sequence 770821, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770821
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-770821
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Query Match 7.4%; Score 168; DB 6; Length 563;

Best Local Similarity 74.6%; Pred. No. 3.9e+03;

Matches 252; Conservative 0; Mismatches 80; Indels 6; Gaps 3;

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Qy 218 TTAAGAGATTTCTTGGAGCCAGGACAGTGTCTACACCTGTAAATTCAGTACTGTGAG 277
Db 493 TTCAAGCATATCTTGAAGCCAGGTACAGTGTCTACACCTGTAAATTCAGTACTGTGAG 434
Qy 278 AGTCCGAGTCAAGAGACTGCTTGAAGCCAGGAGTTCAAGAGCAAGCTTGACACACAGG 337
Db 433 AGTCCGAGTCAAGAGACTGCTTGAAGCCAGGAGTTGAAGCCAGGAGTTGAAGCTTGACATGAT 374
Qy 338 GAGACCTGTACTCAAGAATAAATAATTAAGCCAGGCTTAAGTGTGATCCCTGTGTGT 397
Db 373 GAAACCTGTCTCTTAATAAATAAATAATTAAGCCAGGCTTAAGTGTGATCCCTGTGTGT 314
Qy 398 CCCAGCTACTAGGAGGACAGAGTGTGCTTGT-----CCAGGAGGTCAAGACTGCA 453
Db 313 CCCAGCTACTAGGAGGCTGAGGAGAGAGTGTGATCTTGAACCCAGAGGGGAGAGTGTGCA 254
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Qy	454	GTGAGCTGAACCCAGGCACTGTCATTCAGGCTGGGCAACAAAAGAGACCTGTCTC-	512
Db	253	GTGAGCTGAATTGGCCCA-TTGCACACAGGCTGGGTAACAGACACGAACCTGTCTCA	199
Qy	513	AAAAAATAAAGTTAAATATAAATAATATAAATAAGTT	550
Db	194	AAAAAATAAATCATATAATACATAAATAATATAATCTCT	157

RESULT 6
US-09-925-065A-551304/c
; Sequence 551304, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:

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1  TITLE OF INVENTION: Identification and Mapping of Single
2  TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
3  FILE REFERENCE: 108827.115
4  CURRENT APPLICATION NUMBER: US/09/925,065A
5  CURRENT FILING DATE: 2001-08-08
6  PRIOR APPLICATION NUMBER: US 60/243,036
7  PRIOR FILING DATE: 2000-10-24
8  PRIOR APPLICATION NUMBER: US 60/252,147
9  PRIOR FILING DATE: 2000-11-20
10 PRIOR APPLICATION NUMBER: US 60/250,092
11 PRIOR FILING DATE: 2000-11-30
12 PRIOR APPLICATION NUMBER: US 60/261,766
13 PRIOR FILING DATE: 2001-01-16
14 PRIOR APPLICATION NUMBER: US 60/289,846
15 PRIOR FILING DATE: 2001-05-09
16 NUMBER OF SEQ ID NOS: 957086
17 SOFTWARE: FastSeq for Windows Version 4.0
18 SEQ ID NO 551304
19 LENGTH: 1614
20 TYPE: DNA
21 ORGANISM: Homo sapiens
22 US-09-925-065A-551304

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Query Match %	7.3%	Score 166	DB 6	Length 1614
Best Local Similarity	76.2%	Pred. No. 2.1e+03		
Matches 244	Conservative 0	Mismatches 70	Indels 6	Gaps 3

OY	225	AATTTCTTGGAGCCAGGCA	CAGTGGCTCA	CACTGTAAATTC	CAGTACGTAGAACTCCGA	28
Db	419	AAATTCATGGAGCCAGGCA	CAGTGGCTCA	TGCTGTAAATTC	CAGCACTTTGGAGGCTTA	36
OY	285	GGTGAGAGGACTGTTT	GAGGCCAGAGGTTCA	GAGCAAGCTTGACACACAGGGAGA	CC	34
Db	359	GGCAGGAGATGGCTTT	GAGCCAGGAGTTCA	ATGATAGCTGGGAGAGATGGTGAACCC		300
OY	344	TGTCACTACAAAGAT	TAAATTAATTAGCC	AGGCTTGTGTGCTCATCCCTGTGTGCCAGC		403
Db	299	TGCTCCACAAAAAT	TACAAAAATTAGCC	AAAGTGTGTGTGCACACCTGTGTGCCAGC		240
OY	404	TACTAGGAGGACAGAA	TAGGACTGCTGTG	-----CCGAGAGGCTCA	AGCTGCAGTGAAC	45
Db	239	TACTTGGAGGCTGAGTG	AGAAATGTATTG	AGGCCAAGAGGTCA	AGGCTTCAGTGAAC	180
OY	460	TGAGACCAGCCACTG	GATTCGAGCTGGGCA	CAAAAGAGACCTGTCTCAAAAAAT		510
Db	179	CGAGATCACACCA	CTGCATCCGAGCTGTG	CAACAGAGTGAACCTGTGTCAAAAAAT		122
OY	520	AAATTAAATTAATTAAT	TAAATTAAT			539
Db	120	AAAAAATTAATAATTAAT	CAAT			101

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RESULT 7
US-10-301-480-529254/C
; Sequence 529254, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

```

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: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
: TITLE OF INVENTION: in the Human Genome
: FILE REFERENCE: 108827.137
: CURRENT APPLICATION NUMBER: US/10/301,480
: CURRENT FILING DATE: 2002-11-21
: PRIOR APPLICATION NUMBER: US 10/215,598
: PRIOR FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: US 60/311,695
: PRIOR FILING DATE: 2001-08-10
: NUMBER OF SEQ ID NOS: 122618
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 529254
: LENGTH: 1614
: TYPE: DNA
: ORGANISM: Homo sapien
: US-10-301-480-529254

Query Match          7.3%; Score 166; DB 10; Length 1614;
Best Local Similarity 76.2%; Pred. No. 2,1e+03;
Matches 244; Conservative 0; Mismatches 70; Indels 6; Gaps 3;

```

ORGANISM: Homo sapien
US-10-301-480-529254

Query Match	7.3%	Score 166;	DB 10;	Length 1614;
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Best Local Similarity 10.24; P-vec. NO. 2.14e+03;
Matches 244; Conservative 0; Mismatches 70; Indels 6; Gaps 3

QY	225	AATTTCCTGAAGCCAGGACGACAGTGGCTCAACCTGTAAATTCACATCTGTGAGACTCCGA	284
Db	419	AAATTCATGAGGCCAGGACGACAGTGGCTATGCTGTAAATTCACGACATTTGGAGGCCTA	360
QY	285	GCTCAGAGGACTGCTTTGAGGCCAGGAGTTCAAGAGCAACCTTGACACACAGGAGAG-CC	343
Db	359	GGCAGGCGAGATGGCTTGAGCCAGAGTTCAAGATCAACCTGGGGAGCATGTTGAATCCC	300
QY	344	TGTCACCTCAAGAATATAATAAATTAGCCAGGCTTAGTGCTCATCCCTGTGGTCCAGC	403
Db	299	TGCTCCACAAAAAATACAAAAATTAGCCAAAGTGATGTGTGCAACCTGTGTCCAGC	240
QY	404	TACTTAGGAGGCAGAAAGTAGAGCTGCTGT-----CCAGAGGTAAAGACTGCAATGAGC	459
Db	239	TACTTGGAGGCTAGAGTGAGAAATTATTTAGAGCCCAAGAGGTAAAGCTTCAAGTGAAC	180
QY	460	TGAGACCCAGCCACCTGCAATTCAGCCTGGCCAAACAAAAGAGACCTGTCTCAAAAAAT	519
Db	179	CGAGATCAACCA-CTGCATCTCAAGCCCTGTGCACACAGAGTGAGACCTGTCTCAAAAAAT	121
QY	520	AAAGTAAATAATAATAAT 539	
Db	120	AAAAAATAATAATAATCAT 101	

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RESULT 8
US-10-301-480-1142663/c
; Sequence 1142663, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:

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; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
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; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIORITY FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ. ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1142663
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; LENGTH: 1614
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; TYPE: DNA
;
; ORGANISM: Homo sapien
;
; US-10-301-480-1142663

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Query Match	7.3%	Score 166;	DB 10;	Length 1614;
Best Local Similarity	76.2%	Pred. No. 2.1e+03;		
Matches 244;	Conservative	0;	Mismatches 70;	Indels 6;
				Gaps 3

Query Match	7.3%;	Score 165.6;	DB 9;	Length 1187;
Best Local Similarity	75.9%;	Pred. No. 2.6e+03;		
Matches 243;	Conservative 1;	Mismatches 70;	Indels 6;	Gaps 3;

QY 225 AATTTCCTGGAGCCAGAGGACAGTGGCTCACACTGTAAATTCAGACTGTGAGAGTCCGA 284

Db 419 AAAATCATGAGCCAGAGCCAGATGGCTCATGCTGTAAATTCAGACATTTGGAGGGCTTA 360

QY 285 GGTCTAGAGACTGCTTTGAGAGCCAGAGATTCAAGAGCAGCCTGGACAAACAACAGGAGA-CC 343

Db 359 GGCAGAGCAGATGGCTTTGAGGCCAGAGATTCAAGATCAGCCTGGCAGCATGTGTAAACC 300

QY 344 TGTCACTACAAAGAAATTAATTAATTAAGCCAGCTTAGTGGCTCATCCCTGTGGTCCCAGC 403

Db 299 TGCCCTCCACAAAAAATATACAAAAATTAGCCAAAGTGTGGTGTGACACCTGTGGTCCCAGC 240

QY 404 TACTAGGAGGAGAGAAAGTAGAAGTCTGTTGT---CCAGAGAGGTCAAGACTGAGTAGAGC 459

Db 239 TACTTGGAGAGCTGAGGTGAGAGAAATTAATTGAGGCCCTGAGAGAGGTCAAGGCTCCAAGTAGC 180

QY 460 TGAGACCCAGCCACTGCATTCCTCAGCCTTGAGGCAACAAAAAGAGACCCCTGTCTCAAAAAAT 519

Db 179 CGAGATTCACACCA-CTGCACCTCAGCGCTGTGGAAACAGATGTGAGAACCTGTGCTCAAAAAAT 121

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FEATURES	location/Qualifiers
source	1..3505
ORIGIN	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"

Query Match 100.0%; Score 2270; DB 6; Length 3505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2270; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AACGGAATCTGCCCGCCCTCAAGCTTCCCAAGCTGCGGATTTGACAGCGCTGAGCCACTGAC 60
DB 1 AACGGAATCTGCCCGCCCTCAAGCTTCCCAAGCTGCGGATTTGACAGCGCTGAGCCACTGAC 60
QY 61 CTGAGCTACAAAGTTTCAAAATATACATTTATCTAGTACCATATCTTCAGTTGTGTCCAC 120
DB 61 CTGAGCTACAAAGTTTCAAAATATACATTTATCTAGTACCATATCTTCAGTTGTGTCCAC 120
QY 121 AGGACATCTTATGACTTGAAGCAAGCTGTAAATAATCCAGGGGTGCAAGCTTTGTATGCT 180
DB 121 AGGACATCTTATGACTTGAAGCAAGCTGTAAATAATCCAGGGGTGCAAGCTTTGTATGCT 180
QY 181 ATAGGATTTGCTCAAGATCTGCCCCCACTTGAATAATTTAAGAAATTTCTTGAAGCCAG 240
DB 181 ATAGGATTTGCTCAAGATCTGCCCCCACTTGAATAATTTAAGAAATTTCTTGAAGCCAG 240
QY 241 GCACAGTGGCTCACACCTGTATTTCCAGTACTGTGAGAGTCCGAGGTGAGGAGCTGCTT 300
DB 241 GCACAGTGGCTCACACCTGTATTTCCAGTACTGTGAGAGTCCGAGGTGAGGAGCTGCTT 300
QY 301 GAGGCCAGAGTTCAAGAGCAGCTTGAACAACAGGAGACCTGTCACTAACAAAGATA 360
DB 301 GAGGCCAGAGTTCAAGAGCAGCTTGAACAACAGGAGACCTGTCACTAACAAAGATA 360
QY 361 AATTAATTAAGCAGAGCTTATAGTGGCTCATCCCTGTGTGCTCCAGCTACTATGAGAGGAGAG 420
DB 361 AATTAATTAAGCAGAGCTTATAGTGGCTCATCCCTGTGTGCTCCAGCTACTATGAGAGGAGAG 420
QY 421 TAGGACTGCTGTGCTCCAGAGAGTCAAGACTGAGTGAAGCTGAGACCCAGCCACTGACTT 480
DB 421 TAGGACTGCTGTGCTCCAGAGAGTCAAGACTGAGTGAAGCTGAGACCCAGCCACTGACTT 480
QY 481 CCAGCCTGGGCAACAAAAAGAGCCCTGTCTCAAAAAATTAAGTTAAATTAATAATA 540
DB 481 CCAGCCTGGGCAACAAAAAGAGCCCTGTCTCAAAAAATTAAGTTAAATTAATAATA 540
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DB 541 AAAATAGTTAAACCCCTPAACACATCTTCTTTTCAAGAGAGACTTCTTAAGACTTCAT 600
QY 601 GCTGCGTCTGTGATCTCAACTTCCCTTTTCAAGCGTCAACACTTTTAAAGTCTGTT 660
DB 601 GCTGCGTCTGTGATCTCAACTTCCCTTTTCAAGCGTCAACACTTTTAAAGTCTGTT 660
QY 661 TGCCAAAGATATAATATATATATTTCTGAATCCAGATTCTTCCCTGTTTGAACAGCA 720
DB 661 TGCCAAAGATATAATATATATATTTCTGAATCCAGATTCTTCCCTGTTTGAACAGCA 720
QY 721 GGGGGAACAATTTTGTGTGAGAGCCTTTGATCTGTCTGTCTGTGTGTGATCTCA 780
DB 721 GGGGGAACAATTTTGTGTGAGAGCCTTTGATCTGTCTGTGTGTGTGATCTCA 780
QY 781 CAGCAAAATTTTGCAGAGCTCTCCGGAATGCAACGCGAGACAGAGCTCAGCCCAAAAGCTA 840
DB 781 CAGCAAAATTTTGCAGAGCTCTCCGGAATGCAACGCGAGACAGAGCTCAGCCCAAAAGCTA 840
QY 841 GAGAACTGGCGAGAGAGACTCAACAGTCCCAAAAAATTTATCTTTTCTTTT 900
DB 841 GAGAACTGGCGAGAGAGACTCAACAGTCCCAAAAAATTTATCTTTTCTTTT 900
QY 901 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 960
DB 901 TTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 960
QY 961 CTTCCTTCTCTCTCTTTCTTTCTTTTCTTCAATGAGAGATCTCCCTCATGGAGAAAT 1020
DB 961 CTTCCTTCTCTCTCTTTCTTTCTTTTCTTCAATGAGAGATCTCCCTCATGGAGAAAT 1020
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QY 1021 AATTCGCTTGAATCTTGTGTTTCAACGCTGCTTCTGACAGAGACATGCGCTCGAGTGT 1080
DB 1021 AATTCGCTTGAATCTTGTGTTTCAACGCTGCTTCTGACAGAGACATGCGCTCGAGTGT 1080
QY 1081 TTTCTTCCGCTAATATATATATATATATATATATATATATATATATATATATATATAT 1140
DB 1081 TTTCTTCCGCTAATATATATATATATATATATATATATATATATATATATATATATAT 1140
QY 1141 CAGTCCCTTCTGCTGTAAGAAACATATAGGCGCGGCTGACCAAGAGGTATAGTGTG 1200
DB 1141 CAGTCCCTTCTGCTGTAAGAAACATATAGGCGCGGCTGACCAAGAGGTATAGTGTG 1200
QY 1201 AATATCAGAAAGATGACTGAACGCTTTTGAAGCTTCTCATTTGTAATAATGAGGT 1260
DB 1201 AATATCAGAAAGATGACTGAACGCTTTTGAAGCTTCTCATTTGTAATAATGAGGT 1260
QY 1261 TAATACAGAGCTTCTTACTTCCCAAGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
DB 1261 TAATACAGAGCTTCTTACTTCCCAAGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
QY 1321 TGTGTGCTGTTCAAGCATCAGTTAACCCCAAGAGAGGCTCAGCAATTAAGAGCAACC 1380
DB 1321 TGTGTGCTGTTCAAGCATCAGTTAACCCCAAGAGAGGCTCAGCAATTAAGAGCAACC 1380
QY 1381 AGGCTCGGTCATCTCTGACGCTTTTCTCATCTCAAGGCTGAGACAGGACTGAGCTTG 1440
DB 1381 AGGCTCGGTCATCTCTGACGCTTTTCTCATCTCAAGGCTGAGACAGGACTGAGCTTG 1440
QY 1441 GGCCTCGGCTCTGCTTGTCAAGTGTGCGGGGGCGGCTTGTGTGTGTGTGTGTGTGTGTGT 1500
DB 1441 GGCCTCGGCTCTGCTTGTCAAGTGTGCGGGGGCGGCTTGTGTGTGTGTGTGTGTGTGTGT 1500
QY 1501 CGTGAAGTCAAGCTGAGGTGCTCCGCGCCCGGAGGCTTTAGTGTCTGTGCTCTTAA 1560
DB 1501 CGTGAAGTCAAGCTGAGGTGCTCCGCGCCCGGAGGCTTTAGTGTCTGTGCTCTTAA 1560
QY 1561 GCGGAGGCGCTCCACCGGAGAGAGGCGGAAACCCAGCCGAGCCCAACGCTGTTGT 1620
DB 1561 GCGGAGGCGCTCCACCGGAGAGAGGCGGAAACCCAGCCGAGCCCAACGCTGTTGT 1620
QY 1621 CGGTTGCGGGGCCAAGTGTGTGCAATTTGTTTCTTCCCGGCAACGCGGCG 1680
DB 1621 CGGTTGCGGGGCCAAGTGTGTGCAATTTGTTTCTTCCCGGCAACGCGGCG 1680
QY 1681 GCTGTAAACAATGACAGCGAGCGAGTCCGAGAGCCCAAGTCCGCGCTGAGAGACCA 1740
DB 1681 GCTGTAAACAATGACAGCGAGCGAGTCCGAGAGCCCAAGTCCGCGCTGAGAGACCA 1740
QY 1741 GCGGCGGCTCGCTCGAGAGAGGATGATTTGCCAGCTGTAAGGAGGCTGAGGCCAT 1800
DB 1741 GCGGCGGCTCGCTCGAGAGAGGATGATTTGCCAGCTGTAAGGAGGCTGAGGCCAT 1800
QY 1801 AAAAGAGAGATGACTTAAGACACGCGCCGCTGAGCGCTTGTAAACCCGCTGAGC 1860
DB 1801 AAAAGAGAGATGACTTAAGACACGCGCCGCTGAGCGCTTGTAAACCCGCTGAGC 1860
QY 1861 TGGGAAGCAAGAGTGTGACTGACAAAGACTTGTGCTGAGCGGTCAAGTCTTGCCATC 1920
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QY 1921 CTCACAGAGTTGCGGCGCGGAGAGTGTGAGGACAGAGCGGAGATGAGCAAGAGAGTG 1980
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QY 1981 ACCATCTCGGAGAACAGAGATTAACGCGGTGATGAGGAACGCAACGGAAGTGAAG 2040
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DB 2041 AAAGTCATGAGAGAAACCTTAGGCGGAGGCTCCCGGAGAAAGGCGGCTGCTCAAGGT 2100
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Db	Accession	Source	Organism	Reference	Title	Journal	Authors
Db	2101	CCGCGACCCCAAGTGAAGAGCTGGCAGAGCCCGCCCGCCCGCCGAGCCCAACCCCGAGCC					
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Db	2161	CGGCCCCCGAGGCTTAAAGCCGCGCGCGCGCTGCGGAGAGCCCACTGCGAAGCCAGCT					
Qy	2221	GGCGCGCGCTTGGAGTGAATGCTGCAAGCGCTCGCCCGGCTGCTGCGAAGCG					
Db	2221	GGCGCGCGCTTGGAGTGAATGCTGCAAGCGCTCGCCCGGCTGCTGCGAAGCG					
RESULT 2	AP003531/c	199384 bp	DNA	linear	PRI 27-APR-2002		
LOCUS	AP003531						
DEFINITION	Human sapiens genomic DNA, chromosome 11q clone: RP11-535C12,						
ACCESSION	AP003531						
VERSION	AP003531.2	GI:20334341					
KEYWORDS	HTG.						
SOURCE	Human sapiens (human)						
ORGANISM	Human sapiens						
REFERENCE	1						
AUTHORS	Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,						
TITLE	Fujiyama, A., Yada, T., Totsuki, Y., Watanabe, H. and Sakaki, Y.						
JOURNAL	Human sapiens genomic DNA						
REFERENCE	2						
AUTHORS	Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,						
TITLE	Fujiyama, A., Yada, T., Totsuki, Y., Watanabe, H. and Sakaki, Y.						
JOURNAL	Submitted (18-APR-2001) Maashira Hattori, The Institute of Physical						
COMMENT	and Chemical Research (RIKEN), Genomic Sciences Center (GSC),						
FEATURES	1-7-22 Suenitro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan						
source	(E-mail: hattori@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,						
	Tel: 81-45-503-9111, Fax: 81-45-503-9170)						
	On Apr 26, 2002 this sequence version replaced gi:13699094.						
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	/db_xref="taxon:9606"						
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	/map="11g"						
	/clone="RP11-535C12"						
Query Match	98.6%;	Score 2238.8;	DB 8;	Length 199384;			
Best Local Similarity	99.8%;	Pred. No. 0;					
Matches 2262;	Conservative 0;	Mismatches 2;	Indels 2;	Gaps 2;			
Qy	5	GATTCGCGCGCTCAGCGCTCCCAAGTGTGGAGTTGCAGGCGTGAGCCACTCAGCTGG					
Db	182664	GATTCGCGCGCTCAGCGCTCCCAAGTGTGGAGTTGCAGGCGTGAGCCACTCAGCTGG					
Qy	65	CATCAAGTTTCAAAATACATTTATCTAGTAGCCATPACATTTCTCCAGTTTGTCCACAGA					
Db	182604	CATCAAGTTTCAAAATACATTTATCTAGTAGCCATPACATTTCTCCAGTTTGTCCACAGA					
Qy	125	CATCTATGACTTGAGCAAGCTCTTAATAATCCAGAGGTGCAGCGTTTGATGCTATAG					
Db	182545	CATCTATGACTTGAGCAAGCTCTTAATAATCCAGAGGTGCAGCGTTTGATGCTATAG					
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QY	305	CCAGAGATTCAAGAGCAGCCCTGAGACACACAGGGGAGACTGGACATTAACAAGAATTAATAA	364
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LOCUS Homo sapiens uncoupling protein 2 gene, promoter region and exon 1;
DEFINITION nuclear gene for mitochondrial product.
ACCESSION AF306570
VERSION AF306570.1 GI:11037742
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 3270)
AUTHORS Schmeitler,C., Oberkofler,H., Esterbauer,H. and Patack,W.
TITLE UCP2 promoter region and exon 1
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3270)
AUTHORS Schmeitler,C., Oberkofler,H., Esterbauer,H. and Patack,W.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2000) Laboratory Medicine, Landeskranken
Salzburg, Mueller Hauptstr. 48, Salzburg A-5020, Austria
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QY 65 CTAAAGTTTCAAAATACATTTATCTAGTACCATATCATTTCTCAATTTGTGCACAGAGA 124
DB 981 CTAAAGTTTCAAAATACATTTATCT-GTACCATATCATTTCTCAATTTGTGCACAGAGA 1039
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DB 1040 CATCTTATGACTTGAAGCAAGCTGCTAAATATCAAGGCTGACAGCTTTGATGTCTATAG 1099
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 VERSION
 AP003717.3
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 GI:20334343
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 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 REFERENCE
 1
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 Homo sapiens genomic DNA
 Published Only in Database (2001)
 2 (bases 1 to 156370)
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 Title
 JOURNAL
 AUTHORS
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 JOURNAL
 Submitted (04-JUN-2001) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 1-7-22 Suehiro-Chou,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:hattori@gscc.riken.go.jp, URL:http://hgp.gscc.riken.go.jp/,
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 On Apr 26, 2002 this sequence version replaced gi:16904692.
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DB 43504 TGCCTGGGCACTGTTGTCTGACGTTTGAATTTGTTCTTCCCGAACAAGCGCGGCTG 43445
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DB 43384 CGCGCTGCTGCGAGAGGAGGTAGTTTGCACAGCTTAAAGGAGGCTGAGCCCATAAA 43325
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QY 1925 CAGAGTTTGGCGGCCGAGAGAGTGTGAGGCAAGGCGGAGAGTGTGCAAGGAGTGAACA 1984
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RESULT 5
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LOCUS   197031 bp DNA linear HTG 07-JUL-2000
DEFINITION Homo sapiens chromosome 11 clone Rpl1-535C12, WORKING DRAFT
SEQUENCE, 23 unordered pieces.
AC019121
AC019121.3 GI:8440022
HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eueleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominiidae; Homo.
REFERENCE 1 (bases 1 to 197031)
          Waterston,R.H.
          The sequence of Homo sapiens clone
          Unpublished
          2 (bases 1 to 197031)
          Waterston,R.H.
          Direct Submission
          Submitted (30-DEC-1999) Genome Sequencing Center, Washington
          University School of Medicine, 4444 Forest Park Parkway, St. Louis,
          MO 63108, USA
COMMENT  On Jun 10, 2000 this sequence version replaced gi:7105573.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0535C12
----- Summary Statistics -----
Sequencing vector: M13; 55%
Chemistry: Dye-primer ET; 55% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 182418 bases at least Q40
Consensus quality: 187565 bases at least Q30
Consensus quality: 190012 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 194831; sum-of-contigs
Quality coverage: 4.10 in Q20 bases; agarose-fp
Quality coverage: 4.05 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 2971: contig of 2971 bp in length
* 2972 3071: gap of unknown length
* 3072 5764: contig of 2693 bp in length
* 5765 5864: gap of unknown length
* 5865 8568: contig of 2704 bp in length
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	*	23852	23951	gap of unknown length
	*	23952	28414	contig of 4463 bp in length
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	*	28515	33195	contig of 4681 bp in length
	*	33196	33295	gap of unknown length
	*	33296	38648	contig of 5353 bp in length
	*	38649	38748	gap of unknown length
	*	38749	44925	contig of 6177 bp in length
	*	44926	45025	gap of unknown length
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	*	58956	68289	contig of 9334 bp in length
	*	68290	68389	gap of unknown length
	*	68390	77123	contig of 8734 bp in length
	*	77124	77223	gap of unknown length
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	*	87393	96029	contig of 8637 bp in length
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	*	104892	116912	contig of 12021 bp in length
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	*	142994	143093	gap of unknown length
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ORIGIN

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Best Local Similarity 99.2%; Pred.No. 0;
Matches 2249; Conservative 0; Mismatches 12; Indels 5; Gaps 4;

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QY 305 CCAAGATTCAAGACAGCTGTGACAAACAAGGAGACTGTCTACTAAGAAATTAATA 364
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RESULT 6
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 SEQUENCE, 15 unordered pieces.
 ACCESSION AC024029
 VERSION AC024029.3 GI:7230916
 KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominiidae; Homo.
 1 (bases 1 to 155668)
 Waterston, R.H.
 The sequence of Homo sapiens clone
 Unpublished
 2 (bases 1 to 155668)
 Waterston, R.H.
 Direct Submission
 Submitted (20-FEB-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 On Mar 13, 2000 this sequence version replaced gi:7109555.

COMMENT
 ----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUSGC
 Web site: http://genome.wustl.edu/gsc/index.shtml
 Project Information -----
 Center project name: H NH0167N04
 ----- Summary Statistics -----
 Sequencing vector: MJ3; 100%
 Sequencing method: Dye-terminator Big Dye; 0% of reads
 Chemistry: Dye-terminator Big Dye; 0% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 146450 bases at least Q40
 Consensus quality: 146429 bases at least Q20
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 Insert size: 168000; agarose-fp
 Insert size: 154268; sum-of-contigs
 Quality coverage: 3.98 in Q20 bases; agarose-fp
 Quality coverage: 4.38 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 15 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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 * 20231 25513: contig of 5283 bp in length
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Qy 1805 GAGGAAGTGAAGTGAAGACGCGCGCGCTGTGAAGAACGCTGTGTGTGTGTGT 1864
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Qy 1865 AAGGAAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1924
Db 68552 AAGGAAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 68493
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RESULT 7
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LOCUS
DEFINITION
Homo sapiens uncoupling protein 2 (mitochondrial, proton carrier).
(UCP2) gene, complete cds; nuclear gene for mitochondrial product.
DQ087219
VERSION
DQ087219.1 GI:67515418
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
REFERENCE
1 (bases 1 to 12177)
Livingston,R.J., Rieder,M.J., Shaffer,T., Bertucci,C., Baier,C.N.,
Rajkumar,N., Wills,H.T., Daniels,M., Downing,T.K., Stanaway,I.B.,
Nguyen,C.P., Gilderbieve,H., Cassidy,C.M., Johnson,B.J.,
Swanson,D.E., McFarland,I., Yool,B., Park,C. and Nickerson,D.A.
Direct Submission
JOURNAL
Submitted (07-JUN-2005) Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA
COMMENT
To cite this work please use: NIEHS-SNPs, Environmental Genome
Project, NIEHS S15478, Department of Genome Sciences, Seattle, WA
(URL: http://esp.gs.washington.edu).
FEATURES
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Matches 2065; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Matches 2065; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

[illegible]

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Db	961	CACATATGCGCCCGGCTGACACAGGGGTAAAGTGTGAATATACAGAAATGACTGAC	1020
QY	1223	GTCATTGGGAATCGGTTTCCCTATGTAAAAATGAGGGTTAAATACAGCTTCTCTACTC	1282
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QY	1283	CCCAAGCAGCAGTGTGTGTCCCGGACAGAGGGCCCAATTGTGTGCTGTCCAGTCA	1342
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QY	1343	TACCCCAACAGGACGGGTCAAGCAATTAAAGCGAACCAAGGCCGGTCCATCTCTAGC	1402
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QY	1943	GAGAGTGTGAGGCAAGGCGGGGAGTGGCAAGGAGTGAACATTCGGGGAAACAGAGAG	2002
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QY	2183	GCGCGCGCTGCGGGAGGCCCACTGGAGAACCCAGCTGCGCGGCGCTTGGGATTTGACTG	2242
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Qy      1901 TGGGCGTCAAGTCTGCTGCTCAAGAGTTCGCGCGCGAGAGAGTGTGAGAGAGC 1960
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Qy      2081 AAAAGCGGCTGCTCAAGAGTCTTCGCAACCAAGTGAAGAGTGCAGAGCGCGCGCGCC 2140
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 LOCUS Homo sapiens cDNA: FLJ22089 fis, clone HEP16080, highly similar to
 DEFINITION HSU94592 Human uncoupling protein homolog (UCPH) mRNA.

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ACCESSION AK025742
VERSION AK025742.1 GI:10438154
KEYWORDS oligo capping, fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kawabata, A., Hiki, T., Kobatake, N., Inagaki, H., Ikema, Y.,
Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T.,
Shibahara, T., Tanaka, T., Nakamura, Y., Isoagi, T. and Sugano, S.
TITLE NEPO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2131)
AUTHORS Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail: flicdn@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286,
Fax: 81-3-5449-5416)
COMMENT NEPO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5' - & 3' - end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
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RESULT 10
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LOCUS AR039137 736 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5807740.
ACCESSION AR039137
VERSION AR039137.1 GI:5958500
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 736)
AUTHORS Amaral, M. Catherine, and Chen, J.-L.
TITLE Regulators of UCP2 gene expression
JOURNAL Patent: US 5807740-A 1 15-SEP-1998;
FEATURES
source 1. 736
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ORIGIN

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DEFINITION Sequence 1 from patent US 5849514.
ACCESSION AR05267
VERSION AR05267.1 GI:5995483
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 736)
AUTHORS Amaral, M. Catherine, and Chen, J.-L.
TITLE Method of identifying agents that modulate UCP2 promoter activity
JOURNAL Patent: US 5849514-A 1 15-DEC-1998;
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ORIGIN

Query Match 21.4%; Score 485; DB 6; Length 736;
Best Local Similarity 99.6%; Pred. No. 1.8e-91;
Matches 507; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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DB 300 GAGCGGAGGAGTCCCGCGAGAAAGCGAGTGTCTCAAGGAGTCTCCGACCCCAAGTAGAGAG-T 358
QY 2122 GAGCAGGCCCGGCCCGCCGCGAGAGCCCAACCCCGGAGCCCGCCCGAGGCTTAAAGCGG 2181
DB 359 GAGCAGGCCCGGCCCGCCGCGAGAGCCCAACCCCGGAGCCCGCCCGAGGCTTAAAGCGG 418
QY 2182 CGCGCGCGCTTGGCGGAGAGCCCACTGCGAAGCCCAAGTGTGGCGGCTTGGAGTTGACT 2241
DB 419 CGCGCGCGCTTGGCGGAGAGCCCACTGCGAAGCCCAAGTGTGGCGGCTTGGAGTTGACT 478
QY 2242 GTCCACGCTGCGCGGAGTGTCTCCAGAGCGG 2270
DB 479 GTCCACGCTGCGCGGAGTGTCTCCAGAGCGG 507

RESULT 12
BD061651
LOCUS BD061651 736 bp DNA linear PAT 27-AUG-2002
DEFINITION Regulators of UCP2 gene expression.
ACCESSION BD061651
VERSION BD061651.1 GI:22607256
KEYWORDS JP 2001507943-A/1.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 736)

AUTHORS Amaral, C. M. and Chen, J. L.
 TITLE Regulators of UCP2 gene expression
 JOURNAL Patent: JP 2001507943-A 1 19-JUN-2001;
 COMMENT TULARIK INC
 PN JP 2001507943-A/1
 PD 19-JUN-2001
 PF 22-APR-1998 JP 1998547120
 PR 25-APR-1997 US 08/846012
 PI CATHERINE M AMARAL, JIN LONG CHEN
 PC C12N1/00, C12N5/10, C12N15/11, C12N15/63, C12Q1/02, C12Q1/68 CC
 Strandedness: Double;
 CC Topology: Linear;
 FH Key

FEATURES
 source Location/Qualifiers.
 1. 736
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 21.4%; Score 485; DB 6; Length 736;
 Best Local Similarity 99.6%; Pred. No. 1.8e-91;
 Matches 507; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

1762 GGGTGGAGTATTGCGCAGCGAGGGGCTGGCCCATAAAGAGAGCACTTAAG 1821
 1 GGGTGGAGTATTGCGCAGCGAGGGGCTGGCCCATAAAGAGAGCACTTAAG 60
 1822 ACACGGCCCGCTGAGCGCTTGTAGAAACCGTCTGCTGGAGAGGCAAGAGGTGTG 1881
 61 ACACGGCCCGCTGAGCGC-TGTTAGAAACCGTCTGCTGGAGAGGCAAGAGGTGTG 119
 1882 ACTGGAACAAGCTTTCTGCGCGCTCACTCTTCATCTTCAAGAGCTTGGCGCCG 1941
 120 ACTGGAACAAGCTTTCTGCGCGCTCACTCTTCATCTTCAAGAGCTTGGCGCCG 179
 1942 AGAGAGTGAAGGAGAGGCGGAGTGGCAAGGAGTGAACCATTCGCGGAGCAAGAGA 2001
 180 AGAGAGTGAAGGAGAGGCGGAGTGGCAAGGAGTGAACCATTCGCGGAGCAAGAGA 239
 2002 GTAAACCGCGTATGAGAGCGACCGAAACGAGAGTGAAGAAATCATGAGAGAACCTTA 2061
 240 GTAAACCGCGTATGAGAGCGACCGAAACGAGAGTGAAGAAATCATGAGAGAACCTTA 299
 2062 GCGCGCGCGTCTCCCGCGAAAGCGCGTCTCCAGGCTTCGCAACCAAGTAGAGCT 2121
 300 GCGCGCGCGTCTCCCGCGAAAGCGCGTCTCCAGGCTTCGCAACCAAGTAGAG-T 358
 2122 GCGCGCGCGTCTCCCGCGAGGCGCCACCGCGGCGCGCGCCCGAGGCTTAAGCG 2181
 359 GCGCGCGCGTCTCCCGCGAGGCGCCACCGCGGCGCGCGCCCGAGGCTTAAGCG 418
 2182 GCGCGCGCGTCTCCCGCGAGGCGCCACCTGCAAGACCCAGAGTGGCGCGCTTGGAGTTGACT 2241
 419 GCGCGCGCGTCTCCCGCGAGGCGCCACCTGCAAGACCCAGAGTGGCGCGCTTGGAGTTGACT 478
 2242 GTCCACGCTCGCGCGGCTGTCGACGCG 2270
 479 GTCCACGCTCGCGCGGCTGTCGACGCG 507

RESULT 13
 AX346794
 LOCUS AX346794 5283 bp DNA linear PAT 01-FEB-2002
 DEFINITION Sequence 1865 from Patent WO0200928.
 ACCESSION AX346794
 VERSION AX346794.1 GI:18494680
 KEYWORDS
 SOURCE
 ORGANISM
 other sequences; artificial sequences.
 REFERENCE
 AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.

TITLE Diagnose of diseases associated with the immune system
 JOURNAL Patent: WO 0200928-A 1865 03-JAN-2002;
 EpiGenomics AG (DE)
 FEATURES
 source Location/Qualifiers
 1. 5283
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="chemically treated genomic DNA (Homo sapiens)"

ORIGIN

Query Match 16.0%; Score 364.2; DB 6; Length 5283;
 Best Local Similarity 77.4%; Pred. No. 5.1e-66;
 Matches 467; Conservative 0; Mismatches 133; Indels 3; Gaps 2;

1668 CGACACGCGCGCGCTGTACCAATCGACAGCGCGCGCTGCGAGGCCCACTCCGC 1727
 2 CGATTAACGCGCGCGCTGTATTAATTAATGCGAGGTCGCGAGGCTTTAGTTTCTGT 61
 1728 CTTGCAAGAGCGACCGCGCGCTGCTCGCAGAGGCTGCTTGGCCAGGCTAGG 1787
 62 TTTGTAGAGTATGTCGCGCGCTGCTGTAAGAGGCTGAGTGTGTTAGCGTA-GG 120
 1788 GGGCTGGGCCCATAAAGAGAGAGTGAATTAAGACACGCGCCCGCTGAGCGCTTTAG 1847
 121 GGGCTGGGTTATTAAGAGAGAGTATTAAGATACGTTAG--TGAGCGTTGTTAG 178
 1848 AACCGTCTGCTGCGAGAGGCAAGAGGTGTGAATGACACACCTTTGTCGCGCT 1907
 179 AATCGTTTGTGTTGGAGAGGTAAGAGTGTGATTAAGATTAATTTGTTGGCGCT 238
 1908 CAGCTTGCATCTCTCAAGAGGTTGGCGCGCCGAGAGAGTGAAGAGGCGGAG 1967
 239 TAGTTTGTATTTTATTAAGAGTTGGGTTCAAGAGTGAAGAGTGAAGAGGCGGAG 298
 1968 TGGCAAGGAGTGAACATCTTGGGGAAGAGAGATTAACCGCTGATGAGACGACGA 2027
 239 TGTGAAGAGTGAATTTTCGGGGAAGAGAGTAAACCGGTGATGAGACGACGA 358
 2028 AACGAGTGAAGAAATCATGAGAGAACCTTACGCGCGCGCTCCCGCGAAAGCG 2087
 359 AACGAGTGAAGAAATTAAGAGAAATTTTACGCGCGCGCTTTCGCGAAAGCG 418
 2088 GCTGCTCAGAGTCTCCGACCAAGTAGAGCTGCGAGCGCGCGCGCCCGCAGAGC 2147
 419 GTTGTATTAAGGTTTGTATTAAGAGGTTGATGTTGCTTGTGTTGATAGT 478
 2148 CCCACCGCGCGCGCGCGCCCGAGGCTTAAGCGCGCGCGCTGCGAGGCCCACT 2207
 479 TTTATTTGCGGTTTCGTTTGAAGTTTAAGTCCGCTGCTGTTGCGCGAGTTTAAT 538
 2208 GCGAAGCCACAGCTGCGCGCGCTTGGAGTTGATGCTGACGCTGCGCGCTGCTGAC 2267
 539 GCGAAGTTAAGTGGCGCGCTTGGAGTTGATGTTAAGTGTGTTGCTGCTGTTGAC 598
 2268 GCG 2270
 599 GCG 601

RESULT 14
 AX346795/c
 LOCUS AX346795 5283 bp DNA linear PAT 01-FEB-2002
 DEFINITION Sequence 1866 from Patent WO0200928.
 ACCESSION AX346795
 VERSION AX346795.1 GI:18494681
 KEYWORDS
 SOURCE
 ORGANISM
 other sequences; artificial sequences.
 REFERENCE
 AUTHORS Olek, A., Piepenbrock, C. and Berlin, K.
 TITLE Diagnose of diseases associated with the immune system

JOURNAL									
Patent: WO 0200928-A 1866 03-JAN-2002;									
Epigenomics AG (DE)									
location/Qualifiers									
1..5283									
/organism="synthetic construct"									
/mol_type="unassigned DNA"									
/db_xref="taxon:32630"									
/note="chemically treated genomic DNA (Homo sapiens) "									
ORIGIN									
Query Match	13.8%	Score 312.4	DB 6	Length 5283					
Best Local Similarity	72.0%	Pred. No. 4.9e-55							
Matches 435	Conservative 0	Mismatches 166	Indels 3	Gaps 2					
OY	1667	CCGACAACGCGCGGCTGTAACTCAATGACGACGAGGCGCGTTCGAGAGCCCAAGTCCCG	1726						
DB	5283	CCGACAACGCGACCACTTAATCAATGACGACGAGGCGCGTTCGAGAGCCCAAGTCCCG	5224						
OY	1727	CCCTGACAGAGCCAGCGCGCTTCGCTCGAGAGAGGTGGTATGTTGCCAGCGTAGG	1786						
DB	5223	CCCTACAAAAAACCAACCGCGGCTTCGCTCGAAAAAATAATATTAATTAACCAAGTA-A	5165						
OY	1787	GGGGCTGGGCCCCATTAAGAGAGAGTGAATTAAGACAGCGGCCCGCTGACGCTGTTA	1846						
DB	5164	AAAACTAAACCATTAATAAAAAAATACTTAACCAAGCC-AATAAACCTATTA	5107						
OY	1847	GAACCCGCTCTGCTGAGAGGCAAGAGGTGTGATGACGAAGACTTGTTCGCGCG	1906						
DB	5106	AAACCCGCTCTTAATTAATAAAAAAATAATTAATTAATTAATTAATTAATTAATTAATTA	5047						
OY	1907	TCAGTCTTGCATCTCTCAAGAGGTGGCGCCCGAGAGTGTGAGCAGAGCGCGGA	1966						
DB	5046	TCATCTTACATCTCTCAAAAAATTAACGAGCCGAAAAAATAATTAACAAAAAGAAA	4987						
OY	1967	GTGCGAAGGAGTGACATCTTCGCGGAACGAAGAGTAAAGCGGTGATGGAGCGACCG	2026						
DB	4986	ATTAACAAAAAATAACATCTCTGAAAAACGAAAAATTAACCGCATTAATAAACGACGA	4927						
OY	2027	AAACGGAGTGAGAAAGTCAATGAGAGAACCTTAGCGCGGCGGTCCCGCGAAAAAGC	2086						
DB	4926	AAACGAAATTAATAAAAAATCAATAAAAAACCTTAAGAAACGATCCCGCGAAAAAC	4867						
OY	2087	GGCTGCTCCAGGAGTCCGCAACCCAGTAGAGAGTGGAGGCGCGGCGCCCGCGACAG	2146						
DB	4866	GACTACTCTCAAAATTTCCGCAACCAATTAATACTTAACAAACCGACCCCGCGCAA	4807						
OY	2147	CCCCACCCCGGCGCCCGCCCGAGGCTTAAAGCGCGCGCGCTGCGCGAGACCCAC	2206						
DB	4806	CCCCACCCCGAAACCCCGCCCGGAAACTTTAAACCGCGCGCGCTAAGCAACCCAC	4747						
OY	2207	TGCGAAGCCCAAGCTGGCGGCTTGGGATTTGATCTGACAGCTTGCCCGCTGTCGGA	2266						
DB	4746	TACGAAACCCCAACTACGCGCGCTTTAAATTAATCATCATCAGCTTCGACCACTGTCGA	4687						
OY	2267	CGCG 2270							
DB	4686	CGCG 4683							
RESULT 15									
AC090270/C	AC090270	179222 bp	DNA	linear	HTG 06-AUG-2002				
LOCUS	AC090270	179222 bp	DNA	linear	HTG 06-AUG-2002				
DEFINITION	AC090270	179222 bp	DNA	linear	HTG 06-AUG-2002				
SEQUENCE	AC090270	179222 bp	DNA	linear	HTG 06-AUG-2002				
ACCESSION	AC090270	179222 bp	DNA	linear	HTG 06-AUG-2002				
VERSION	AC090270.3	GI:22123606							
KEYWORDS	HTG, HTGS_PHASE1, HTGS_DRAFT, HTGS_FULLTOP.								
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;								
	Homnidae; Homo.								
REFERENCE	1 (bases 1 to 179222)								

AUTHORS
TITLE
JOURNAL
REFERENCES
AUTHORS

Birren, B., Nusbaum, C. and Lander, E.
 Homo sapiens chromosome 15, clone RP11-1653
 Unpublished
 2 (bases 1 to 179222)

TITLE
JOURNAL
REFERENCES
AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
 Barna, N., Beattie, V., Boguslavsky, L., Bouhagalter, B., Brown, A.,
 Camarata, J., Campoliano, A., Choquel, Y., Colangelo, M., Collins, S.,
 Collymore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S.,
 Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J.,
 Gardyna, S., Glnde, S., Goyette, M., Graham, L., Hulme, I., Johnson, R.,
 Hago, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
 Jones, C., Karates, A., Larocque, K., Lamazares, R., Lander, T.,
 Lehotcký, J., Levine, R., Liu, G., Maclean, C., MacDonald, P.,
 McGrath, N., Matthews, C., McCarthy, M., McGowan, P., McDermott, K.,
 McPheters, R., Meldrum, J., Menes, L., Mihova, T., Mings, V.,
 Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,
 O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
 Plunkhang, P., Pierre, R., Pollara, V., Raymond, C., Retta, R.,
 Riebeck, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rossetti, M.,
 Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P.,
 Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, M., Subramanian, A., Talmes, J., Tsafaye, S., Theodore, J.,
 Travers, M., Travis, N., Trigglio, J., Vassiliev, H., Vei, R., Vo, A.,
 Wilson, B., Wu, X., Wyman, D., Ye, M., Young, G., Zainoun, J.,
 Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 179222)

TITLE
JOURNAL
REFERENCES
AUTHORS

Birren, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
 Barna, N., Beattie, V., Bloom, T., Boguslavsky, L., Bouhagalter, B.,
 Camarata, J., Chang, J., Chazaro, B., Choquel, Y., Collymore, A.,
 Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
 Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
 Gardyna, S., Gord, S., Graham, L., Grand-pierre, N., Hago, B.,
 Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
 Karates, A., Kells, C., Lander, T., Levine, R., Lindblad-Toh, K.,
 Liu, G., Maclean, C., MacDonald, P., Major, J., Matthews, C.,
 McCarthy, M., Meldrum, J., Menes, L., Mihova, T., Mings, V.,
 Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
 O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
 Plunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
 Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severy, P.,
 Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talmes, J.,
 Tsafaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
 Vei, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
 Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Aug 6, 2002 this sequence version replaced g113273418.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 --- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 --- Project Information
 Center project name: L12470
 Center clone name: 16.E.3
 --- Summary Statistics
 Sequencing vector: Plasmid, n/a, 100% of reads
 Chemistry: Dye-terminator Big Dye, 100% of reads
 Assembly program: Phrap, version 0.960731
 Consensus quality: 17207 bases at least Q40
 Consensus quality: 17560 bases at least Q30
 Consensus quality: 17670 bases at least Q20
 Insert size: 17600, agarose-fp
 Insert size: 17772, sum-of-contigs
 Quality coverage: 9.4 in Q20 bases, sum-of-contigs
 Quality coverage: 9.3 in Q20 bases, sum-of-contigs

[illegible]

Db 72596 CAAAAATTAGCTGTGCA CAGTGGCGCA CGTCTGTAA TCCAGCTACTTGGGAGGCTGAGG 72537
 Qy 419 -AGTAGGACTGCTTGTGTC CAGAGAGGTCAAGA CTGCAGTGAGCTGAG ACCCAGCCACTGC 477
 Db 72536 CAGGAGAA TCCCTTGAA ACCAGAGGCGAGAGGTTGCAGTAA GCTGAGACTGTGCCACTGC 72477
 Qy 478 ATTCCAGCCTGGGCA CAAAAAGAGACCCTGTCTCAAAAAATTAAGTTAA 527
 Db 72476 ACTCCAGTCTGGTGACAGAGCGAGAGTCTGTCTCAAAAAA AAAAAA 72427

Search completed: December 21, 2005, 21:08:07
 Job time : 11049 secs

ORIGIN (NIMH/NIHRI, National Institutes of Health). Note: this is a NIH_MGC Library."

Query Match 26.1%; Score 593.2; DB 2; Length 941;

Best Local Similarity 95.3%; Pred. No. 9.9e-74;

Matches 667; Conservative 0; Mismatches 23; Indels 10; Gaps 5;

QY 763 TGTTCAGCAATCTCAGCAAAATTTCCGAGCTTCCGAAATGACAGCCAGCAG 822
 DB TTTTCAGCAATCTCAGCAGC-AATTTCCGAGCTTCCGAAATGACAGCCAGCAG 644
 QY 823 AGCTCAGGCAAAAGCTGAGAACTGCGGAGGAGACTCACTGTCGCAAAAAAAT 882
 DB AGCTCAGGCAAAAGCTGAGAACTGCGGAGGAGACTCACTGTCGCAAAAAAAT 584
 QY 883 TTATC---TTTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 938
 DB TTATCAGTCTCCGCTGTTGTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 524
 QY 939 TCTTTCCT 994
 DB TCTTTCCT 464
 QY 995 TGGCAAGATCT 1054
 DB TGGCAAGATCT 404
 QY 1055 GCCAGAGCATGCGCTGCGGCGTGTCTTTCTTTCCGCTATTA-TTATCCAGGCCATCCCA 1113
 DB GCCAGAGCATGCGCTGCGGCGTGTCTTTCTTTCCGCTATTAAGTATCCAGGCCATCCCA 344
 QY 1114 GCTCTGCTCCCTCAGCTGTTTCCCTGCGAGTCCCTTCTGCTGTGTAAGAAACATATGCG 1173
 DB GCTCTGCTCCCTCAGCTGTTTCCCTGCGAGTCCCTTCTGCTGTGTAAGAAACATATGCG 284
 QY 1174 CCGGCTTACCAAGGCTGTAAGTGTGTAATCAGAAAGATGACTGAACGTTTGGGAC 1233
 DB CCGGCTTACCAAGGCTGTAAGTGTGTAATCAGAAAGATGACTGAACGTTTGGGAC 224
 QY 1234 TCCGTTCTCTATTTGTAATAATGAGAGTTAATACAGCTTCTCTACTCCCAACGAC 1293
 DB TCCGTTCTCTATTTGTAATAATGAGAGTTAATACAGCTTCTCTACTCCCAACGAC 164
 QY 1294 GTGTTTGTCCGCGCAGAGGCGCCATTTGCTGTGTCAGCATCACTTACCCCAAG 1353
 DB GTGTTTGTCCGCGCAGAGGCGCCATTTGCTGTGTCAGCATCACTTACCCCAAG 104
 QY 1354 GACGGGTACGCAATTAAGGCAACGAGGCCGCTCATCTCTGACGCTTTTTCAT 1413
 DB GACGGGTACGCAATTAAGGCAACGAGGCCGCTCATCTCTGACGCTTTTTCAT 44
 QY 1414 CCCAGGCTGAGACGAGCTGAGCTGAGGCCGCTGAGC 1453
 DB CCCAGGCTGAGACGAGCTGAGGCCGCTGAGC 4

RESULT 2
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 LOCUS OK6405.81 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1518728 3'
 DEFINITION similar to gb:K17360_rnal HOMOBBOX PROTEIN HOX-D4 (HUMAN); mRNA
 sequence.
 ACCESSION AA903751
 VERSION AA903751.1 GI:3038874
 KEYWORDS EST.
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 314)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 Bismert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINU at:
www-bio.llnl.gov/dbp/image/image.html
 Insert Length: 521 Std Error: 0.00
 Seq primer: -40ml3 fwd. RT from Amersham
 High quality sequence stop: 297.

FEATURES

Source

1..314
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/db_xref="taxon:9606"

/clone="IMAGE:1518728"

/tissue_type="pooled germ cell tumors"

/lab_host="DH10B"

/clone_id="NCI_CGAP GC4"

/note="Vector: pT73D-Pac (Pharmacia) with a modified
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 germ cell tumors, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT73
 vector. Library is normalized. Library was constructed by
 Bento Soares and M. Fatima Bernaldo."

ORIGIN

Query Match 13.3%; Score 303; DB 1; Length 314;

Best Local Similarity 99.7%; Pred. No. 7.5e-33;

Matches 314; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 907 TTCTTCT 966
 DB 1 TTCTTCT 60
 QY 967 TTCT 1026
 DB 1 TTCT 120
 QY 1027 CTTGACTTCTGTTTCCAGCTGCTTCTGCAAGACATGCGCTGCGGCTTTTCTTT 1086
 DB 121 CTTGACTTCTGTTTCCAGCTGCTTCTGCAAGACATGCGCTGCGGCTTTTCTTT 180
 QY 1087 CCGCTATTAATATCAGAGCCCATCCAGCTTGTCCCTGAGCTGTTCCCTGAGCTCC 1146
 DB 181 CCGCTATTAATATCAGAGCCCATCCAGCTTGTCCCTGAGCTGTTCCCTGAGCTCC 240
 QY 1147 CTTCTGCTGTGAAGAACATATGCGCGGCTGACACAGGCTGTAAGTGTGTAATATC 1206
 DB 241 CTTCTGCTGTGAAGAACATATGCGCGGCTGACACAGGCTGTAAGTGTGTAATATC 299
 QY 1207 AGGAAGATGACTGA 1221
 DB 300 AGGAAGATGACTGA 314

RESULT 3
 B1222607 427 bp mRNA linear EST 11-JUL-2001
 LOCUS B1222607 602940387F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5103573 5',
 DEFINITION mRNA sequence.
 ACCESSION B1222607
 VERSION B1222607.1 GI:14676051
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Euteleostomi; Mammalia; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.
TITLE	1 (bases 1 to 592)
JOURNAL	Ansoerge,W., Krieger,S., Regiert,T., Rittmüller,C., Schwager,B., Mewes,H.W., Well,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
COMMENT	EST (Ansoerge,W., Krieger,S., Regiert,T., Rittmüller,C., et al.) Unpublished (2003) Contact: MIPS MIPS
FEATURES	IngoIsaetler Landstr.1, D-85764 Neuherberg, Germany this is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. No BL clone available. This clone (DKFP686B08251) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcencentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers 1..592 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="DKFP686B08251" /dev_stage="adult" /lab_host="DH10B" /clone_id="686 (synonym: hlcc3)" /note="Vector: pTriplex2; Site_1: SfIIA; Site_2: SfIIB; cDNA-collection"
SOURCE	ORIGIN
Query Match	7.1%; Score 161; DB 5; Length 592;
Best Local Similarity	74.8%; Pred. No. 5.2e-13;
Matches 228; Conservative	0; Mismatches 75; Indels 2; Gaps 2;
OY	234 AGGCCAGGACAGGTGGCTCACACCTGTAATTCAGTACTGAGAGTCCGAGTCAGAGG 293
Db	308 AGCGCCGGCCGGTGCTTACACTGTAAATCCAGCAGCTTTGGAGAGCTGAGGCAGGTGG 249
OY	294 ACTGCTTAGGCGCCAGAGATTCAAGAGAGCGCTGGACAACACAGGAGAAGCTT-GTCACTTAC 352
Db	248 ATCATCTGAAGTCCAGAGATTGSAACACAGCGCTGGCAAATAGAGAACCTCATCTCTAC 189
OY	353 AAAAATAATTAATTTAGCCAGGCTTAGTGCTCATCCCTGTGCTGCCAGTACTTAGGGA 412
Db	188 AAAAAAATACAAAATTATGACGAGCTGTGTGGCGCATCTGTATGTTCTAGCTACTCGGGA 129
OY	413 GGCAAGATGAGGAGTGTCTGTCCAGAGAGGCAAGACATGACAGTGAAGCTGAGACCACGCA 472
Db	128 GACTCAGGTGATCATCTTAGACCCCGGAGAGAGGATTACGTAGCTGAGATGTACCA 69
OY	473 CCTGCATTCCAGCCTTGAGCAACAAAAGAGACCTGTCTCAAAAAAATAGTTAATAAT 532
Db	68 -CTGCACCTCCAGCCTGGGCAACAGAGTGAAGACCTGTCTCAAAAAAAAAAAAAAAAAA 10
OY	533 AAATA 537
Db	9 AAACA 5
RESULT 5	BMS56801/c
LOCUS	BMS56801 LOCUS DEFINITION
DEFINITION	BM556801 1033 bp mRNA linear EST 20-FEB-2002
ACCESSION	AGNCNCOURT 6540722 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737964
VERSION	BMS56801
KEYWORDS	EST.
SOURCE	Homo sapiens (human)

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 1033)
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
AUTHORS	Contact: Robert Strusberg, Ph.D.
TITLE	Email: cgsphs-remail.nih.gov
JOURNAL	Tissue Procurement: ATCC
COMMENT	cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Plate: LLM12748 row: 0 column: 21 High quality sequence stop: 606. Location/Qualifiers 1..1033 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone IMAGE:5737964" /tissue_type="duodenal adenocarcinoma, cell line" /lab_host="DH10B (phage-resistant)" /clone_idb="NIH_MGC_88" /note="Organ: small_intestine; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."
ORIGIN	
Query Match	7.1%; Score 160.6; DB 3; Length 1033;
Best Local Similarity	77.0%; Pred. No. 5e-13; Indels 6; Gaps 3;
Matches	235; Conservative 0; Mismatches 64;
Db	231 TTGAGGCCAGACAGTAGTGCTCACCTGTATTCAGTACTGTGTAGAATCGAAGTCAG 290
Db	341 TTTAGGCCAGAGTGGTGGCTGCGCCTATATCCACAATTGGAGAGCCGAGGTGG 282
Oy	231 AGGACTGCTTGAGGCCAGAGATTCAAGACAGCTTGGACACACAGGGAGA-CCTGTAC 349
Db	281 AGGATGGCTTAGATGCAGATGATTCAAAGACAGCCCTGGGCAACATAGGAACCCCTGACTC 222
Oy	350 TACAAAGATATAATTAATTAGCCAGAGCTTAAAGTGTCACTCCCTGTGGTCCAGACTAG 409
Db	221 TACAAATATATTTAAAAATTCGTGGGTGTAGTGGACATACCTGTGGTCCAGCTAGTTG 162
Oy	410 GGAGGAGAAATGAGA---CTGCTTGTCCAGAGAGTCAAAGACTGCAGTAGCTGAGAC 465
Db	161 GGAGGCCAGAGAGAGAGATGCTTGAAGCCAGAGAGTCCAAGAGCTGCATATAGCTGCAT 102
Oy	466 CCAGCCACCTGATTCAGAGCTCGGGGCAAAAAGAGACCCTGTCTCAAAAATAAGTTA 525
Db	101 CTTGCCA-CTGCATCTCGAGCTTGGGCAACAGCCAGAACCTGTCTCAAAAACAAAAAC 43
Oy	526 AATAA 530
Db	42 AAAAA 38
RESULT 6	
LOCUS	BC029972
DEFINITION	Human sapiens clusterin (complement lysis inhibitor, SP-40, 40, sulfolip glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein U), mRNA (cDNA clone IMAGE:493961).
ACCESSION	BC029972
VERSION	BC029972.1 GI:20455818
KEYWORDS	HTC.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Bakayote, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Homidae, Homo.
REFERENCE	1 (bases 1 to 2821)
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klauser, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Bluetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, A.F., Jordan, H., Moore, C., Max, S.T., Wang, J., Hsieh, F., Diatchenko, L., Marisina, K., Farmer, A.A., Rubin, G.M., Hong, L., Sapleton, M., Soares, M.B., Bonaldi, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Tothiyak, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, A.A., McGowan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hult, S.W., Vallatton, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Pahey, J., Halton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shavchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.T., Skalski, U., Smallos, D.E., Schmeckel, A., Schein, J.E., Jones, S.V. and Marra, M.A.
CONSTRM	MMMLLian Gene Collection Program Team
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED	12477932
REFERENCES	2 (bases 1 to 2821)
AUTHORS	
CONSTRM	
TITLE	
JOURNAL	
REMARK	
COMMENT	
	NIH MGC Project Direct Submission Submitted (06-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA NIH-MGC project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: gcgaps-remail.nih.gov Tissue Procurement: David N. Louis, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunnarsson, P.H., Garcia, A.M., Lu, X., Hult, S.W., Louis, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Naveau, A.N., Gibbs, R.A.
FEATURES	
SOURCE	
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 42 Row: h Column: 7 This clone has the following problem: no 5' EST match. Location/Qualifiers 1..2821 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:493961" /tissue_type="Brain, anaplastic oligodendroglioma with 1p/19q loss" /clone_1lb="NCI CGAP_Brn67" /lab_host="DH10B" /note="Vector: pCMV-SPORT6"
ORIGIN	
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220 AAGAGATTTCCTGAGGCCAGGCACAGTGGCTCACACCTGTATTCCAGTACTGTGAGAG 279

—

Db 357 ACAAACACAGTGGCCAGGTGTGCTACACCTGTATCCAGACCCCTGGAGGCC 298
QY 283 GAGGTCAAGAGACTCTTGAAGCCAGAGTTCAAGAGACCTGAGACACAGGAGAC 342
Db 297 AGGTAGGTGAGACGCTTGAAGCCAGAGGCTCAAGAACAGCTGGGACATACCAAAAC 238
QY 343 CT-GTCACTACAAAGATTAATTAATTAAGCCAGGCTTAGTGGCTCATCCCTGTGTCCCA 401
Db 237 TTCACTCTCTCAAAAAATTAAGAAATTAAGTGAAGCAGGTGTGCATGCTGTGTCCCA 178
QY 402 GCTACTGGAGGAGGAGTAGTA-----CTGCTTGTCCAGAGAGTCAAGCTGCACTGA 457
Db 177 GCTACTCTGAGAGCTGAGGTTGAGAGATCACTTAACCCAGAGGCTCAAGGCTTCAGTGA 118
QY 458 GCTGAGACCCAGCAGCTGATTCAGCTGGGCGCAAAAAAGAGACCTGTCTCAAAA 517
Db 117 GCTGTGATCAACACACC-ACATTCAGCTGGGTGGTAAGAGTGAAGACCTGTGTCCAAAA 59
QY 518 ATTAAGTTAATTAATTAATTAATTAATTAAGTTAAACCTTAACACA 564
Db 58 AAAAAAAAAAAAAAAAAAATTAAGAAAAAAGAAAAATTAATAATA 12

RESULT 9
AG014791 749 bp DNA linear GSS 16-FEB-2005
LOCUS AG014791 Homo sapiens genomic DNA, 21q region, clone: 762015N19, genomic

ACCESSION AG014791 AG006506
VERSION AG014791.1 GI:3650009
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
REFERENCE 2 (bases 1 to 749)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (23-SEP-1998) Masahira Hattori, RIKEN Genomic Sciences
Center, RIKEN Yokohama Institute, Yokohama Research Promotion
Division, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa,
230-0045, Japan (E-mail:hattori@gs.c.riken.jp, Tel:81-45-503-9111,
Fax:81-45-503-9113)
COMMENT On Feb 6, 1999 this sequence version replaced gi:2992384.
AG006506: Submitted (27-Mar-1998).

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/map="21q"
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Best Local Similarity 71.9%; Pred. No. 1.5e-12;
Matches 241; Conservative 0; Mismatches 88; Indels 6; Gaps 3;

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QY 293 GACTGCTTGAAGCCAGAGTTCAGAGAGGCTGGACAAACAGGAGAG-CTGTCACTA 351
Db 306 AATGGCTTGAAGCCAGAGTTCAGAGAGGCTGGAGAAACATGCAAAACCCACCTCTA 365
QY 352 CAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 411

Db 366 CAAAAAATACAAAAATTAAGCCAGCATTAATGACATGCTGTATCTCAGCTACCTGGG 425
QY 412 AGCAGAGATGAGACTGCTGT-----CCGAGAGGTCAAGACTGAGTGAAGACC 467
Db 426 AGCTAGGTGAGAGGCTCTTGAAGCCAGAGGCGCAAGGCTGAGTGAAGTCA 485
QY 468 AGCCACCTGATTCAGAGCTGGGCAAAAAAGAGACCTGTCTCAAAAAATTAAGTTAA 527
Db 486 CGCCA-CTGTACTCCAGCTGGGTGAAGAGCCAGACCTGTCTTAAAAAAG 544
QY 528 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 562
Db 545 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 579

RESULT 10
BX504185/c 476 bp mRNA linear EST 04-SEP-2003
LOCUS BX504185 DKFP686G1812.21 686 (synonym: h1cc3) Homo sapiens cDNA clone
DEFINITION DKFP686G1812.3', mRNA sequence.
ACCESSION BX504185
VERSION BX504185.1 GI:32030197
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 476)
AUTHORS Pousetka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Weill,B., Amid,C., Oeinger,A., Fodor,G., Han,M. and
Wiemann,S.
TITLE EST (Pousetka,A., Albert,R., Moosmayer,P., Schupp,I.,
Wellenreuther,R., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS

REFERENCE 2
AUTHORS Ingolstaedter Landstr.1, D-85764 Neubherg, Germany
TITLE This is the 3' sequence of the clone insert
JOURNAL Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email:s.wiemann@dkfz-heidelberg.de,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
COMMENT r1 sequence also available.
This clone (DKFP686G1812) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
location/Qualifiers

FEATURES
source location/Qualifiers
1..476
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFP686G1812"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1lb="586 (synonym: h1cc3)"
/note="Vector: pTribEx2; site_1: sf11A; site_2: sf11B;
cDNA-collection"

ORIGIN

Query Match 6.9%; Score 157; DB 5; Length 476;
Best Local Similarity 69.7%; Pred. No. 2e-12;
Matches 242; Conservative 0; Mismatches 100; Indels 5; Gaps 2;

QY 211 AAAGATTTAAGAAATTTCTTGAAGCCAGGACAGTGGCTCAACCTGTATTCAGTA 270
Db 400 AGAAGATTAAGAAATTTCTTGAAGCCAGGACAGTGGCTCAACCTGTATTCAGTA 341
QY 271 CTGTGAGAGTCCAGAGTCAAGAGTCTTGAAGCCAGGAGTTCAAGAGAGCTGACA 330
Db 340 CTTGGGATTTGAGAGTGGGAGATCACTTGAAGTCAAGAGTTCAAGAGAGCTGGCCA 281

Query Match	6.9%	Score 157	DB 9	Length 680
Best Local Similarity	74.8%	Pred. No. 1.8e-12		
Matches 237	Conservative	0	Mismatches 75	Indels 5
Gaps				3

QY	215	TAAAGAAATTTCTTGAAGCGCAGACGACGACGCTCAACCTGATATTCACATCTGTGAGAA	278
DB	215	TAAACAAATATATTTGGGCGCAGGACACAGTGGCTCCACCTGTATATCCAGCACATTTAGGA	274

Email: cgapbbs-rt@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.G.E. Consortium (LIML)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.shgc.stanford.edu>

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2005, 09:39:26 ; Search time 1254 Seconds
(without alignments)
12064.475 Million cell updates/sec

Title: US-09-869-098A-1_COPY_1_2270
Perfect score: 2270
Sequence: 1 aacgacatcgccgcgcacg.....cgccgcgctcgtccgacgcg 2270

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 496997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_21:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2270	100.0	3505	AAA62932	Aaa62932 DNA cont.
2	846.8	37.3	9314	ADG55405	Adg55405 Human unc
3	485	21.4	736	AAV44874	Aav44874 UCP2 gene
4	485	21.4	736	AAV08879	Aav08879 UCP2 prom
5	447.4	19.7	1161	AAV44599	Aav44599 Human unc
6	364.2	16.0	5283	AB133892	Ab133892 Human imm
7	312.4	13.8	5283	AB133893	Ab133893 Human imm
8	188.4	8.3	41150	ADL13819	Adl13819 Osteoarthritis
9	188.4	8.3	44348	ADN48556	Adn48556 Human Not
10	172.8	7.6	11172	AA829967	Aa829967 Human lun
11	172.8	7.6	11172	ADB33304	Adb33304 Human nov
12	168.4	7.4	25825	ABA19375	Ab19375 Human ner
13	167.2	7.4	135005	ADQ19501	Adq19501 Human sof
14	166.6	7.3	52342	ADA02666	Ada02666 Human MDM
15	166.6	7.3	52342	ADB72404	Adb72404 Human MDM
16	166.6	7.3	52342	ADG55414	Adg55414 Human MDM
17	164	7.2	186510	ADE24797	Ade24797 Human end
18	162.6	7.2	81099	ACN45018	Acn45018 Human gen
19	162.2	7.1	46275	AB110145	Ab110145 Human bre

C	20	162.2	7.1	46275	10	ADL13621	Adl13621 Osteoarthritis
C	21	162	7.1	125910	3	AA64370	Aa64370 Human KCN
C	22	161.8	7.1	7759	4	AAK77916	Aak77916 Human imm
C	23	161.8	7.1	109906	6	ABK94411	Abk94411 DNA encod
C	24	161.8	7.1	109906	12	ADL08112	Adl08112 Human gen
C	25	161.6	7.1	10899	5	ABA15344	Ab15344 Human ner
C	26	161.6	7.1	12758	5	ABA15345	Ab15345 Human ner
C	27	161.4	7.1	93500	13	ADT77142	Adt77142 Type II d
C	28	161.4	7.1	110000	14	AB61124	Ab61124 Human SLIC
C	29	161.2	7.1	56737	6	AB69895	Ab69895 Human hyp
C	30	160.8	7.1	60815	11	ACN43882	Acn43882 Human gen
C	31	160.8	7.1	110000	12	ADN06353_0	Adn06353 Human FLA
C	32	160.8	7.1	110000	13	AD894372_0	Ad894372 Human 5-1
C	33	160.6	7.1	7739	4	AA136824	Aa136824 Human mus
C	34	160.6	7.1	7739	8	ABX59812	Abx59812 CDNA enco
C	35	160.6	7.1	7739	12	ADJ30562	Adj30562 Human mus
C	36	160.6	7.1	8133	6	ABN99663	Abn99663 Human clu
C	37	160.6	7.1	20000	14	AD270132	Ad270132 Human clu
C	38	160.4	7.1	31749	4	AAK72959	Aak72959 Human can
C	39	160.4	7.1	78925	3	AA89888	Aa89888 Human FN
C	40	160	7.0	110000	10	ADG70447_0	Adg70447 Human ANG
C	41	160	7.0	110000	10	AB279565_0	Ab279565 CLID8 and
C	42	160	7.0	169659	12	ADQ59434	Adq59434 Human can
C	43	160	7.0	187851	14	AD213735	Ad213735 Human can
C	44	159.8	7.0	563	14	ACL58953	Ac158953 Human col
C	45	159.8	7.0	30030	11	ACN44714	Acn44714 Human gen

ALIGNMENTS

RESULT 1	AAA62932	standard; DNA, 3505 BP.
ID	AAA62932	
AC	AAA62932;	
DT	02-NOV-2000	(first entry)
DE	DNA containing human uncoupling protein-2 (UCP-2) promoter region.	
KW	Promoter; human; uncoupling protein-2; UCP-2; obesity; diabetes;	
KW	hypertension; hyperlipidaemia; anti-pyretic; de.	
OS	Homo sapiens.	
PN	WO200039315-A1.	
PD	06-JUL-2000.	
PF	22-DEC-1999;	99WO-JP007198.
PR	24-DEC-1998;	98JP-00366719.
PA	(TAKE) TAKEDA CHEM IND LTD.	
PI	Toyoda Y, Kobayashi M, Igaki S;	
DR	WPI; 2000-452407/39.	
PT	DNA with promoter region containing regulator sequence of uncoupling protein-2 (UCP-2), applicable in screening anti-obesity, anti-diabetic, hypotensive, anti-hyperlipidemic and anti-pyretic drugs for use in therapy.	
PS	Claim 4; Fig 1-6; 43pp; Japanese.	
CC	This invention relates to DNA comprising a promoter region containing the regulatory sequences of human uncoupling protein-2 (UCP-2). Included in the invention are a recombinant vector containing the DNA sequence, cells transformed by the vector, and a method for screening for compounds or salts that can promote or inhibit the UCP-2 promoter activity using the transformants. The DNA and cells transformed using it can be used to	

CC screen for anti-obesity, anti-diabetic, hypotensive, anti-hyperlipidemic
CC and anti-pyretic drugs. The present sequence represents DNA containing
CC the UCP-2 promoter sequences
XX

Sequence 3505 BP; 671 A; 1053 C; 894 G; 887 T; 0 U; 0 Other;

Query Match 100.0%; Score 2270; DB 3; Length 3505;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2270; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AACGATCTGCCCGCTCAGCCTCCCAAAGTCTGGGATTTGACAGCGTGAAGCCACCTCAC 60
Qy 61 CTGGCTCAAGTTTCAAAATACATTTATCTAGTACCATCATCTTCCAGTTTGTCCAC 120
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Db 361 AATAAATTTAGCAGAGCTTATGAGCTATCCCTGTGCTCCAGCTACTAGGGAGGAGAG 420
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Db 421 TAGGACTGTCTTGTCCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCCACTGCAAT 480
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Db 841 GAGAACTGTGGGAGGAGACTCAACGTGCACAAAAACTTTATCTTTTCTTTT 900
Qy 901 TTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 960
Db 901 TTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 960
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Db 961 CTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 1020
Qy 1021 AATTCGCTTGAATCTGTGTTTCCAGCTGCTTTGCGCAAGACCAATGCGCTGCGCTTT 1080
Db 1021 AATTCGCTTGAATCTGTGTTTCCAGCTGCTTTGCGCAAGACCAATGCGCTGCGCTTT 1080
Qy 1081 TTTCTTCCGCTAATTAATTCAGAGCCATCCAGCTCTGTGCTCCCTCAGCTGTTCCTTG 1140
Db 1081 TTTCTTCCGCTAATTAATTCAGAGCCATCCAGCTCTGTGCTCCCTCAGCTGTTCCTTG 1140
Qy 1141 CAGTCCCTTCTGTGTGAAGAAACAATATGCGCGCGCTGACCAAGAGTGAATGTGTG 1200
Db 1141 CAGTCCCTTCTGTGTGAAGAAACAATATGCGCGCGCTGACCAAGAGTGAATGTGTG 1200
Qy 1201 AATATCAGAAATGACTGAACGCTTTTGGAACTCGTGTCTCTATTTGTAATGAGGT 1260
Db 1201 AATATCAGAAATGACTGAACGCTTTTGGAACTCGTGTCTCTATTTGTAATGAGGT 1260
Qy 1261 TAATACAGGCTTCTTCTACTCCCAAGCAGTGTGTTGCTCCGCGCAGAGGCGCAAT 1320
Db 1261 TAATACAGGCTTCTTCTACTCCCAAGCAGTGTGTTGCTCCGCGCAGAGGCGCAAT 1320
Qy 1321 TGTGTGCTGTTCAAGCATCAGTTAACCCCAAGAGCAGGATCAAGCAATTAAGCGCAACC 1380
Db 1321 TGTGTGCTGTTCAAGCATCAGTTAACCCCAAGAGCAGGATCAAGCAATTAAGCGCAACC 1380
Qy 1381 AGGCGCGGTCAATCTCTGACGCTTTTCTCATCTCCAGAGGCTGAGACAGCTGCGCTG 1440
Db 1381 AGGCGCGGTCAATCTCTGACGCTTTTCTCATCTCCAGAGGCTGAGACAGCTGCGCTG 1440
Qy 1441 GGCCTGGCTCTGCTGTGTCAGTGTGCGGAGGCGGAGCGGCTGTGCTGTGTAGAG 1500
Db 1441 GGCCTGGCTCTGCTGTGTCAGTGTGCGGAGGCGGAGCGGCTGTGCTGTGTAGAG 1500
Qy 1501 CGTAGAGTCAAGCTGTGTGCTCCCGCGCGCGGAGCTTTAGTGTCTGTGCTCTTAA 1560
Db 1501 CGTAGAGTCAAGCTGTGTGCTCCCGCGCGCGGAGCTTTAGTGTCTGTGCTCTTAA 1560
Qy 1561 CGCAGGCGCTCTCAACGCGGAGGAGAAAGCGCGAAACCCAGCCAGCCCAACGCTGTGT 1620
Db 1561 CGCAGGCGCTCTCAACGCGGAGGAGAAAGCGCGAAACCCAGCCAGCCCAACGCTGTGT 1620
Qy 1621 CGGTTGCGGAGCACTGTGTTGTCAGTGTCTGATTTGCTTCCCGCAACAGCGGCG 1680
Db 1621 CGGTTGCGGAGCACTGTGTTGTCAGTGTCTGATTTGCTTCCCGCAACAGCGGCG 1680
Qy 1681 GCTGTAAACAATGACAGCGAGGCGGCTCGAGAGCCCGAGTCCCGCTGCAAGAGCCA 1740
Db 1681 GCTGTAAACAATGACAGCGAGGCGGCTCGAGAGCCCGAGTCCCGCTGCAAGAGCCA 1740
Qy 1741 GCGCGCGCTGCTCGCAGAGAGGAGGTGTGTTTCCAGCGTGAAGGAGGAGCTGAGCCAT 1800
Db 1741 GCGCGCGCTGCTCGCAGAGAGGAGGTGTGTTTCCAGCGTGAAGGAGGAGCTGAGCCAT 1800
Qy 1801 AAAAGAGAAAGTGAACCTTAAGACACGAGCCCGCTGAGCGCTGTGTAAACCGTCTGAG 1860
Db 1801 AAAAGAGAAAGTGAACCTTAAGACACGAGCCCGCTGAGCGCTGTGTAAACCGTCTGAG 1860
Qy 1861 TGGAGAGCAAGAGTGTGATCTGACCAAGACTTGTCTTGTGCGGCTCAGTCTTGCATC 1920
Db 1861 TGGAGAGCAAGAGTGTGATCTGACCAAGACTTGTCTTGTGCGGCTCAGTCTTGCATC 1920
Qy 1921 CTCAAGAGGTTGCGGCGCCGAGAGAGTGTGAGGCAAGCGCGAGATGTGCAAGGAGGTG 1980
Db 1921 CTCAAGAGGTTGCGGCGCCGAGAGAGTGTGAGGCAAGCGCGAGATGTGCAAGGAGGTG 1980
Qy 1981 ACCATCTCGGAGAAAGAAAGAGTAAACGCGAGTGAAGGAGCGACCGAGAAAGGAGTGGAG 2040
Db 1981 ACCATCTCGGAGAAAGAAAGAGTAAACGCGAGTGAAGGAGCGACCGAGAAAGGAGTGGAG 2040
```


PF 16-JUL-2002; 200205-00197019.
 XX 25-JAN-2001; 2001WO-US002485.
 XX
 PA (CHEW/) CHEW A.
 PA (DENT/) DENTON R. R.
 PA (GILS/) GILSON C. R.
 PA (NAND/) NANDABALAN K.
 PA (PARK/) PARKS K. E.
 PI Chew A, Denton RR, Gilson CR, Nandabalan K, Parke KE.
 XX
 DR MPI; 2004-051505/05.
 DR P-PSDB; ADG65407.
 XX
 PT Haployping Uncoupling Protein 2 gene of an individual comprises
 PT identifying the phased sequence of nucleotides at polymorphic sites of
 PT the gene and assigning a haplotype or haplotype pair consistent with the
 PT phased sequence.
 XX
 PS Claim 1; SEQ ID NO 1; 64bp; English.

CC The invention describes haployping the uncoupling protein 2
 CC (mitochondrial, protein carrier) (UCP2) gene of an individual comprising
 CC identifying the phased sequence of nucleotides at polymorphic sites (PS) 1
 CC -23 for at least one copy of the individual's UCP2 gene and assigning to
 CC the individual a UCP2 haplotype or haplotype pair that is consistent with
 CC the phased sequence. The composition and methods are useful in
 CC haployping and/or genotyping the UCP2 gene in an individual to e.g.
 CC screen for drugs targeting the UCP2 protein to treat a condition or
 CC disease predicted to be associated with UCP2 activity. The disease or
 CC condition may include obesity, diabetes, immunological disorders and
 CC other diseases associated with defects in body mass and thermoregulation.
 CC This sequence represents the human uncoupling protein 2 (UCP2) gene.
 XX
 SQ Sequence 9314 BP; 1904 A; 2619 C; 2371 G; 2397 T; 0 U; 23 Other;

Query Match 37.3%; Score 846.8; DB 12; Length 9314;
 Best Local Similarity 98.9%; Pred. No. 7.5e-156;
 Matches 874; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

QY 1387 GGTTCATCTCTGAGAGGCTTTCTCATCTCCAGGGCTGACAGGAGCTGCTGGGCGG 1446
 Db 1 GGTTCATCTCTGAGAGGCTTTCTCATCTCCAGGGCTGACAGGAGCTGCTGGGCGG 60
 QY 1447 GCTCTGCTTGTCACTGACGGGAGGCGGCGCTTGTGCTGTGTAGAGAGCTGAG 1506
 Db 61 GCTCTGCTTGTCACTGACGGGAGGCGGCGCTTGTGCTGTGTGTAGAGAGCTGAG 120
 QY 1507 GTCAAGCTGAGTGTCTCCGCGCGCGGAGCTTTAGTGTCTTGTCTTAAAGCCGAG 1566
 Db 121 GTCAAGCTGAGTGTCTCCGCGCGCGGAGCTTTAGTGTCTTGTCTTAAAGCCGAG 180
 QY 1567 GCGGCTCCACGGGGGAGAGAGGCGGAAAGCCGAGCCGAGCCGAGCTGTGTGCGGTG 1626
 Db 181 GCGGCTCCACGGGGGAGAGAGGCGGAAAGCCGAGCCGAGCCGAGCTGTGTGCGGTG 240
 QY 1627 CCGGGCCACCTGTGTGCTGCACTTCTGATTTCTTCCCGGCAAGCGGCGGCTGTA 1686
 Db 241 CCGGGCCACCTGTGTGCTGCACTTCTGATTTCTTCCCGGCAAGCGGCGGCTGTA 300
 QY 1687 ACCAATGACAGCAGGCGGCTGCGAGGCGCCGAGTCCCGCTGACAGAGCCAGCGCG 1746
 Db 301 ACCAATGACAGCAGGCGGCTGCGAGGCGCCGAGTCCCGCTGACAGAGCCAGCGCG 360
 QY 1747 CGCTCGCTCGAGAGAGGTGTGTGTTGCTCCAGCGTGAAGGGGCTGAGCCCAATAAAGA 1806
 Db 361 CGCTCGCTCGAGAGAGGTGTGTGTTGCTCCAGCGTGAAGGGGCTGAGCCCAATAAAGA 419
 QY 1807 GGAAGTGACATTAGAACAAGGCGCGCTGAGAGCTGTGTGAACCGGCTGTGGGAAA 1866
 Db 420 GGAAGTGACATTAGAACAAGGCGCGCTGAGAGCTGTGTGAACCGGCTGTGGGAAA 477

QY 1867 GGCAGAGAGTGTGTGACTGAGCAAGACTTTGTTCTGGCGGTGACTGTTCATCTTACA 1926
 Db 478 GGCAGAGAGTGTGTGACTGAGCAAGACTTTGTTCTGGCGGTGACTGTTCATCTTACA 537
 QY 1927 GAGTTGACCGCCCGGAGAGGTGTGAGGCGAGGCGGAGGTGGCAAGAGTGAACATC 1986
 Db 538 GAGTTGACCGCCCGGAGAGGTGTGAGGCGAGGCGGAGGTGGCAAGAGTGAACATC 597
 QY 1987 TCGGGGAAAGAAAGTAAAGCGGCTGATGGAGCGACAGGAAACGGGAGTGAAGAAATC 2046
 Db 598 TCGGGGAAAGAAAGTAAAGCGGCTGATGGAGCGACAGGAAACGGGAGTGAAGAAATC 657
 QY 2047 ATGAGAGAAACCTTAGCGGCGGCGGTCTCCCGGAAAGCGGCTCTTCAAGGCTTCGCG 2106
 Db 658 ATGAGAGAAACCTTAGCGGCGGCGGTCTCCCGGAAAGCGGCTCTTCAAGGCTTCGCG 717
 QY 2107 ACCCAATAGAGCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2166
 Db 718 ACCCAATAGAGCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 777
 QY 2167 CCGAGGCTTAAGCG 2226
 Db 778 CCGAGGCTTAAGCG 837
 QY 2227 GCTTGGAGATTGACTGTTCACAGCTCGCGCGCTGCTTCCAGCGCG 2270
 Db 838 GCTTGGAGATTGACTGTTCACAGCTCGCGCGCTGCTTCCAGCGCG 881

RESULT 3
 AAV4974
 ID AAV4974 standard; cDNA; 736 BP.
 XX
 AC AAV4974;
 XX

DT 16-NOV-1998 (first entry)
 XX
 XX UCP2 gene transcriptional promoter sequence.

DE Uncoupling protein 2; UCP2 gene; transcriptional promoter; mouse;
 XX mitochondrial protein; cis transcriptional regulatory activity; therapy;
 KM expression modulator screening; fat feeding; diabetes; obesity; de.

OS Mus BP.
 XX

PN US5807740-A.
 XX

PD 15-SEP-1998.
 XX

PF 25-APR-1997; 97US-00846012.
 XX

PR 25-APR-1997; 97US-00846012.
 XX

PA (TULA-) TULARIK INC.
 XX

PI Chen J, Amaral MC;
 XX

DR MPI; 1998-520130/44.
 XX

PT Mouse UCP2 gene promoter - useful for forming transfected cell lines
 PT employed in drug screening assays.
 XX

PS Claim 1; Col 7-8; 9p; English.
 XX

CC This sequence represents the mouse mitochondrial uncoupling protein 2
 CC (UCP2) gene transcriptional promoter of the invention. The promoter has
 CC cis transcriptional regulatory activity. Cells containing the promoter
 CC attached to a non-UCP2 gene, in which the non-UCP2 gene is a reporter
 CC gene can be used in screening assays for modulators of UCP2 gene
 CC expression, which may be useful for treating disorders in which the UCP2
 CC gene is upregulated in response to fat feeding, e.g. diabetes and obesity

Sequence 736 BP; 119 A; 236 C; 235 G; 146 T; 0 U; 0 Other;
 SQ

Query Match 21.4%; Score 485; DB 2; Length 736;
 Best Local Similarity 99.6%; Pred. No. 2.8e-85;
 Matches 507; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

```

QY 1762 GGGTGGGTAAGTTTCCAGCGTAGGGGGGCTGGGCCATTAAGAGAGAGCACTTAAG 1821
DB 1 GGGTGGGTAAGTTTCCAGCGTAGGGGGGCTGGGCCATTAAGAGAGAGCACTTAAG 60
QY 1822 ACAGGCCCCCGCTGAGCGCTTGTGAAACCGTCTGCTGGAGAGGCAAGAGTGTGTG 1881
DB 61 ACAGGCCCCCGCTGAGCGCTTGTGAAACCGTCTGCTGGAGAGGCAAGAGTGTGTG 119
QY 1882 ACTGGACAAAGCTGTTCTGGCGGCTGAGTCTGTCATCTCCACAGAGAGTGGCGGCGG 1941
DB 120 ACTGGACAAAGCTGTTCTGGCGGCTGAGTCTGTCATCTCCACAGAGAGTGGCGGCGG 179
QY 1942 AGAGAGTGTGAGGAGCGAGAGCGGAGTGGCAAGAGAGTACCATCTCGGAGACGAAGA 2001
DB 180 AGAGAGTGTGAGGAGCGAGAGCGGAGTGGCAAGAGAGTACCATCTCGGAGAGCAAGA 239
QY 2002 GTAAACCGGCTGATGAGCGACGGAACGGAGTGAAGAAAGTCATGAGAGAAACCTTA 2061
DB 240 GTAAACCGGCTGATGAGCGACGGAACGGAGTGAAGAAAGTCATGAGAGAAACCTTA 299
QY 2062 GCGCGGCGGCTGCGCGGAGAAAGCGGCTGCTCCAGGCTCTCCGACCCAGTAGAGACT 2121
DB 300 GCGCGGCGGCTGCGCGGAGAAAGCGGCTGCTCCAGGCTCTCCGACCCAGTAGAGAG-T 358
QY 2122 GCGAGGCGGCGGCGGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2181
DB 359 GCGAGGCGGCGGCGGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 418
QY 2182 GCGCGGCGGCTGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2241
DB 419 GCGCGGCGGCTGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 478
QY 2242 GTCCACGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2270
DB 479 GTCCACGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 507

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RESULT 4

AAV08879 standard; cDNA, 736 BP.

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XX AC AAV08879;
XX AC 20-MAR-2003 (revised)
DT 25-FEB-1999 (first entry)
XX DE UCP2 promoter.
XX KW UCP2; promoter; transcription factor; modulator; diabetes; obesity;
XX KW therapy; ds.
XX OS Homo sapiens.
XX PN US5849514-A.
XX PD 15-DEC-1998.
XX PF 19-JUN-1998; 98US-00100297.
XX PR 25-APR-1997; 97US-00846012.
XX PA (TULAR-) TULARIK INC.
XX PI Chen J, Amaral MC;
XX DR WPI, 1999-069722/06.
XX PT Screening assay for modulators of UCP2 gene expression - based on

```

PT interaction of transcription factor and defined UCP2 promoter sequence.
 XX Claim 1; Col 7-8; 9pp; English.

CC This sequence represents the UCP2 promoter, and is used in the method of
 CC the invention. The method is a screening assay for agents that modulate
 CC the effect of a transcription factor on a UCP2 promoter comprises
 CC combining the promoter and transcription factor in the presence and
 CC absence of a candidate agent and determining any change in the effect of
 CC the transcription factor on the promoter. The promoter comprises at least
 CC 50 nucleotides of a sequence comprising nucleotides 1-460 of the UCP2
 CC promoter. The method is used to identify agents that modulate UCP2 gene
 CC transcription (agents that upregulate UCP2 are potentially useful for
 CC treating diabetes and obesity). (Updated on 20-MAR-2003 to correct PF
 CC field.)

XX Sequence 736 BP; 119 A; 236 C; 225 G; 146 T; 0 U; 0 Other;

Query Match 21.4%; Score 485; DB 2; Length 736;
 Best Local Similarity 99.6%; Pred. No. 2.8e-85;
 Matches 507; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

```

QY 1762 GGGTGGGTAAGTTTCCAGCGTAGGGGGGCTGGGCCATTAAGAGAGAGCACTTAAG 1821
DB 1 GGGTGGGTAAGTTTCCAGCGTAGGGGGGCTGGGCCATTAAGAGAGAGCACTTAAG 60
QY 1822 ACAGGCCCCCGCTGAGCGCTTGTGAAACCGTCTGCTGGAGAGGCAAGAGTGTGTG 1881
DB 61 ACAGGCCCCCGCTGAGCGCTTGTGAAACCGTCTGCTGGAGAGGCAAGAGTGTGTG 119
QY 1882 ACTGGACAAAGCTGTTCTGGCGGCTGAGTCTGTCATCTCCACAGAGAGTGGCGGCGG 1941
DB 120 ACTGGACAAAGCTGTTCTGGCGGCTGAGTCTGTCATCTCCACAGAGAGTGGCGGCGG 179
QY 1942 AGAGAGTGTGAGGAGCGAGAGCGGAGTGGCAAGAGAGTACCATCTCGGAGACGAAGA 2001
DB 180 AGAGAGTGTGAGGAGCGAGAGCGGAGTGGCAAGAGAGTACCATCTCGGAGAGCAAGA 239
QY 2002 GTAAACCGGCTGATGAGCGACGGAACGGAGTGAAGAAAGTCATGAGAGAAACCTTA 2061
DB 240 GTAAACCGGCTGATGAGCGACGGAACGGAGTGAAGAAAGTCATGAGAGAAACCTTA 299
QY 2062 GCGCGGCGGCTGCGCGGAGAAAGCGGCTGCTCCAGGCTCTCCGACCCAGTAGAGACT 2121
DB 300 GCGCGGCGGCTGCGCGGAGAAAGCGGCTGCTCCAGGCTCTCCGACCCAGTAGAGAG-T 358
QY 2122 GCGAGGCGGCGGCGGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2181
DB 359 GCGAGGCGGCGGCGGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 418
QY 2182 GCGCGGCGGCTGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2241
DB 419 GCGCGGCGGCTGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 478
QY 2242 GTCCACGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2270
DB 479 GTCCACGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 507

```

RESULT 5

AAV44599 standard; DNA, 1161 BP.

```

XX AC AAV44599;
XX AC 24-NOV-1998 (first entry)
XX DE Human uncoupling protein-2 UCP2 gene clone hUCP2-g2 sequence 2.
XX KW Uncoupling protein-2; UCP2 gene; human; respiration; thermogenesis;
XX KW obesity; hyperinulinaemia; glucose intolerance; diabetes; syndrome X;
XX KW hypothermia; wasting; cachexia; anorexia; inflammation; fever;
XX KW hyperthermia; gene therapy; diagnosis; ds.

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XX	Homo sapiens.
OS	MO9631396-A1.
XX	23-JUL-1998.
PD	22-APR-1997; 97WO-US006864.
PF	15-JAN-1997; 97US-0034960P.
PR	(UYDU-) UNIV DUKE.
PA	(REGC) UNIV CALIFORNIA.
PA	(CNRS) CENT NAT RECH SCI.
XX	Surwit RS, Collins SA, Warden CH, Seldin MF, Riquier D,
PI	Bouilland F;
DR	WPI; 1998-413823/35.
XX	
PT	Method for treating disease associated with altered UCP-2 expression - by
PT	administering agent which enhances or inhibits UCP-2 activity,
PT	effectively to treat obesity, diabetes, fever, hyperthermia, cachexia
XX	etc.
PS	Example II; Fig 10b; 98pp; English.
XX	
CC	This is the nucleotide sequence of a region (sequence 1) of the human
CC	uncoupling protein-2 (UCP2) gene present in genomic clone hUCP2-g2 (I-
CC	1867). 4 Regions (see V4598-601) of hUCP2-g2 are provided. The hUCP2-g2
CC	clone was isolated from a human placenta genomic DNA library constructed
CC	in lambda EMBL3 phage using a partial genomic fragment as probe. Sequence
CC	2 corresponds to DNA from positions bp -511 to +650 and includes the
CC	putative proximal human UCP2 promoter. The UCP2 gene maps to a
CC	chromosomal region (11q13) linked to obesity and hyperinsulinaemia. The
CC	invention provides methods for the treatment of disorders associated with
CC	diminished or elevated UCP2 expression or activity. An agent which
CC	enhances UCP2 expression (e.g. an expression construct comprising a UCP2
CC	encoding sequence) can be used to treat obesity, diabetes, syndrome X,
CC	hypochetmia, hyperinsulinaemia, or glucose intolerance. An inhibitor of
CC	UCP2 (e.g. an antisense construct) is used to treat wasting, anorexia,
CC	inflammation, cachexia, fever or hyperthermia (all claimed). The
CC	invention also relates to diagnostic and drug screening methodologies
XX	
SQ	Sequence 1161 BP; 209 A; 346 C; 323 G; 234 T; 0 U; 49 Other;
Query Match	19.7%; Score 447.4; DB 2; Length 1161;
Best Local Similarity	94.9%; Pident No. 76-78; 22; Indels 6; Gaps 5;
Matches 516; Conservative 0; Mismatches 22; Indels 6; Gaps 5;	
OY	1733 AGAGGCCACGCGCGCTGTGCAGAGAAGGTGGTAGTTGCCACAGCT--AGGAGGG 1790
DB	2 ANGAACCAACGCGCGGCTTGTTCGAGAGAGTGTTAGTTGCCACAGGGTAAGGGGG 61
OY	1791 CTGGGCCCCATAAAGAGAAATGC-ACTTAAACAACGCGCCCGCTGACGCTTTAGAA 1849
DB	62 CTGGGCCCATAAAGAGAAATGCACCTTAACAACGCGCCCGCTGACGCTTTAGAA 121
OY	1850 ACCGTCCT-GGCTGGGAAAGGCAAGAGGTGTGACTGCAAGAAATTGTTCT--GGCGGT 1907
DB	122 ACCTTCTGGAGTTGGGAAGGCAAGAGGTGTGACTGCAAGAAATTGTTCTGGGCGGT 181
OY	1908 CAGTCTTGCATCTTCACAGAAGTTGCGCGCCCGAGAGAGTGTGAGGAGGCGGGAG 1967
DB	182 CAGTCTTGCATCTTCACAGAAGTTGCGCGCCCGAGAGAGTGTGAGGAGGCGGGAG 241
OY	1968 TGCCAAAGGAGTGACCATTCGGGGAAAGAAAGAGTAAACGCGGTGATGGACGACGG- 2028
DB	242 TGCCAAAGGAGTGACCATTCGGGGAAAGAAAGAGTAAACGCGGTGATGGACGACGA 301
OY	2027 AAACGGAGTGGAGAAAGTCAATGAGAGAAACCTTACGCGGGCGGTCCCGCGGAAAAGC 2086
DB	302 AAACGGAGTGGAGAAAGTCAATGAGAGAAACCTTACGCGGGCGGTCCCGCGGAAAAGC 361

QY	2087	GGCTGCTCCAGAGCTCCGACCCCAAGTAGAGCTGGGAGGCCCCGCCCCGACAG	2146
Db	362	GGCTGCTCCAGAGCTCCGACCCCAAGTAGAGCTGGGAGGCCCCGCCCCGACAG	421
QY	2147	CCCCACCCCGGAGCCCCCGCCCAAGGCTTAAAGCCGCGCCGCTCGCGGAGCCCCAC	2206
Db	422	CCCCACCCCGGAGCCCCCGCCCAAGGCTTAAAGCCGCGCCGCTCGCGGAGCCCCAC	481
QY	2207	TGCGAAGCCCAAGCTCGCGGCGCCCTTGGGATTGACTGTGCCAGCTCGCCCGGCTGTCCGA	2266
Db	482	TGCGAAGCCCAAGCTCGCGGCGCCCTTGGGATTGACTGTGCCAGCTCGCCCGGCTGTCCGA	541
QY	2267	CGCG 2270	
Db	542	CGCG 545	
RESULT 6			
ABLJ3892			
ID	ABLJ3892	standard; DNA; 5283 BP.	
AC	ABLJ3892;		
XX			
DT	26-MAR-2002	(first entry)	
XX			
DE	Human immune system associated gene SEQ ID NO: 1865.		
KM	Human; immune system disease; cytosine methylation; antiaesthetic;		
KM	antiartherosclerotic; antianemic; cytosolic; noctropic;		
KM	neuroprotective; anti-HIV; anticonvulsant; ophthalmological;		
KM	antirheumatic; antiarthritic; antidiabetic; antiparasitic;		
KM	antiinflammatory; cancer; eye disease; arteriosclerosis; anemia;		
KM	acute myeloid leukemia; Alzheimer's disease; AIDS; epilepsy;		
KM	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;		
KM	ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200200928-A2.		
XX			
PD	03-JAN-2002.		
XX			
PF	02-JUL-2001; 2001WO-EP007537.		
XX			
PR	30-JUN-2000; 2000DE-01032529.		
PR	01-SEP-2000; 2000DE-01043826.		
XX			
PA	(EPIG-) EPIGENOMICS AG.		
XX			
PI	Olek A. Piepenbrock C, Berlin K;		
XX			
DR	WPI; 2002-130909/17.		
XX			
PT	Nucleic acid comprising fragment of chemically modified gene, useful for		
PT	diagnosis and treatment of diseases associated with abnormal cytosine		
PT	methylation.		
XX			
PS	Claim 1; SEQ ID NO 1865; 32pp + Sequence Listing; German.		
XX			
CC	The present invention provides a number of human immune system associated		
CC	genes which are modified by the methylation of cytosines. The sequences		
CC	can be used in the diagnosis and treatment of immune system disorders,		
CC	including eye diseases such as retinopathy, neovascular glaucoma and		
CC	macular degeneration, arteriosclerosis, anemia, cancer, acute myeloid		
CC	leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,		
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel		
CC	diseases. The present sequence is a gene of the invention		
XX			
SO	Sequence 5283 BP; 1097 A; 136 C; 1369 G; 2681 T; 0 U; 0 Other;		
Query Match			
16.0%; Score 364.2; DB 6; Length 5283;			
Best Local Similarity 77.4%; Pred. No. 1.8e-61;			

Db 4686 CGCG 4683

RESULT 8

ADL13819 ID ADL13819 standard; DNA; 41150 BP.

XX ADL13819;

XX 06-MAY-2004 (first entry)

DE Osteoarthritis-associated polymorphic nucleotide #351.

XX

KM ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;

KM joint space narrowing; osteophyte development; joint pain;

KM osteoarthritis; SNP; single nucleotide polymorphism.

XX

OS Homo sapiens.

PN M02003054166-A2.

XX

PD 03-JUL-2003.

XX

PF 19-DEC-2002; 2002MO-US041225.

XX

PR 20-DEC-2001; 2001US-0342603P.

XX

PA (INCY-) INCYTE GENOMICS INC.

PI Jones KA, Schaefer A;

XX WPI; 2003-559141/52.

XX

PT Determining susceptibility of an individual to joint space narrowing,

PT osteophyte development and/or joint pain comprises identifying whether

PT the individual has at least one polymorphism in a polymucleotide encoding

PT a protein.

XX

PS Disclosure; SEQ ID NO 351; 297bp; English.

XX

CC The invention relates to a method of determining susceptibility of an

CC individual to joint space narrowing and/or osteophyte development and/or

CC joint pain comprising identifying whether the individual has at least one

CC polymorphism in a polymucleotide encoding at least one of the protein

CC listed in the specification. The methods, composition and agent are

CC useful for modulating the susceptibility of an individual to joint space

CC narrowing and/or osteophyte development and/or joint pain that is

CC associated with a disease, preferably osteoarthritis. The cell line and

CC the non-human animal are useful for screening for an agent for diagnosing

CC an individual having susceptibility to joint space narrowing and/or

CC osteophyte development and/or joint pain. This sequence corresponds to

CC the polymucleotide encoding a protein listed in the specification. (Note:

CC The sequence data for this patent did not form part of the printed

CC specification but was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pat_sequences).

XX

XX Sequence 41150 BP; 10143 A; 11252 C; 10866 G; 8889 T; 0 U; 0 Other;

XX

Query Match 8.3%; Score 188.4; DB 10; Length 41150;

Best Local Similarity 63.7%; Pred. NO. 7.1e-27;

Matches 354; Conservative 0; Mismatches 191; Indels 11; Gaps 4;

QY 5 GATCTGCCGCTCAGCTCCCAAGTGTGGATTGACGCGTGAAGCACTTCACTG 64

DB 32914 GATCTGCCGCTCAGCTCCCAAGTGTGGATTGACGCGTGAAGCACTTCACTG 32973

QY 65 CTACAAAGTTTCAAAATTCATTTA---TCTAGTACCCATACATTTCTCCAGTTTGCCACA 121

DB 32974 CCTGTGTTTATTAACCTAAACAGATTTAGAGTGTCTTTTATATTCATTTATTA 33033

QY 122 GGAATCTTATGACTTGGACGACGCTCTAAATTCGAAGGTCAGCGCTTTGTATGTCTTA 181

DB 33034 TGAAGAACTATCAACATACAGAAAAAGTTGACCAATTCATATACCAACGACTTGAATTC 33093

QY 182 TAGAATTGCTCAGATCTGCCCCCACCCTGAAAAGAT---TTAAGAGATTTCTTGAGGCC 238

DB 33094 TATTGTTAGCTTAATCTACCAATCTTCTTTCTAAACATTTAAAAATTAATTGCAGACC 33153

QY 239 AGGCACAGTGTGCTCACACCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCAAGACTGC 298

DB 33154 GGGCACAGTGTGCTCACAGTCTAATATCTTAGCACTTTGGAGAGCAAGAGTGAATGCATCGC 33213

QY 299 TTGAGGCCAGAGATTTCAAGACGCTTGAACAACAAGGAGACCTGTCACTTCAAAAGAA 358

DB 33214 TTGAGTTCAAGAGTTCAAGACGCTTGGCAATATATGAGACCCGTCTTCAAAAAA 33273

QY 359 TAAATAAATTAAGCAAGCTTAAGTGTGCTCATCCCTGTGTGTCCTCACTACTAGAGAGCAGA 418

DB 33274 TACAAAGCTTAAGCCGGGACATGATGGGACACGCTGTAAATCCAGACTACTTGGGGACTGA 33333

QY 419 AGTAGGA---CTGCTTGTCCCAAGAGTCAAGACTGCAAGTGAAGCCACCACTACC 474

DB 33334 GGTGGAGAGATCACTTGAAGCCCAAGAAAGTGAAGCTGCAGTGAAGTCAATGCCA-C 33392

QY 475 TGCATTCAGCTGGGCAACAAAAGACCCGTGTCAAAAAATAGTTAAATTAATAA 534

DB 33393 TGTACTTCAGCTGGGGTGAACAAAGTGAAGACTGTCTCAAAAAATAAATTAATTTG 33452

QY 535 ATATATAAATTAAGTTT 550

DB 33453 CAATCATCCACATATT 33468

RESULT 9

ADN48556/c

ID ADN48556 standard; DNA; 44348 BP.

XX

AC ADN48556;

XX

DT 12-AUG-2004 (first entry)

XX

DE Human Notch3 genomic DNA #2.

XX

KM Human; Notch3; gene; ds; antisense oligonucleotide;

KM phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;

KM 5-methylcytosine; hyperproliferative disorder; cancer; cytostatic.

XX

OS Homo sapiens.

XX

PN US2004102390-A1.

XX

PD 27-MAY-2004.

XX

PF 21-NOV-2002; 2002US-00301832.

XX

PR 21-NOV-2002; 2002US-00301832.

XX

PA (ISIS-) ISIS PHARM INC.

PI Freiler SM, Dobie KM;

XX

PT WPI; 2004-399720/37.

DR GENBANK; NM_000435.

XX

PT New compound, particularly oligonucleotides targeted to a nucleic acid

PT encoding Notch3, useful for treating diseases associated with Notch3,

PT e.g. hyperproliferative disorders.

XX

PS Example 15; SEQ ID NO 11; 74bp; English.

XX

XX The invention relates to a compound targeted to a nucleic acid molecule

XX encoding the human Notch3 polypeptide. The compound is an antisense

XX oligonucleotide that specifically hybridizes with the nucleic acid and

XX inhibits expression of the polypeptide. The antisense oligonucleotide

XX comprises at least one modified internucleoside linkage i.e. a

XX phosphorothioate linkage, at least one modified sugar moiety, preferably

CC a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase
CC comprising a 5-methylcytosine. The antisense compounds are useful for
CC modulating the expression of the human Notch3 polypeptide and in
CC preparation of a composition for treating hyperproliferative disorders,
CC e.g. cancer. This sequence represents genomic DNA encoding the human
CC Notch3 polypeptide of the invention.

XX Sequence 44348 BP; 9445 A; 11931 C; 12348 G; 10624 T; 0 U; 0 Other;

Query Match 8.3%; Score 188.4; DB 12; Length 44348;

Best Local Similarity 63.7%; Pred. No. 7.2e-27;

Matches 354; Conservative 0; Mismatches 191; Indels 11; Gaps 4;

QY 5 GATCGCCGCGCTGACCTCCCAAGTGTGGGATTTGAGGCGGAGCCACTGCTGG 64
DB 12725 GATCGCTGCTGCTGACCTCCCAAGTGTGGGATTTGAGGCGGAGCCACTG 12666
QY 65 CTACAGTTTCAAAATACATTTA---TCTAGTACCATACATTCCTCCAGTTTGTCCACA 121
DB 12665 CCGTGTGTTTATTAACCTTAAACAGTATTTAGTAGGCGCTTTTATATCATTTATTA 12606
QY 122 GGAATCTTTATGACTTTGAGCAAGCTGCTTAAATCCAAAGGCTGCGAGCTTGTATGCTTA 181
DB 12605 TGAGAACTATCAAAACATACAGAAAGTTGACCATTCATATACCCACACTAGATTCAAC 12546
QY 182 TAGAGTTGCTGAGATCTGCGCCCGCCACCTGAAAGAT---TTAGAGAAATTTCTTAGGCC 238
DB 12545 TATGTTAGCTTAATCTTACCAATCTTCTTTCTTAAACATTTAAATTAATTTGAGAC 12486
QY 239 AGGCAAGTGTGCTGACCTGTAATTCAGTACTGTAGAGTCCGAGGTCAGAGACTGC 298
DB 12485 GGGCACTATGGCTGACGCTATTAATCTTGAAGCTTTGGAGGCTCAAGGTGATGCTGC 12486
QY 299 TTGAGCCAGAGATTCAAGAGAGCTGTGACAAACAGGAGACTGTGACTTACAAAGAA 358
DB 12425 TTGATTTCAAGAGTTCAAGAGAGCTGTGAGCAATATAGTGAACCCGCTCTACAAAAA 12366
QY 359 TAAATTAATTAAGGAGCTTGTAGTGTGCTATCCCTGTGGCCCGAGCTACTAGGAGAGCGA 418
DB 12365 TACAAAGCTTACCCGAGGATGTGTGGCGACGCTGTAAATCCAGCTACTTGGGAGCTGA 12306
QY 419 AGTAGA---CTGCTTGTCCAGAGAGGTCAAGACTGCAAGTGTGAGCTGAGACCCAGCC 474
DB 12305 GGTGGAGAGATCACTTGAAGCCAGAGAGTCCAGAGGCTGAGTGAAGTATATGCCA-C 12247
QY 475 TGCATTCCAGCTGGGCAACAAAGAGACCTGTCTCAAAAATTAAGTTAAATTAATPA 534
DB 12246 TGTACTCCAGCTGGGTGACAAAGTGAAGCTGTCTCAAAAATTAATTAATTAATTTG 12187
QY 535 AATAAATAATAGTTT 550
DB 12186 CAATATCCACATATT 12171

RESULT 10

AAS29967/C

ID AAS29967 standard; DNA; 11172 BP.

XX AAS29967;

DT 21-NOV-2001 (first entry)

XX Human lung antigen genomic DNA #37.

XX Lung antigen protein; human; mouse; rabbit; goat; horse; cat; dog;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic;
KW antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective;
KW cerebroprotective; nootropic; antibacterial; vinuclide; fungicide; cancer;
KW ophthalmological; veterinary; gene therapy; autoimmune disease; neoplasm;
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; db;
KW cerebrovascular disorder; nervous system disorder; bacterial infection;
KW fungal infection; viral infection; ocular disorder; endocrine disorder;
KW gastrointestinal disorder; renal disorder; respiratory disorder;

KW wound healing; skin aging; organ transplantation; food preservative;
KW tissue regeneration; anti-infertility; food additive.

OS Homo sapiens.

XX WO200155303-A2.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US001301.

XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
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PR 11-JUL-2000; 2000US-0217487P.
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PR 26-JUL-2000; 2000US-0218299P.
PR 26-JUL-2000; 2000US-0220963P.
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PR 14-AUG-2000; 2000US-0224518P.
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PR 18-AUG-2000; 2000US-0226279P.
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PR 22-AUG-2000; 2000US-0227182P.
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PR 01-SEP-2000; 2000US-0229287P.
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PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
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PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
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PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234222P.
PR 21-SEP-2000; 2000US-0234274P.

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PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
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PR 02-OCT-2000; 2000US-0236802P.
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PR 20-OCT-2000; 2000US-0240960P.
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PR 20-OCT-2000; 2000US-0241825P.
PR 01-NOV-2000; 2000US-0244617P.
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PR 08-NOV-2000; 2000US-0246475P.
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PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
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PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 06-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.

PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-457723/49.
XX
XX Isolated polypeptide for treating, preventing and/or prognosing
PT respiratory disorders related to the lung including lung cancers and also
PT for testing and detection e.g. diagnosis.
XX
PS Claim 1; SEQ ID NO 231; 507bp; English.
XX
XX Sequences AA829931-AA830164 represent genomic DNA molecules, which encode
CC the lung antigen polypeptides of the invention. Lung antigen polypeptides
CC and their associated polymucosides are useful in the diagnosis,
CC treatment and prevention of various types of disorders in e.g. humans,
CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A
CC pathological condition can be determined by detecting the presence or
CC absence of a mutation in a lung antigen polymucoside. The treatable
CC disorders include autoimmune diseases such as rheumatoid arthritis,
CC hyperproliferative disorders such as neoplasms of the breast or liver,
CC cardiovascular disorders such as cardiac arrest, cerebrovascular
CC disorders such as cerebral ischaemia, nervous system disorders such as
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi,
CC ocular disorders such as corneal infection, endocrine disorders such as
CC premature labour and infertility, gastrointestinal disorders such as
CC Crohn's disease, renal disorders such as glomerulonephritis and
CC respiratory disorders such as asthma and pleurisy. The polypeptides can
CC also be used to aid wound healing, to prevent skin aging due to sunburn,
CC to maintain organs before transplantation, to regenerate tissues and in
CC chemocaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

Query Match 7.64; Score 172.8; DB 5; Length 11172;
Best Local Similarity 58.54; Pred. No. 6.1e-24;
Matches 337; Conservative 0; Mismatches 237; Indels 2; Gaps 2;

QY 1 AACGATCTGCCGCTCAGCTCCCAAGTCTGGATTGCGGCTGACCTCTAC 60
DB 8630 AAGTATCCCTGCTGCTGCTCCCAAGTCTGATTAACGATTAACGCTACCCAC 8571

QY 61 CTGGCTACAGTTTCAATAATATATATAGTACCAATTCCTCCAGTTTGCCAC 120
DB 8570 CTGGCTCCCTTAAGATATTAACATTAATCCAGCTCAACAAACATGAAGACAAA 8511

QY 121 AGGACATCTTATGACTTGAAGCAAGCTGCTAAATCCAGGGTGCAGCGTTGTATGCT 180
DB 8510 AGGACTAATTAATTAAGTATAGTAAATTAATTAATTTCTGTGTATTAAGAGACGTT 8451

QY 181 ATAGATGCTCAGATGCTGCCCACTGAAAGAAATTAAGAAATTTCTTAGAGCCAG 240
DB 8450 TCCCTCAGACAAAGATGATTAATTTGGCTTTTCTTTTAAGAGTAGGAGACTGCCAG 8391

QY 241 GCACAGTGGCTACACCTGTAATTCAGTCTGTGAGAGTCCAGGCTCAGAGCTGCTT 300
DB 8390 GCACAGTGGCTCACAACCTGTAATTCAGCACTTTGGAGGCGAGGGGTGAGGACCT 8331

QY 301 GAGGCCAGAGTTCAAGAGCAGCTGAGCAACAGAGAGA-CCTGTCACTACAAAGAT 359
DB 8330 GAGGTCAAGAGTTCAAGAGCAGCTGAGCAATTAAGTAAACCCCACTTACTAATAAAT 8271

QY 360 AATTAATTAAGCAGGCTTAAGTGTATCTGTGTGCTCCAGCTACTAGAGAGCGAGAA 419
DB 8270 ACAAATTAAGCAGGCGCGGTGCGTACCTGTAGTCCAGCTACTAAGAGGCTGAG 8211

QY 420 GTAGGACTGCTTGTCCAGAGAGTCA-AGAATGAGAGTACAGACCAAGCACTGCA 478
DB 8210 ACAGAATGCTTGAACCGGAGGAGGAGGTTACAAGTGAAGCTTAGATTGTGCACTGAC 8151

PR	08-NOV-2000;	2000US-0246613P.
PR	08-NOV-2000;	2000US-0246613P.
PR	17-NOV-2000;	2000US-0249207P.
PR	17-NOV-2000;	2000US-0249208P.
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PR	17-NOV-2000;	2000US-0249210P.
PR	17-NOV-2000;	2000US-0249211P.
PR	17-NOV-2000;	2000US-0249212P.
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PR	17-NOV-2000;	2000US-0249219P.
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PR	17-NOV-2000;	2000US-0249246P.
PR	17-NOV-2000;	2000US-0249265P.
PR	17-NOV-2000;	2000US-0249287P.
PR	17-NOV-2000;	2000US-0249299P.
PR	01-DEC-2000;	2000US-0249300P.
PR	01-DEC-2000;	2000US-0250160P.
PR	01-DEC-2000;	2000US-0250311P.
PR	05-DEC-2000;	2000US-0251033P.
PR	05-DEC-2000;	2000US-0251988P.
PR	05-DEC-2000;	2000US-0256719P.
PR	06-DEC-2000;	2000US-0251479P.
PR	08-DEC-2000;	2000US-0251856P.
PR	08-DEC-2000;	2000US-0251868P.
PR	08-DEC-2000;	2000US-0251869P.
PR	08-DEC-2000;	2000US-0251989P.
PR	08-DEC-2000;	2000US-0251990P.
PR	11-DEC-2000;	2000US-0254097P.
PR	05-JAN-2001;	2001US-0259678P.
PR	17-JAN-2001;	2001US-00764878.
XX		
PA	(HUMA-)	HUMAN GENOMES SCI INC.
XX		
FI	Rosen CA,	Ruben SM, Barash SC;
XX		
DR	WPI;	2003-695900/66.

PT Novel isolated lung antigen polypeptides useful for treating, preventing,
 PT diagnosing acute myelogenous leukemias, adenocarcinoma, thrombocytopenia,
 PT Von Willebrand's disease.
 PS
 PS
 PS Disclosure; SEQ ID NO 231; 178bp; English.
 XX
 CC
 CC The invention relates to an isolated lung antigen polypeptide sequence or
 CC encoded sequence in a cDNA clone. The polypeptide and its polynucleotide
 CC are useful for treating, preventing, diagnosing and/or prognosing
 CC diseases and/or disorders such as pathological cell proliferative
 CC neoplasias e.g. acute myelogenous leukemias, adenocarcinoma, respiratory
 CC disorders such as chronic rhinitis, sinusitis; immunodeficiencies such as
 CC X-linked agammaglobulinemia, X-linked infantile agammaglobulinemia;
 CC inflammatory disorders such as adrenaritis, alveolitis; immune complex
 CC diseases such as serum sickness, polyarteritis nodosa; bleeding disorders
 CC such as thrombocytopenia, Von Willebrand's disease; acquired platelet
 CC dysfunction such as kidney failure, multiple myeloma; disorders
 CC associated with macrophage numbers and/or macrophage function such as
 CC Gaucher's disease, Niemann-Pick disease; tumours such as colon cancer,
 CC pancreatic cancer; renal disorders such as kidney failure, nephritis;
 CC bone disorders such as Albers-schonberg disease, bowlegs; muscle
 CC disorders such as Becker's muscular dystrophy, Duchenne's muscular
 CC dystrophy; nervous disorders such as ischaemic lesions, traumatic lesions
 CC / endocrine disorders such as Cushing's syndrome, corticosteroid
 CC
 Query Match 7.6%; Score 172.8; DB 10; Length 11172;
 Best Local Similarity 58.5%; Pred. No. 6,1e-24;
 Matches 337; Conservative 0; Mismatches 237; Indels 2; Gaps 2
 1 AACGATGTGCCCGCTCAGCTCCCAAGTGTGGATTGGACGGCGTGAGCCACTCAGC 60

Db	8630	AAAGTATCCGCTCGCTTGGCTCCCAAGTGTAGATTTACAGACATAGACTACCGCAC	8571
Oy	61	CTGGCTCAAGATTCTTCAAAATACATTTATCTAGTACCCATACATCTTCAGATTGTCCAC	120
Db	8570	CTGGCTCTCCCTTAAGAATCTAACATTAATCCAGAGCTCACAAACAACTGAAGACAAA	8511
Oy	121	AGGACATCTTATGACTTGGACAGACTGTAAAAATCCAAAGGTGCAGCGTTGTATGCT	180
Db	8510	AGGACTAAATATATAGATATAGTTAATATAGATTTTCTGTGTACTATATAGAGACGT	8451
Oy	181	ATAGAGATTGCTCAGATCTGACCCGCCACCCCTGAAAATTTAAGAAATTTCTTGAGGCCAG	240
Db	8450	TCCTCTCAGACAAAGATGATTAATTTGGGTTTTTCTTTTAAAGATAGGACCTGCGCAG	8391
Oy	241	GCAcAGTGGCTCACACCTGTATTCAGTACTGTAGAGTCCAGGCTCAGAGACTGCTT	300
Db	8390	GCAcAGTGGCTCACACCTGTATTCAGGACCTTTGGAGGCGGAGGTGGGTGAGACCT	8311
Oy	301	GAGGCCAGAGTTCAAGAGCAGCTTGACAAcACAGGGAGA - CCTGTCACTACAAAGAT	359
Db	8330	GAGCTCAGAGATTCAAGACCGACTGCACATATGTATTAACCCCATCTCTACATAAAT	8271
Oy	360	AAATTAATTAACCGCAGGCTTATGTGCTCATCCCTGTGTCCAGTACTAGGAGAGCAGAA	419
Db	8270	ACAAAATTTAGCCAGGCGCGGTGCCTGACACTGTATGTCCAGCTACTAGGAGAGCTGAG	8211
Oy	420	GTAGGACTGCTTGTCCcAGAGAGTCA - AGACTGcAGTGAAGTGAACCCAGCACCCTGCA	478
Db	8210	ACAGATTTGCTTGAACCCGGAAGGCAAGGTTACAGTGAAGCTTGATTTGTGCCACTGCAC	8151
Oy	479	TTCCAGCTGGGCAACAAAAGAGACCTGTCTCAAAAAATTAAGTTAATTAATTAATAA	538
Db	8150	TCCAGCTAGGTGTGACAGAGTGAAGACTATCTCAAAAAAAAAAAAAAAAAAAAAA	8091
Oy	539	TAAAAATATGTTAAACCTTAACACATCTCTTTTT 574	
Db	8090	AAAAAGAGTGGAGCCATGACTTTATTTATTTGT 8055	

RESULT 12	
ABAI9375/c	
ID	ABAI9375 standard; DNA; 25525 BP.
XX	
AC	
XX	ABAI9375;
DT	
XX	23-JAN-2002 (first entry)
DE	
XX	Human nervous system related polynucleotide SEQ ID NO 11706.
XX	
KW	Human; noctropic; neuroprotective; cytosatic; dermatological; virucide;
KW	immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
KW	antiparkinsonian; antisticking; antianaemic; antiarthritic; cancer;
KW	antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW	antiallegic; antidiabetic; antifurcer; anticonvulsant; antifungal;
KW	antiparasitic; cardiac; immune disorder; cardiovascular disorder;
XX	neurological disease; infection; nephrotropic; gene therapy; vaccine; ds
XX	
OS	Homo sapiens.
XX	
PN	WO200159063-A2.
XX	
PD	16-AUG-2001.
XX	
PF	17-JAN-2001; 2001WO-US01334.
XX	
PR	31-JAN-2000; 2000US-0179065P.
PR	04-FEB-2000; 2000US-0180628P.
PR	24-FEB-2000; 2000US-0184664P.
PR	02-MAR-2000; 2000US-0186350P.
PR	16-MAR-2000; 2000US-0189874P.
PR	17-MAR-2000; 2000US-0190076P.
PR	18-APR-2000; 2000US-0198123P.
PR	19-MAY-2000; 2000US-0205515P.

CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
CC / (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at http://wipo.int/pub/published_pct_sequences

XX Sequence 25525 BP; 6205 A; 6343 C; 6691 G; 6286 T; 0 U; 0 Other;

Query Match 7.4%; Score 168.4; DB 5; Length 25525;

Best Local Similarity 62.1%; Pred. No. 5.3e-23;
Matches 334; Conservative 0; Mismatches 196; Indels 8; Gaps 4;

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DB 6911 AACTGACTGCGCACTCAGCTCCCAAGTCTGGAGTTGACAGCGTGAACCTTCAC 6852
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DB 6851 CCATCTTCTTATGAGGATTTGATATATATATATATATATATATATATATATATAT 6792
QY 121 AGGACATCTTATGACTTATGAGCAAGCTGTAAATATCCAAAGGATGAGGTTATGCT 180
DB 6791 CAGCCCACTTATGACATGAGCAAAATATATATATATATATATATATATATATATAT 6732
QY 181 ATAGATTTCTCAGATCT--GCCGCCACCTGAAAGAAATTTAAGAAATTTTGAAGC 237
DB 6731 GAAAGACTTCTTGTCTCTGCGCAAGGCTGGCTTTATGTTAAGAAATGATCTCCGC 6672
QY 238 CAGGACAGTGGCTCAGACCTGTATTTCCAGTACTGTAGAGTCCGAGTCAAGAGCTG 297
DB 6671 CAGGCTGGTGGCTCAGACCTGTATTTCCAGTACTGTAGAGTCCGAGTCAAGAGCTG 6612
QY 298 CTTGAGGCGAGAGTTCAGAGCCTGAGCAACACAGGAGAGCTGTCTACTCAAAAGA 357
DB 6611 CTTAGAGTGGAGAGTTTGAACAGCAGCTGACTGATGAGAAACCCCATCTTACTTAA 6552
QY 358 ATAAATATATATAGCAGCTTATGAGTCTATCCCTGTGCTCCAGTACTTAAAGGAG 417
DB 6551 AACCAAAATATAGCAGGCTTGTGTGAGATGCTGTATCCAGTACTTGGAGGCTG 6492
QY 418 A--AGTGAAGTCTGTTTCCAGAGAGTCAAGACTGAGTGAAGTGAAGCCAGCC 474
DB 6491 AGGAGGAGATTCGCTTGAAGTGAAGGAGGAGTGAAGCCAGATCGACCA-C 6433
QY 475 TGCAATTCAGGCTGGGCAACAA-AAAGAGCCTGTCTCAAAAATATATATATAT 531
DB 6432 TGCACTCGAGCTGGGCAACAAAGAAATCTGTCTCAAAAATATATATATAT 6375
```

RESULT 13
ADQ19501/c
ID ADQ19501 standard; DNA; 135005 BP.

AC ADQ19501;

XX 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 2320.

XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;

XX ds.

XX Homo sapiens.

XX OS

XX WO2004048938-A2.

XX

PD 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

PR (PROT-) PROTEIN DESIGN LABS INC.

PA Aziz N, Ginsburg WM, Zlotnik A;

XX WPI; 2004-441206/41.

XX Early detection of soft tissue sarcoma comprises determining expression

PT of a gene in a first soft tissue sample and a normal soft tissue sample

PT and comparing the gene expression, also useful in treating soft tissue

PS sarcoma.

XX Example 2; SEQ ID NO 2320; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma

CC which comprises obtaining a first soft tissue sample from an individual,

CC and a normal soft tissue sample from the same or different individual,

CC determining the expression of a gene in both samples and comparing the

CC expression of the gene in both soft tissue samples, where a higher level

CC of protein expression in the first soft tissue sample indicates the

CC presence of soft tissue sarcoma. The method of the invention has

CC cytostatic applications and may be useful for detecting soft tissue

CC sarcoma, possibly via gene therapy or vaccine production. The nucleic

CC acid sequences may be useful in diagnostic and screening applications.

CC The current sequence is that of a human soft tissue sarcoma-upregulated

CC DNA of the invention. The current sequence is not shown within the

CC specification per se but was submitted in CD format by the inventor.

XX Sequence 135005 BP; 32951 A; 33605 C; 32661 G; 35788 T; 0 U; 0 Other;

Query Match 7.4%; Score 167.2; DB 12; Length 135005;

Best Local Similarity 80.3%; Pred. No. 1.3e-22;

Matches 233; Conservative 0; Mismatches 53; Indels 4; Gaps 3;

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QY 235 GGCCAGGACAGAGGCTCAGACCTGTATTTCCAGTACTGTGAGAGTCCGAGTCAAGAG 294
DB 8440 GGCTGAGCAAGTGGCTCAGATCTGTATTTCCAGTACTTTGGAGGAGAGTGAAGA 84781
QY 295 CTGCTTGAAGCCAGAGTTCAGAGCCTGAGCAACACAGGAGAG--CCTGTACTTAC 352
DB 84780 TTGCTTGAAGGAGAGATTTCAAGCTATCTCTGGGCAACATATGAGAGCCCTGTCTTAC 84721
QY 353 AAAAATTAATTAATTAGCAGCTTATGAGTCTATCCCTGTGCTCCAGTACTTAAAGGA 412
DB 84720 AAAAATTAAGAAATTAATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 84661
QY 413 GGCAAGATGAGAGTCTCTTG--TCCAGAGAGTCAAGACTGAGTGAAGCCAGCC 471
DB 84660 GGCTGAGTATGAGATTTGTTAGCTTCAAGAGTCAAGGCGGAGTGAAGTGAAGAGTCC 84601
QY 472 ACCTGATTCAGGCTGGGCAACAAAAGAGCCTGTCTCAAAAATAT 521
DB 84600 A-CTGTACTCAACCTGGGCAACAGAGCAAGACCTGTCTCAAAAATAT 84552
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RESULT 14
ADA02666
ID ADA02666 standard; DNA; 52242 BP.

XX ADA02666;

XX 06-NOV-2003 (first entry)

XX Human MDM2 carcinoma associated gene, SEQ ID NO:1184.

XX Human; carcinoma associated; oncogene; carcinoma; cancer; breast;

XX prostate; lymphoma; leukemia; cytostatic; gene therapy; drug screening;

XX gene; ds.

XX Homo sapiens.
OS
XX WO2003057146-A2.
XX
XX 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041414.
XX
XX 26-DEC-2001; 2001US-00035832.
XX
XX (SAGR-) SAGRES DISCOVERY.
XX
XX Morris DW;
XX WPI; 2003-587068/55.
XX
XX New recombinant nucleic acid encoding carcinoma associated protein,
XX useful for preparing compositions for treating carcinomas.
XX
XX Claim 1; SEQ ID NO 1184; 245bp; English.
XX
XX The invention relates to recombinant carcinoma associated (CA) nucleic
XX acid sequences from mouse and human (ADA01482-ADA03094), and to
XX recombinant carcinoma associated proteins (CAP) encoded by them. The
XX invention also encompasses expression vectors and host cells comprising a
XX CA nucleic acid, a polypeptide (especially an antibody) that specifically
XX binds to the protein, and a biochip comprising CA nucleic acid or
XX fragments thereof. The sequences of the invention were identified using
XX oncogenic retroviruses, which insert into the genome of the host organism
XX at random. Many of these do not carry transduced host oncogenes or
XX pathogenic trans-acting viral genes meaning that cancer incidence is a
XX direct consequence of the effects of proviral integration into host
XX proto-oncogenes. The CA nucleic acid sequences can be used to diagnose
XX carcinoma (especially breast cancer, prostate cancer, lymphoma or
XX leukemia) or a propensity to carcinoma by determination of the sequence
XX of a CA gene, or by determination of CA gene expression in particular
XX tissues. CA nucleic acids, proteins and antibodies are also useful as
XX therapeutic agents and in screening and evaluating drug candidates. The
XX present sequence represents a specifically claimed human CA nucleic acid
XX sequence of the invention. Note: The complete sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 52242 BP; 14384 A; 10354 C; 10997 G; 16487 T; 0 U; 20 Other;
SQ
Query Match 7.3%; Score 166.6; DB 9; Length 52242;
Best Local Similarity 62.9%; Pred. No. 1.4e-22;
Matches 344; Conservative 0; Mismatches 189; Indels 14; Gaps 5;
QY 5 GATCTGCCCGCTCAGCTCCCAAGTCTGAGTTCAGAGCGGTGAGCCACTCCACTCG 64
DB 5228 GATCTGCCCGCTCAGCTCCCAAGTCTGAGTTCAGAGCGGTGAGCCACTCGCG 5287
QY 65 CTACAGTTTCAAAATACATTATCTAGTACCCATACATCTCCAGTTTGTCCACAGA 124
DB 5288 CCCGATTTCCTTTAAATACATATTCAGTTCCAGATTTTGAAGAATMAAGA 5347
QY 125 CATCTTAAGACTTGAGCA-----ACCTGATAAAATCCAGAGGTGACGTTGATGTC 179
DB 5348 ATTGAACCTACTCTCTGTAATTTTATAGTCTCAATAATTTGTAACTCAGCATTTCTA 5407
QY 180 TATAGAGTTGCTCAGATCTGCCCC--ACCTGAAGAATTTAAGAAATTTCTTGAGG 236
DB 5408 AACAGGTTTCTGACCTAAATCTTTAGTTTACACATGCTTTAAAGATTAGTTGG 5467
QY 237 CCAGCAGAGTGGCTCACACCTGTAATCCAGTACTGTGAGAGTCCGAGGTGAGGAGCT 296
DB 5468 CCAGCAGAGTGGCTCACACCTGTAATCCAGTACTGTGAGAGTCCGAGGTGAGGAGCT 5527
QY 297 GCTTGAAGCCAGAGATTCAAGAGCCTGAGCAACACAGGAGA-CCTGTCACTACAA 355

DB 5528 ACCTGAGCCAGAGATTGCGAGACCAAGCTGGCCAAATAGTAATCCCGTCTACTAA 5587
QY 356 GAATTAATAATTAATGAGCGTTAGTGGCTCATCCCTGTGGTCCAGTACTAGGAGGC 415
DB 5588 AAATACAAAATATGAGCGGTATGTGGCACAAAGCTGTATCCAGTACTCGGAGGC 5647
QY 416 AGAAGTAGA-----CTGCTTGTCCAGAGAGTCAAGACTGAGCTGAGACCCAGCC 471
DB 5648 TGAGCAGAGAAATCACTTGAACCCAGAGAGTGAAGGCTGAATGAGCTGATCTGCC 5707
QY 472 ACCTGATTCAGCTGGGCAAAAGAGACCTGTCTCAAAAAATAGTTAAATAA 531
DB 5708 A-CTGCACTCCAACTGGTGAAGAGTGAAGTCTCCGTCTCAAAAAAGAA 5766
QY 532 TAATTA 538
DB 5767 AGACAAA 5773
RESULT 15
ADB72404
ID ADB72404 standard; DNA; 52242 BP.
AC ADB72404;
XX 04-DEC-2003 (first entry)
DT
XX Human MDN2 gene.
DE
XX human; ds; cytosstatic; gene therapy; vaccine; carcinoma; lymphomas;
XX cancer; neoplasm; adenocarcinoma; sarcoma; gene.
XX
XX Homo sapiens.
XX
XX WO2003008583-A2.
XX
XX 30-JAN-2003.
XX
XX 26-DEC-2001; 2001WO-US051291.
XX
XX 02-MAR-2001; 2001US-00798586.
XX 23-OCT-2001; 2001US-00004113.
XX 08-NOV-2001; 2001US-00052482.
XX 30-NOV-2001; 2001US-00997722.
XX 20-DEC-2001; 2001US-00034650.
XX
XX (SAGR-) SAGRES DISCOVERY.
XX
XX Morris DW, Engelhard EK;
XX
XX WPI; 2003-239337/23.
XX
XX New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
XX cancers, neoplasm, adenocarcinoma, or sarcomas.
XX
XX Claim 1; SEQ ID NO 232; 2304bp; English.
XX
XX The invention relates to a novel recombinant nucleic acid comprising a
XX nucleotide sequence selected from any of the 660 sequences fully defined
XX in the specification. A polynucleotide of the invention has cytosstatic
XX activity, and may have a use in gene therapy, or in a vaccine. The
XX recombinant nucleic acids and polypeptides are useful for treating
XX carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
XX sarcomas. The present sequence represents a human gene of the invention.
XX
XX Sequence 52242 BP; 14384 A; 10354 C; 10997 G; 16487 T; 0 U; 20 Other;
SQ
Query Match 7.3%; Score 166.6; DB 10; Length 52242;
Best Local Similarity 62.9%; Pred. No. 1.4e-22;
Matches 344; Conservative 0; Mismatches 189; Indels 14; Gaps 5;
QY 5 GATCTGCCCGCTCAGCTCCCAAGTCTGAGTTCAGAGCGGTGAGCCACTCCACTCG 64

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Db 5228 GATCTGCTGTCTTGGCTCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGGCTCCG 5287
QY 65 CTACAAGTTTCCAAAATATCATTTATCTAGTACCATCATTCCTCCAGTTTGTCCACAGGA 124
Db 5288 CCGGATTTTGGCTTTTAAATATCACTATTCAGATGTTCCAGATGTTGAAAGACATTAAGGA 5347
QY 125 CATCTTATGACTTGAGCA----AGCTGCTAAAAATCCAAAGGTGACGCGTTGTATGTC 179
Db 5348 ATTGAACCTACTCTCTGTAAATTTTAGATGTCCTCATTAATATTTGGAACCTCAGCATTCCTA 5407
QY 180 TATAGGATTTGCTCAGATCTGCCCC--ACCTGAAAGAAATTTAAGAAATTTCTTGAGG 236
Db 5408 AACCGGTTCTGAGCTAAATCTGTGTAGTTTTCACCATGCTTTAAAGATTAGTTGTGG 5467
QY 237 CCAAGCACAGTGTCTCACACCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACT 296
Db 5468 CCAAGCACAGTGTCTCACACCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACT 5527
QY 297 GCTTGAAGGCCAGAGGTTCAAGAGCAGCTTGACAAACAAGGAGA-CCTGTCACTACAAA 355
Db 5528 ACCTGAAGGCCAGAGGTTCAAGAGCAGCTTGACAAACAAGGAGA-CCTGTCACTACAAA 5587
QY 356 GAATTAATTAATTGAGGCTTATGAGCTCATCCCTGTGTGTCCTCAGCTACTAGGAGGC 415
Db 5588 AAATTAATAAATTTAGCCGGTATGTGGCACAAGCTTGTATCCAGCTACTCGGAGAGGC 5647
QY 416 AGAAGTAGGA----CTGCTTGTCCAGAGAGGTCAAGACTGAGAGCTGAGACCCAGCC 471
Db 5648 TGAAGCAGAGAAATCATCTTGAAACCCAGAGAGGTGAGAGCTGCAATGAGCTGAGATCGTGC 5707
QY 472 ACCTGCAATTCAGGCTTGAGGCAACAAAAAGAGACCTGTGTCTCAAAAAAATAAGTTAATPAA 531
Db 5708 A-CTGCACTCCAACTGGGTGACAGAGTGAGACTCCGCTCAAAAAAATAAGTTAATPAA 5766
QY 532 TAAATPAA 538
Db 5767 AGACAAA 5773
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Job time : 1260 secs

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2005, 17:43:12 ; Search time 1635 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	846.8	37.3	9314	US-10-197-019-1	Sequence 1, Appl1
2	550.6	24.3	562	US-09-925-065A-566754	Sequence 566754,
3	531.6	23.4	554	US-09-925-065A-177131	Sequence 177131,
4	447.4	19.7	1161	US-10-265-689-27	Sequence 27, Appl
5	364.2	16.0	5283	US-10-311-455-1865	Sequence 1865, Ap
6	312.4	13.8	5283	US-10-311-455-1866	Sequence 1866, Ap
7	188.4	8.3	44348	US-10-301-832-11	Sequence 11, Appl
8	175	7.7	160556	US-10-719-993-6827	Sequence 6827, Ap
9	172.8	7.6	11172	US-09-764-878-231	Sequence 231, App
10	172.8	7.6	11172	US-10-079-854-231	Sequence 11, App
11	168	7.4	563	US-09-925-065A-770821	Sequence 770821,
12	167.2	7.4	135005	US-10-723-860-2320	Sequence 2320, Ap
13	167.2	7.4	135005	US-10-756-149-1719	Sequence 1719, Ap
14	166.8	7.3	3030	US-10-027-632-115210	Sequence 115210,
15	166.8	7.3	3030	US-10-027-632-115211	Sequence 115211,
16	166.8	7.3	3030	US-10-027-632-115210	Sequence 115210,
17	166.8	7.3	3030	US-10-027-632-115211	Sequence 115211,
18	166.6	7.3	52242	US-10-052-482-172	Sequence 172, App
19	166	7.3	1614	US-09-925-065A-551304	Sequence 551304,
20	165.6	7.3	1187	US-09-925-065A-71294	Sequence 71294, A
21	165.6	7.3	1187	US-09-925-065A-71295	Sequence 71295, A
22	164	7.2	1369	US-10-027-632-86881	Sequence 86881, A
23	164	7.2	1369	US-10-027-632-178961	Sequence 178961,

c 24	164	7.2	1369	6	US-10-027-632-86881	Sequence 86881, A
c 25	164	7.2	1369	6	US-10-027-632-178961	Sequence 178961,
c 26	164	7.2	1369	6	US-10-043-715-1	Sequence 1, Appl1
c 27	163.4	7.2	558	4	US-09-925-065A-822292	Sequence 822292,
c 28	163.4	7.2	558	4	US-09-925-065A-839930	Sequence 839930,
c 29	163.2	7.2	561515	8	US-10-741-601-5682	Sequence 5682, Ap
c 30	163.2	7.2	561515	8	US-10-741-600-17730	Sequence 17730, A
c 31	163.6	7.2	81099	5	US-10-087-192-1756	Sequence 1756, Ap
c 32	161.8	7.1	109906	7	US-10-235-182A-31	Sequence 31, Appl
c 33	161.4	7.1	383432	9	US-10-737-082-34	Sequence 34, Appl
c 34	161.4	7.1	383432	9	US-10-765-790-34	Sequence 34, Appl
c 35	161.2	7.1	56737	3	US-09-782-378A-17	Sequence 17, Appl
c 36	160.8	7.1	60815	5	US-10-087-192-52	Sequence 52, Appl
c 37	160.6	7.1	599	4	US-09-925-065A-875725	Sequence 875725,
c 38	160.6	7.1	599	4	US-09-925-065A-905153	Sequence 905153,
c 39	160.6	7.1	7739	3	US-09-764-877-1189	Sequence 3189, Ap
c 40	160.6	7.1	7739	6	US-10-242-515-3189	Sequence 3189, Ap
c 41	160.6	7.1	8133	7	US-10-380-124-10	Sequence 10, Appl
c 42	160.4	7.1	87467	7	US-10-741-600-15634	Sequence 5634, Ap
c 43	160.4	7.1	87467	8	US-10-741-600-17624	Sequence 17624, A
c 44	160.4	7.1	136436	9	US-10-756-149-3773	Sequence 3773, Ap
c 45	160.2	7.1	492	5	US-10-027-632-84916	Sequence 84916, A

ALIGNMENTS

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RESULT 1
US-10-197-019-1
Sequence 1, Application US/10197019
Publication No. US20030207284A1
GENERAL INFORMATION:
APPLICANT: Chew, Anne
APPLICANT: Denton, R. Rex
APPLICANT: Gilson, Christopher Raleigh
APPLICANT: Nandabalan, Krishnan
APPLICANT: Parks, Katie E.
TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
FILE REFERENCE: MMH-0042US
CURRENT APPLICATION NUMBER: US/10/197, 019
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: PCT/US01/02485
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 9314
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (1283)..(1283)
OTHER INFORMATION: P81: polymorphic base cytosine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (1714)..(1714)
OTHER INFORMATION: P82: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (2051)..(2051)
OTHER INFORMATION: P83: polymorphic base thymine or cytosine
FEATURE:
NAME/KEY: allele
LOCATION: (214)..(2124)
OTHER INFORMATION: P84: polymorphic base cytosine or thymine
FEATURE:
NAME/KEY: allele
LOCATION: (2287)..(2287)
OTHER INFORMATION: P85: polymorphic base cytosine or guanine
FEATURE:
NAME/KEY: allele
LOCATION: (2408)..(2408)
OTHER INFORMATION: P86: polymorphic base adenine or guanine

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1 FEATURE:
2 NAME/KEY: allele
3 LOCATION: (4768)..(4768)
4 OTHER INFORMATION: PS7: polymorphic base adenine or guanine
5 FEATURE:
6 NAME/KEY: allele
7 LOCATION: (4785)..(4785)
8 OTHER INFORMATION: PS8: polymorphic base guanine or adenine
9 FEATURE:
10 NAME/KEY: allele
11 LOCATION: (4813)..(4813)
12 OTHER INFORMATION: PS9: polymorphic base thymine or cytosine
13 FEATURE:
14 NAME/KEY: allele
15 LOCATION: (4882)..(4882)
16 OTHER INFORMATION: PS10: polymorphic base adenine or cytosine
17 FEATURE:
18 NAME/KEY: allele
19 LOCATION: (4976)..(4976)
20 OTHER INFORMATION: PS11: polymorphic base thymine or adenine
21 FEATURE:
22 NAME/KEY: allele
23 LOCATION: (5600)..(5600)
24 OTHER INFORMATION: PS12: polymorphic base cytosine or thymine
25 FEATURE:
26 NAME/KEY: allele
27 LOCATION: (5820)..(5820)
28 OTHER INFORMATION: PS13: polymorphic base thymine or guanine
29 FEATURE:
30 NAME/KEY: allele
31 LOCATION: (6536)..(6536)
32 OTHER INFORMATION: PS14: polymorphic base thymine or adenine
33 FEATURE:
34 NAME/KEY: allele
35 LOCATION: (6607)..(6607)
36 OTHER INFORMATION: PS15: polymorphic base guanine or adenine
37 FEATURE:
38 NAME/KEY: allele
39 LOCATION: (6617)..(6617)
40 OTHER INFORMATION: PS16: polymorphic base cytosine or thymine
41 FEATURE:
42 NAME/KEY: allele
43 LOCATION: (6872)..(6872)
44 OTHER INFORMATION: PS17: polymorphic base cytosine or guanine
45 FEATURE:
46 NAME/KEY: allele
47 LOCATION: (6966)..(6966)
48 OTHER INFORMATION: PS18: polymorphic base guanine or adenine
49 FEATURE:
50 NAME/KEY: allele
51 LOCATION: (7036)..(7036)
52 OTHER INFORMATION: PS19: polymorphic base cytosine or thymine
53 FEATURE:
54 NAME/KEY: allele
55 LOCATION: (7086)..(7086)
56 OTHER INFORMATION: PS20: polymorphic base adenine or guanine
57 FEATURE:
58 NAME/KEY: allele
59 LOCATION: (8100)..(8100)
60 OTHER INFORMATION: PS21: polymorphic base cytosine or thymine
61 FEATURE:
62 NAME/KEY: allele
63 LOCATION: (8221)..(8221)
64 OTHER INFORMATION: PS22: polymorphic base guanine or adenine
65 FEATURE:
66 NAME/KEY: allele
67 LOCATION: (8677)..(8677)
68 OTHER INFORMATION: PS23: polymorphic base thymine or adenine
69 OS-10-197-019-1

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Query Match	37.3%	Score 846.8;	DB 6;	Length 9314;
Best Local Similarity	98.9%	Pred. No. 2e-204;		
Matches 874; Conservative	0;	Mismatches 7;	Indels 3;	Gaps 2

[illegible]

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US-09-925-065A-566754
RESULT 2
Sequence 566754, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.15
CURRENT APPLICATION NUMBER: US/09/925, 065A
CURRENT FILING DATE: 2001-08-08

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1 PRIOR APPLICATION NUMBER: US 60/243,096
2 PRIOR FILING DATE: 2000-10-24
3 PRIOR APPLICATION NUMBER: US 60/252,147
4 PRIOR FILING DATE: 2000-11-20
5 PRIOR APPLICATION NUMBER: US 60/250,092
6 PRIOR FILING DATE: 2000-11-30
7 PRIOR APPLICATION NUMBER: US 60/261,766
8 PRIOR FILING DATE: 2001-01-16
9 PRIOR APPLICATION NUMBER: US 60/289,846
10 PRIOR FILING DATE: 2001-05-09
11 NUMBER OF SEQ ID NOS: 957086
12 SOFTWARE: FASTCUS for Windows Version 4.0
13 SEQ ID NO: 566754
14 LENGTH: 562
15 TYPE: DNA
16 ORGANISM: Homo sapiens
17 US-09-925-065A-566754

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Query Match%	24.3%	Score 550.6;	DB 4;	Length 562;
Best Local Similarity	99.6%	Pred. No. 1.4e-129;		
Matches 561, Conservative	1;	Mismatches 0;	Indels 1;	Gaps 1.

[illegible]

RESULT 3
 US-09-925-065A-177131/C
 ; Sequence 177131, Application US/09925065A
 ; Publication No. US20050228172A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108627.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A

```

1  CURRENT FILING DATE: 2001-08-08
2  PRIOR APPLICATION NUMBER: US 60/243,096
3  PRIOR FILING DATE: 2000-10-24
4  PRIOR APPLICATION NUMBER: US 60/252,147
5  PRIOR FILING DATE: 2000-11-20
6  PRIOR APPLICATION NUMBER: US 60/250,092
7  PRIOR FILING DATE: 2000-11-30
8  PRIOR APPLICATION NUMBER: US 60/261,766
9  PRIOR FILING DATE: 2001-01-16
10 PRIOR APPLICATION NUMBER: US 60/289,846
11 PRIOR FILING DATE: 2001-05-09
12 NUMBER OF SEQ ID NOS: 957086
13 SOFTWARE: PstSeq for Windows Version 4.0
14 SEQ ID NO 177131
15 LENGTH: 554
16 TYPE: DNA
17 ORGANISM: Homo sapiens
18
19 US-09-925-065A-177131

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Query Match	23.4%	Score 531.6;	DB 4;	Length 554;
Best Local Similarity	99.5%;	Pred. No. 9.8e-125;		
Matches 553; Conservative	1;	Mismatches 0;	Indels 2;	Gaps 2;

QY	1131	IGTTCCCTGGAGGCGCCCTTCGTCGTCGGTGAAGAAACAATATGGCGCGGCTACACAGGGTG	1190
Db	554	TGTTCCCTGGAGGCGCCCTTCGTCGTCGGTGAAGAAACAATATGGCGCGGCTACACAGGGTG	495
QY	1191	TAACTGTGTGAATATACAGGAAGATGACTGAAAGCTCTTTGGGACTCCGTTTCCCTATTGTA	1250
Db	494	TAACTGTGTGAATATACAGGAAGATGACTGAAAGCTCTTTGGGACTCCGTTTCCCTATTGTA	435
QY	1251	AAATGAGGTTTAATATACAGAGCCTTCTTCTACTCTCCCAAAAGCAAGTGTGTTGTCGCGGCAG	1311
Db	434	AAATGAGGTTTAATATACAGAGCCTTCTTCTACTCTCCCAAAAGCAAGTGTGTTGTCGCGGCAG	375
QY	1311	AGGGGCCCAATGTTGGGCTGTACAGCAATCAGTTATCCCAAGGACGCGGCTCAGGCAATTA	1370
Db	374	AGGGGCCCAATGTTGGGCTGTACAGCAATCAGTTATCCCAAGGACGCGGCTCAGGCAATTA	316
QY	1371	AAGCGAACAACAGGCGCGGTCATCTCTGACGCGCTTTTCTCATCCAGAGGCTGACAGGC	1430
Db	315	AAGCGAACAACAGGCGCGGTCATCTCTGACGCGCTTTTCTCATCCAGAGGCTGACAGGC	256
QY	1431	AGCTGGCTGGGCGCGGCTCTGCTTGTACAGTGGGGGGGCGGCGGTTTGTCTGTCTG	1490
Db	255	AGCTGGCTGGGCGCGGCTCTGCTTGTACAGTGGGGGGGCGGCGGTTTGTCTGTCTG	197
QY	1491	TGTGTAGGAGGAGTACAGTCAAGCTGGGGGTCGCCGCCCGCGGCGGCTTTAGTGTCCCT	1550
Db	196	TGTGTAGGAGGAGTACAGTCAAGCTGGGGGTCGCCGCCCGCGGCGGCTTTAGTGTCCCT	137
QY	1551	GATCCCTTAAACGACAGGCGGCTCAACCGGAGGAGNAGGCGGAACCCACAGCGAGCCCA	1610
Db	136	GATCCCTTAAACGACAGGCGGCTCAACCGGAGGAGNAGGCGGAACCCACAGCGAGCCCA	77
QY	1611	CGGCTGTTGTGGTTGCCGGGCAACCTGTGCTGCAAGTTCTGATTTGTTCTTCTTCCCGCA	1670
Db	76	CGGCTGTTGTGGTTGCCGGGCAACCTGTGCTGCAAGTTCTGATTTGTTCTTCTTCCCGCA	17
QY	1671	CAACGCGGCGGCTGTA	1686
Db	16	CAACGCGGCGGCTGTA	1

US-10-265-689-27
 RESULT 4
 ; Sequence 27, Application US/10265689
 ; Publication No. US2003011975A1
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: STRUTT, RICHARD S.
 ; APPLICANT: COLLINS, SHEILA A.
 ; APPLICANT: WARDEN, CRAIG H.
 ; APPLICANT: SELDIN, MICHAEL F.

```

; APPLICANT: RICOUIER, DANIEL
; APPLICANT: BOUILLAUD, FREDERIC
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
; FILE REFERENCE: 1579-376
; CURRENT APPLICATION NUMBER: US/10/265,689
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/353,645
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: PCT/US97/06864
; PRIOR FILING DATE: 1997-04-22
; PRIOR APPLICATION NUMBER: 60/034,960
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: "n" bases may be a, t, c, g, modified or unknown
US-10-265-689-27

```

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Query Match      19.7%; Score 447.4; DB 6; Length 1161;
Best Local Similarity 94.9%; Pred. No. 3.9e-103;
Matches 516; Conservative 0; Mismatches 22; Indels 6; Gaps 5;

QY 1733 AGAGGCCAGCCGCGCTCGCTCGCAGAGGAGTGTGAGTTGCTCCAGCGT--AGGGGG 1790
DB 2  ANGAACACACCGCGCGTTCGTCGAGAGGTTGTTAGTTGCTCCAGGGTAAAGGGGG 61
QY 1791 CTGGGCCCATTAAGAGAGAGTGC-ACCTTAAGACACGCGCCCGCTGACGCTTTTGA 1849
DB 62  CTGGGCCCATTAAGAGAGAGTGC-ACCTTAAGACACGCGCCCGCTGACGCTTTGA 121
QY 1850 ACCGCTCT-GGCTGGGAAGGAGAGAGTGTGAGCTGACAAAGCTTTCT--GGCGGT 1907
DB 122  ACTCTTCGAGTTGGAGAGGAGAGAGTGTGAGCTGACAAAGTGTTCGAGCGGT 181
QY 1908 CAGTCTTCATCTCTCACAAGAGTGTGCGCGCCCGAGAGTGTGAGGAGAGCGGGAG 1967
DB 182  CAGTCTTCATCTCTCACAAGAGTGTGCGCGCCCGAGAGTGTGAGGAGAGCGGGAG 241
QY 1968 TGGCAAGGAGTGTGACATCTCGGGAGACGAAGAGTAAACCGGTGATGGACGACGG- 2026
DB 242  TGGCAAGGAGTGTGACATCTCGGGAGACGAAGAGTAAACCGGTGATGGACGACG 301
QY 2027 AAACGGAGTGTGAGAAAGTCAATGAGAGAACCTTAGCGGGGCGGTCCCGCGGAAAGC 2086
DB 302  AAACGGAGTGTGAGAAAGTCAATGAGAGAACCTTAGCGGGGCGGTCCCGCGGAAAG 361
QY 2087 GAGTGTCTCAGAGTCTCCGCAACCAAGTGAAGAGTGTGAGAGCGCGCCCGCGCAG 2146
DB 362  GAGTGTCTCAGAGTCTCCGCAACCAAGTGAAGAGTGTGAGAGCGCGCCCGCGCAG 421
QY 2147 CCCCACCCCGGGCCCCCGCCCGAGGCTTAAAGCGCGCGCGCTGCGCGAGCCAC 2206
DB 422  CCCCACCCCGGGCCCCCGCCCGAGGCTTAAAGCGCGCGCGCTGCGCGAGCCAC 481
QY 2207 TGGCAAGCCAGCTGTGCGCGCGCTTGGATTGACTGTCCAGCTGTGCGCGCGCTGTCCA 2266
DB 482  TGGCAAGCCAGCTGTGCGCGCGCTTGGATTGACTGTCCAGCTGTGCGCGCGCTGTCCA 541
QY 2267 GCGG 2270
DB 542  GCGG 545

```

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RESULT 5
US-10-311-455-1865
; Sequence 1865, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander

```

```

; APPLICANT: PIEPENROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1865
; LENGTH: 5283
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1865

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Query Match      16.0%; Score 364.2; DB 6; Length 5283;
Best Local Similarity 77.4%; Pred. No. 1.3e-81;
Matches 467; Conservative 0; Mismatches 133; Indels 3; Gaps 2;

QY 1668 GCACACGCGCGCGCTGTAACATCGACACGAGCGCGGTTCGCAAGCCCACTCCGC 1727
DB 2  CGATACGCGCGCGGTGTATATATATATATATATATATATATATATATATATATATATAT 61
QY 1728 CTGACAGACCCAGCGCGCTGCTCGCAGAGAGGTGTGAGTTTCCAGCGTAAAGG 1787
DB 62  TTGTAGAGATGTAGTCCGCGGTTCGTCGAGAGCGGTGTGAGTTTCCAGCGTAAAGG 120
QY 1788 GGGGTGGCCCATTAAGAGAGAGTGTGACCTTAAGACACGCGCCCGCTGAGCGCTGTAG 1847
DB 121  GGGGTGGGTATTAAGAGAGAGTGTGATTAAGATACGCTTTAG--TGAAGCTTTAG 178
QY 1848 AAACCGTCTGTGTGAGAGAGCAAGAGTGTGATGTAACAAGTCTTTCTGCGCGT 1907
DB 179  AAATCGTTTGTGTGAGAGAGTGTGATGTAAGAGTGTGATGTAAGTGTGTTTGGCGGT 238
QY 1908 CAGTCTTCATCTCTCACAAGAGTGTGCGCGCCCGAGAGTGTGAGCAAGCGGGAG 1967
DB 239  TAGTTTGTATTTTATTAAGAGTGTGCGCGTTCGAGAGAGTGTGAGAGCGGGAG 298
QY 1968 TGGCAAGGAGTGTGACATCTCGGGAGACGAAGAGTAAACCGGTGATGGACGACGGA 2027
DB 299  TGGCAAGGAGTGTGATTTTCGGGGAGACGAAGAGTAAACCGGTGATGGACGACGGA 358
QY 2028 AACGGAGTGTGAGAAAGTCAATGAGAGAACCTTAGCGGGGCGGTCCCGCGGAAAGCG 2087
DB 359  AACGGAGTGTGAGAAAGTCAATGAGAGAAATTTAGCGGGGCGGTTCGCGGAAAGCG 418
QY 2088 GCTGTCTCAGAGTCTCCGCAACCAAGTGAAGAGTGTGAGAGCGCGCCCGCGCAGGC 2147
DB 419  GTTGTTTAGAGTGTGTGATTTTAAGTGAAGTGTGATGAGTGTGCTGTTGTAAGT 478
QY 2148 CCCCACCCCGGGCCCCCGCCCGAGGCTTAAAGCGCGCGCGCTGCGCGAGCCCACT 2207
DB 479  TTTATTTTGGGTTCGTTTCGAGAGTGTAAAGTCCGCGTGTGCGCGAGGTTTATTT 538
QY 2208 GCGAAGCCAGCTGTGCGCGCTTGGATTGACTGTCCAGCTGTGCGCGCGCTGTCCA 2267
DB 539  GCGAAGTGTGATGCGCGCGTTTGGATTGATGTTTACGTTCCGTTCCGTTCCGAC 598
QY 2268 GCG 2270
DB 599  GCG 601

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RESULT 6
US-10-311-455-1866/c

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? Sequence 1866, Application US/10311455
? Publication No. US20030143606A1
? GENERAL INFORMATION:
? APPLICANT: OLEK, Alexander
? APPLICANT: PIPENBROCK, Christian
? APPLICANT: BERLIN, Kurt
? TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining
? TITLE OF INVENTION: Cytosine methylation
? FILE REFERENCE: 5013.1014
? CURRENT APPLICATION NUMBER: US/10/311,455
? CURRENT FILING DATE: 2002-12-16
? PRIOR APPLICATION NUMBER: PCT/EP01/07537
? PRIOR FILING DATE: 2001-07-02
? PRIOR APPLICATION NUMBER: DE 10032529.7
? PRIOR FILING DATE: 2000-06-30
? PRIOR APPLICATION NUMBER: DE 10043826.1
? PRIOR FILING DATE: 2000-09-01
? NUMBER OF SEQ ID NOS: 2424
? SEQ ID NO 1866
? LENGTH: 5283
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
? US-10-311-455-1866

```

Query Match	13.8%	Score 312.4	DB 6	Length 5283
Best Local Similarity	72.0%	Pred No. 2e-68		
Matches 435, Conservative	0	Mismatches 166	Indels 3	Gaps 2

QY	1667	CCGACAAACGCGCGGCTGTAACATATGACAGACGCGCGCGGTGCGAGAGCCCAAGTCCCG	1726
Db	5283	CCGACAAACGCGACGACTTAACCAATCGACACGAAACCGATCGCGAAACCCCAATCCCG	5224
QY	1727	CCCTGCGAGAGCCAGCCCGCGCTGCTCGACGAGAGGGGTGGATGTTTGCCCAAGCTGAGG	1786
Db	5223	CCCTACAAACAAACCGCGCGCTGCTCGCAAAACAAATTAATATTTAACCAACGTA-A	5165
QY	1787	GGGGCTGGGCCCCATTAAGAGAGAGTGCATTTAAGACCGGCCCGCTGACGCTTGTA	1846
Db	5164	AAAACTAACCCATTAACAAACAAATATACATTAAACACGACCC--AATTAACGCTATTA	5107
QY	1847	GAAACCGTCTGGCTGGGAGGCAAGAGGTGTGACTGGAACAAGCTTGTTCGGCGG	1906
Db	5106	AAAACCGTCTTAATTAACAAACAAATATATTAACCAACAACTTATTTCTAACGA	5047
QY	1907	TCAGTCTTTCATCTCAACAGAGTTGCGCGCCGAGAGTGTGAGGCAGAGGCGGGGA	1966
Db	5046	TCAATCTTACCATCTTCAACAAACAAATTAACGACCCGAAACAAATATATTAACAAACGAAAA	4987
QY	1967	GTGGCAAGGAGTGCACATCTTCGGGGAACGAAGAGTAAACGGGTGATGGGACGCACGG	2026
Db	4986	ATAACAAACAAATTAACATCTTCGAAAAACGAAAAATTAACGCGATTAATTAACGACAGA	4927
QY	2027	AAACGGAGTGGAGAAAGTTCATGAGAGAACCTTGAAGCGGCGGTCTCCCGCGAAAGGC	2086
Db	4926	AAACGAAATTAACAAATTAATCAATTAACAAACCTTAACGAAACGATTCCTCCGCAAAAAAC	4867
QY	2087	GGCTGCTCAAGGTTTCGCGACCCAGTAGAGTGTGCAAGCGCGCGCCCGCCCGCAGG	2146
Db	4866	GACTACTCCAAATATCTCCGCAACCAATTAACATTAACAAACCCGACCCCGCCGCAAA	4807
QY	2147	CCCCACCCCGGGCCCCCGCCCCGGAAGCTTAAGCGCGCGCGCGCTGCGCGAGGCCAC	2206
Db	4806	CCCCACCCCGAAACCCCGCCCCCGAAACCTTAACCGCGCGCGCGCTTAACGCAAAACCCAC	4747
QY	2207	TGCGAAGCCCAAGCTTGCAGCGCGCTTGGAGTTGACTGTCAACGCTTGCACCGGCTGTCCGA	2266
Db	4746	TACGAAACCAACTACGCGCGCTTAATAATTAATATCAACGCTTGCACCGCTGTCCGA	4687
QY	2267	CGCG 2270	
Db	4686	CGCG 4683	

```

RESULT 7
US-10-301-832-11/c
; Sequence 11, Application US/10301832
; Publication No.: US20040102390A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Pfeifer
; TITLE OF INVENTION: MODULATION OF NOTCH3 EXPRESSION
; FILE REFERENCE: RTS-0414
; CURRENT APPLICATION NUMBER: US/10/301,832
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 155
; SEQ ID NO 11
; LENGTH: 44348
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
US-10-301-832-11

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Query Match	8.3%;	Score 188.4;	DB 7;	Length 44348;
Best Local Similarity	63.7%;	Pred. No. 2.2e-36;		
Matches 354;	Conservative 0;	Mismatches 191;	Indels 11;	Gaps 4

QY	5	GATTCGCCCGCCCTCAGGCTCCCAAAATGGCTGGGAATTGCAGGGGTAGGCACTCACCTGG	64
Db	12725	GATTCGCTCCTCCAGCTCCCAAAAGCTGGGATTTACAGGCTGAGCCACCGCCCGG	12666
QY	65	CTACAACTTTTCAAAATACATTTA---TCTAGTACCCATACATCTCCAGTTTGCACA	121
Db	12665	CGTGTGTTTTTTTATTAACCTAAACAGTATTTAGTAGCTGCTTTTTTAATCCATTTATTA	12606
QY	122	GGACATCTTATGACTTGGACAGCTGCTAAAATCCAAAGGTGCAGCGTTTGTATGTCTA	181
Db	12605	TGAGAACTATCAAAACATACAGAAAAGTTGACCATTCATATACCAACCACTTGATTTCAAC	12546
QY	182	TAGGATTTGCTCAGATCTGGCCCCCAGCCTGAAAAGAT---TTAAGAAATTTCTGAGGCC	238
Db	12345	TATTTGTAAGTTATATCATCAACATCTTTCTTTTCAAAACATTTAAAATATAATTGCAGACC	12486
QY	239	AGGCACAGTGGCTCACAACCTGTAAATTCAGTACTGTGAGAGTCCGAGTCAAGAGACTGC	298
Db	12485	GGGACACAGTGGCTCAGTGTATATATCTGTAGCACTTTGGGAGGCCAAAGTGAATGATGGC	12426
QY	299	TTGAGGCCAGAGGTTGAAGAGCAGCTTGAACAACACAGGGAACCTGTCTACTACAAAGAA	358
Db	12425	TTGAGTTCAAGAGTTCAAGACACAGCTGGGGCAATATAGTGAACCCGTCTCTACAAAAAA	12366
QY	359	TAAATTAATTAAGCCAGAGCTTAAAGGCTCAATCCCTGTGGTCCAGCTACTAGGGAAGCGA	418
Db	12365	TACAAAGCTTAAGCCGGGCAATGGTGGGCGCAGCCTGTAAATCCAGCTACTTGGGGACGTGA	12306
QY	419	AGTAGA-----CTGCTTTGTCACGAGAGGTCAAGACTGCAAGTAGAGCTGAGACCCAGCAAC	474
Db	12305	GGTGGAGGATCACTTGAGGCCACGAAAGTGTAGAGCTGCAGTGAAGCTAGATCAATGCCA-C	12247
QY	475	TGCATTTCCAGCTGGGGCAAAAAAGAACCTGTCTCAAAAAATTAAGTTAAATTAATTA	534
Db	12246	TGTACTCCAGCTGGGGTGAACAAAGTAGACTGTGTCTCAAAAAATTAATTAATTAATTG	12187
QY	535	ATATATAAATAAGTTT 550	
Db	12186	CAAAACATCCACATATT 12171	

RESULT 8
US-10-719-993-6827/c
; Sequence 6827, Application US/10719993
; Publication No. US20040255849A1
; GENERAL INFORMATION:
; APPLICANT: CARILU, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

```

; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 6827
; LENGTH: 160556
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(160556)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-719-993-6827

Query Match          7.7%; Score 175; DB 8; Length 160556;
Best Local Similarity 67.7%; Pred. No. 1e-32;
Matches 258; Conservative 2; Mismatches 117; Indels 4; Gaps 1;

Qy 216 ATTAAAGAAATTTCTTGAAGCCAGGACAGTGGCTCACTGTAAATTCAGTACTGTG 275
Db 30112 ATTCAAAATATACATATCTCACCCGGGTGCACTGCTCAAGCTTAATCTTGAACCTTTG 30053
Qy 276 AGAGTCCGAGGTCAAGAGACTGTCTTGAAGCCAGAGATTCAAGAGAGCTGGACAACACA 335
Db 30052 GGAAGCCCAAGGACAGGTGATTACGTGAGTCAAGAGATTCAAGAGAGCTGGACAACATG 29993
Qy 336 GGGAGACCTGTCTACTACAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 395
Db 29992 GTGACACTGTCTCTACTAAAAAATACAAAATTAAGCCAGGTGTGTGTGTGCGCGCTGTGA 29933
Qy 396 GTCCAGCTACTAGGAGAGGAGAGAGTGA---CTGCTTGTCCAGAGAGGTCAAGACTG 451
Db 29932 GTCCAGCTACTTGGAGAGCTGAGGACAGAGATCACTTGAACCCAGAGAGGTGAAGTTA 29873
Qy 452 CAGTGAAGTGAAGCCAGCCACTGTGATTCAAGCTTGGGCAACAAAAGAGAGCCCTGTCT 511
Db 29872 CAGTGAAGTGAAGTTTGACCACTGCACTCCAGCTGGGTGACAGAGAGAGACTGTCT 29813
Qy 512 CAAAAAATTAAGTTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 571
Db 29812 CAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 29753
Qy 572 TTCAAAAGAGAGCTCTTAAG 592
Db 29752 TGACAAAAATGTCTTACTAAG 29732

RESULT 9
US-09-764-878-231/c
; Sequence 231, Application US/09764878
; Patent No. US20020090615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121
; CURRENT APPLICATION NUMBER: US/09/764,878
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 231
; LENGTH: 11172
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-878-231

Query Match          7.6%; Score 172.8; DB 3; Length 11172;
Best Local Similarity 58.5%; Pred. No. 1e-32;
Matches 337; Conservative 0; Mismatches 237; Indels 2; Gaps 2;

Qy 1 AACGATCTGCCCGCTCAGCCTCCCAAAAGTGTGGATTGCAAGCGTGAAGCCACTTAC 60
Db 1 AACGATCTGCCCGCTCAGCCTCCCAAAAGTGTGGATTGCAAGCGTGAAGCCACTTAC 60
```

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Db 8630 AAGGATCCCGCTGCGCTTGCCCTCCCAAGTGTAGATTACAGAGCATGACTCCGCAC 8571
Qy 61 CTGGCTACAAAGTTTCAAAATATACATTATCTAGTACCACATATTCCTCCAGTTTGTCCAC 120
Db 8570 CTGGCTACCGCTTAAGATCTACATATAATCCAGGCTCAACAAACATGAAACAAA 8511
Qy 121 AGGACATCTTATGACTTGAAGCAAGCTGTAAATAATCCAAAGGTGACCGTTGTATGCT 180
Db 8510 AGGACTAATTAATTAAGATATAGTTAATTAAGATTTTCTGTGTGTACTATGAGAGAGCT 8451
Qy 181 ATAGGATTTGCTCAGATCTGCCCCCACTTGAAGAAATTTAAGAAATTTCTTGAAGCCAG 240
Db 8450 TCCCTCAGACAAAGATGATGAATAAATTTGGGTTTTTCTTTTAAAGATGAGGACTGCCAG 8391
Qy 241 GCACAGTGGCTCACACCTGTAAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTT 300
Db 8390 GCACAGTGGCTCACACCTGTAAATTCAGTACTTGGAGAGCCGAGGTGGTGAAGACCT 8331
Qy 301 GAGGCCAGAGATTCAAGAGAGAGCTGTGACAAACACAGGAGAG-CCTGTCACTACAAAGAT 359
Db 8330 GAGGTCAAGAGATTCAAGAGAGAGCTGTGACAAATATGTAAATCCCATCTTACTTAAAT 8271
Qy 360 AATTAATTAAGCCAGGCTTATGTGCTATCCTGTGTCCAGTACTTGAAGAGGCGAA 419
Db 8270 ACAAATTAAGCCAGGCGCGGTGCTTACACTGTATCTCCAGTACTTGAAGAGGCTGAG 8211
Qy 420 GTAGGACTGTGTGCCAGAGGTCA-AGA CTGCAAGTGAAGTGAAGCCAGCCAGCTGCA 478
Db 8210 ACAGAAATTTGCTGAACCCGAGAGGAGAGTTACAGTGAAGCTTGAATTTGTGCCACTGCAC 8151
Qy 479 TTCCAGCTGTGGCAACAAAAGAGAGCCGTGTCAAAAATTAAGTTAATTAATTAATTA 538
Db 8150 TCAGAGCTAGGTGTGACAGAGTGAAGCTCATCTCAAAAAAATTAATTAATTAATTAATTA 8091
Qy 539 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 574
Db 8090 AAAAAAGATGAGGAGCATGATTAATTAATTAATTTGT 8055

RESULT 10
US-10-079-854-231/c
; Sequence 231, Application US/10079854
; Publication No. US20030054368A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121C1
; CURRENT APPLICATION NUMBER: US/10/079,854
; CURRENT FILING DATE: 2002-02-22
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 231
; LENGTH: 11172
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-079-854-231

Query Match          7.6%; Score 172.8; DB 5; Length 11172;
Best Local Similarity 58.5%; Pred. No. 1e-32;
Matches 337; Conservative 0; Mismatches 237; Indels 2; Gaps 2;

Qy 1 AACGATCTGCCCGCTCAGCCTCCCAAAAGTGTGGATTGCAAGCGTGAAGCCACTTAC 60
Db 8630 AAGGATCCCGCTGCGCTTGCCCTCCCAAGTGTAGATTACAGAGCATGACTCCGCAC 8571
Qy 61 CTGGCTACAAAGTTTCAAAATATACATTATCTAGTACCACATATTCCTCCAGTTTGTCCAC 120
Db 8570 CTGGCTACCGCTTAAGATCTACATATAATCCAGGCTCAACAAACATGAAACAAA 8511
Qy 121 AGGACATCTTATGACTTGAAGCAAGCTGTAAATAATCCAAAGGTGACCGTTGTATGCT 180
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Db 8510 AGCACTAATTAATAGATATATATTAATTAAGATTTTCTGTGTACTATGAGACGCTT 8451
Qy 181 ATAGATTGCTCAGATCTGCCCCCAGCCTGAAAGAAATTTAGAGAAATTTCTTGAGCCAG 240
Db 8450 TCCCTCAGACAAAGATGATTAATTTGGGTTTTCTTTTAAAGTGGAGCGACGTGCGAG 8391
Qy 241 GCACAGTGGCTCACACCTGTATTTCCAGTACTGTGAGAGTCCGAGGTGAGAGACTGCTT 300
Db 8390 GCACAGTGGCTCACACCTGTATTTCCAGTACTGTGAGAGTCCGAGGTGAGAGACTGCTT 8331
Qy 301 GAGGCCAGAGTTCAGAGCAGCTGTGACAAACAGAGGAGA-CCTGTCACTACAAAGAAAT 359
Db 8330 GAGGTCAAGAGTTCAGAGCAGCTGTGACCAATATGTATAAACCCCATCTCTATAAAT 8271
Qy 360 AATAAATTAAGCCGCTTATGTGCTCATCCCTGTGTGCTCCAGCTACTAGAGGAGCAGAA 419
Db 8270 ACAAATTAATTAAGCCGCTTATGTGCTCATCCCTGTGTGCTCCAGCTACTAGAGGAGCTGAG 8211
Qy 420 GTAGGACTGCTTGTCCAGAGAGTCA-AGACTGAGTGTGAGACCCAGCAGCTGCA 478
Db 8210 ACAGAATGCTTGAACCCGGAAGAGAGGTTACAGTACGCTAGATTGTGCTGAC 8151
Qy 479 TTCAGCCTGGGCAACAAAAGAGACCTGTCTCAAAAATTAAGTTAAATTAATTA 538
Db 8150 TCCAGCCTAGGTGTGACAGAGTGAGACTATCTCAAAAAAATTAATTAATTAATTA 8091
Qy 539 TAAATATGTTAAACCTTAACACATCTCTTTT 574
Db 8090 AAAAAAGTAGGAGCCATGACTTATATATTTGT 8055

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RESULT 11

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US-09-925-065A-770821/c
; Sequence 770821, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: US/09/925.065A
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770821
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-770821

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Query Match 7.4%; Score 168; DB 4; Length 563;
Best Local Similarity 74.6%; Pred. No. 4,1e-32;
Matches 252; Conservative 0; Mismatches 80; Indels 6; Gaps 3;

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Qy 218 TTAAGAAATTTCTTGAAGCCAGGACAGTGGCTCACACCTGTAAATTCAGTACTGTGAG 277
Db 493 TTCAAGATATCTTGAAGCCAGGATACAGTGGCTCACACCTGTAAATTCAGTACTGTGAG 434
Qy 278 AGTCCAGGTGAGAGTCTGTTGAGGCCAGAGTTCAAGAGACCTGTCGACACAGG 337
Db 433 AGTGAAGGTGGTGAATCACTTGAAGGTGAGAGTTTGAACACACCTGTCGACACATGAT 374
Qy 338 GAGACCTGTCACTAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 397

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Db 373 GAAACCTGTCTATTAATAAATACAAAATTAAGCTKXGCAATGATGGACATGCTGTAT 314
Qy 398 CCCAGCTACTRAGGAGGACAGAAATGAGACTGCTT-----CCGAGAGTCAAGACTGCA 453
Db 313 CCCAGCTACTRAGGAGGCTGTGAGGAGAAATTCCTTGAACCCGAGGAGGAGGTTGCA 254
Qy 454 GTGAGTGAAGCCAGCAGCCTGATTCAGCCTGGGCAACAAAAGAGACCTGTCTC- 512
Db 253 GTGAGTGAAGTTGCGCA-TTGACCAACAGCTGGGTGACAGAGCAAGACTGTCTCA 195
Qy 513 AAAAAATTAAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 550
Db 194 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 157

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RESULT 12

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US-10-723-860-2320/c
; Sequence 2320, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natsaba
; APPLICANT: Gineburg, Wendy M.
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT FILING DATE: US/10/723.860
; PRIOR APPLICATION NUMBER: 2003-11-26
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2320
; LENGTH: 135005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2320

```

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Query Match 7.4%; Score 167.2; DB 8; Length 135005;
Best Local Similarity 80.3%; Pred. No. 9.3e-33;
Matches 233; Conservative 0; Mismatches 53; Indels 4; Gaps 3;

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Qy 235 GGCAGGACAGTGGCTCACACCTGTAAATTCAGTACTGTGAGAGTCCGAGGTGAGGA 294
Db 84840 GGCAGGACAGTGGCTCACACCTGTAAATTCAGTACTGTGAGAGTCCGAGGTGAGGA 84781
Qy 295 CTGCTGAGGCGAGAGTTCAGAGCAGCTGTGACAAACAGGAGA--CCTGTCACTAC 352
Db 84780 TTGCTTGAAGGCGAGAGTTCAGAGCTATCTGAGCAATATGTAGAGACCTGTCTCTAC 84721
Qy 353 AAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 412
Db 84720 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 84661
Qy 413 GGCAGAGTGAAGTCTGTG-TCCAGAGGTCAAGACTGAGTGAAGTGAAGTGAAGTGAAG 471
Db 84660 GGCAGAGTGAAGTCTGTG-TCCAGAGGTCAAGACTGAGTGAAGTGAAGTGAAGTGAAG 84601
Qy 472 ACTGATTCAGGCTGGGCAACAAAAGAGACCTGTCTCAAAAATTA 521
Db 84600 A-CTGTACTCAACCTGGGCAACAGAACAGACCTGTCTCAAAAATTA 84552

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RESULT 13

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US-10-756-149-1719/c
; Sequence 1719, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natsaba
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER

```


FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1719
LENGTH: 135005
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-756-149-1719

Query Match 7.4%; Score 167.2; DB 9; Length 135005;
Best Local Similarity 80.3%; Pred. No. 9.3e-31;
Matches 233; Conservative 0; Mismatches 53; Indels 4; Gaps 3;

Qy 235 GGCCAGGACAGTGGCTCAACCTGTATATCCAGTACTGTGAGAGTCCGAGGTCAGAGGA 294
Db 84840 GGCTGACACAGTGGCTCACTGTATATCTCAGCACTTTGGAGGCGAGGTAGAGGA 84781
Qy 295 CTGCTTGAAGCCAGAGTTCAAGAGCAGCTTGAACAACAGGAGGA--CCTGTCACTAC 352
Db 84780 TTGCTTGAAGGACAGAGTTCAAGACTATCTGGCAACATAGTAGAGCCCTGTCTCTAC 84721
Qy 353 AAAAATTAATTAATTAAGCCAGGCTTATGCTCATCCTTGTGTTCCAGTACTAGGGA 412
Db 84720 AAAAAATGAATAATTAATGCTGATGTGTGACACATGCTTATGCTCCAGTACTAGGA 84661
Qy 413 GGCAAGATAGAGTCTGCTTG--TCCAGAGAGGTCAAGATGTCAGTGAAGTCAAGCC 471
Db 84660 GGCTGAGTATGATTTGCTTGAAGTCAAGAGGTCAAGGCGGAGTGAAGTGAACATGCC 84601
Qy 472 ACTGCAATTCAGCTGGGCAACAAAGAGACCCCTGTCTCAAAATAA 521
Db 84600 A-CTGTACTCCAACTGGGCAACAGAACAGACCCCTGTCTCAAAAAA 84552

RESULT 14
US-10-027-632-115210/c
Sequence 115210, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 115210
LENGTH: 3030
TYPE: DNA
ORGANISM: Human
US-10-027-632-115210

Query Match 7.3%; Score 166.8; DB 5; Length 3030;
Best Local Similarity 61.8%; Pred. No. 1.9e-31;
Matches 336; Conservative 0; Mismatches 197; Indels 11; Gaps 4;

Qy 1 AACGATCTGCCCGCTCAGCTCCCAAGTGTGGATTTGACAGGCTGAGCCACTTAC 60
Db 2458 AAGGATCTTCTGCGCTCAGCTTACCAAAATGCTGAGATTAACAGGTGTGATCAGAC 2399
Qy 61 CTGGCTACAGTTTCAAAATATATTATCTAGTACCAATTCATCTCCAGTTTGTCCAC 120
Db 2398 CTGGCCCTTAATTAATCTTTGACATTTGATTTATTTTGAAGAGTACTCTTCTAA 2339
Qy 121 AGGACATCTTATGACTTGAAGCAAGCTGTAAATAATCCAGGAGTGAAGCTTTGATGCT 180
Db 2338 GACAAAGCCACATGATATCTTCAAGTTTATTAAGTTTATATGAAATCTTTTAATGT 2279
Qy 181 ATAGATTTCTCAGATCTGCCCACTGAA-----AGAAATTAAGAAATTTCTTGA 234
Db 2278 AAGAAATGAATACAGATCTCTGAGCTTGAATTTTCAATATTAATAAAGCCTTGA 2219
Qy 235 GGCCAGGACAGTGGCTCAACCTGTATATCCAGTACTGTGAGAGTCCGAGGTCAGAGGA 294
Db 2218 GGCTGACACAGTGGCTCACTGTATATTCAGCACTTTAGAGAGCCAAAGTGAAGA 2159
Qy 295 CTGCTTGAAGCCAGAGTTCAAGAGCAGCTTGAACAACAGGAGAGC--TGTCACTA 351
Db 2158 TGGTTTGGGCGCAGAGTTTGAACAGCCTGGCAACCTAGTAGAGCCCGTTTCAACA 2099
Qy 352 CAAAGATTAATTAATTAAGCCAGGCTTATGCTCATCCTTGTGTTCCAGTACTAGGG 411
Db 2098 AAATTTTATTAATTAATGCTGGGCAATGCTGTAAATGCTGTGTCTCAACTACTGGG 2039
Qy 412 AGGAGAGTATGAGTCTGCTTG--TCCAGAGAGTCAAGATGTCAGTGAAGTCAAGCC 470
Db 2038 AGGAGAGTATGAGTCACTTGAAGCCAGAGTTTGAAGCTGCAATGAGTATGCTGT 1979
Qy 471 CACCTGATTCAGCTGGGCAACAAAGAGACCCCTGTCTCAAAATAATTAATAA 530
Db 1978 CA-CTGACTCCAGCTGGGCAACAGATTAATTCCTGTCTCAAAAAAAGGTCTTA 1920
Qy 531 ATAA 534
Db 1919 AAAA 1916

RESULT 15
US-10-027-632-115211/c
Sequence 115211, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 115211
LENGTH: 3030
TYPE: DNA
ORGANISM: Human
US-10-027-632-115211

Query Match 7.3%; Score 166.8; DB 5; Length 3030;
 Best Local Similarity 61.8%; Pred No. 1.9e-31;
 Matches 336; Conservative 0; Mismatches 197; Indels 11; Gaps 4;

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QY 1 AACGATCTGCCCGCTCAGCCCTCCCAAAGTGTGGATGTGAGGCGTGAAGCACTTCAC 60
   |||||
Db 2458 AAGCATCTTCCTGCTCAGCTTACCAAAATGCTGAGATTACAGGTGTAATCAGCAGC 2399
   |||||
QY 61 CTGGCTACAGTTTCAAAATATCTATCTAGTACCATATCTCCAGTTTGTCCAC 120
   |||||
Db 2398 CTGGCCCTTAATTAATCTTTGCAATTATATGTTCTTGAAAGTACCTCTTTCTAA 2339
   |||||
QY 121 AGGACATCTTATGATGTAGCAAGCTGCTAAATCAAGGGTGCAGGGTTTGTATGCT 180
   |||||
Db 2338 GACAAAGCCACATGATCTTCAAGTTTATMAAGTTTATATATGTAACCTTTATATGT 2279
   |||||
QY 181 ATAGATTGCTCAGATCTGCCCCCACTGAA-----AGATTTAAGAAATTTCTTGA 234
   |||||
Db 2278 AAAGAAATGAATACGATTTCTGTGAGCTGATTTTCCAAATACATATTAAGCTTGA 2219
   |||||
QY 235 GGCAGGCAAGTGTCTCAACCTGTAAATCCATCTGTGAGAGTCCGAGGTCAAGGA 294
   |||||
Db 2218 GGTAGGCAAGTGTCTCATGCTTGAATTCAGCACTTGAAGGCAAGGTGGAAGA 2159
   |||||
QY 295 CTGCTGAGGCGAGGTTCAAGAGCAAGCTGGAACAACAAGGAGACC---TGTCACTA 351
   |||||
Db 2158 TGGTTTGGGGCCAGAGTTTGAGACCAAGCTGAGCACTTATGAGACCCGTTTCACA 2099
   |||||
QY 352 CAAGAATATAATTAATTAAGCCAGGCTTAGTGTCTATCCCTGTGTCCAGCTACTAGGG 411
   |||||
Db 2098 AAATTTTATTAATTAAGTGTGGGATGTGTAAATGCTGTGTCTCAACTACTTGGG 2039
   |||||
QY 412 AGGCAAGATAGAGCTGCTTG-TCCGAGAGGTCAAGACTGAGTGAAGCCAGC 470
   |||||
Db 2038 AGGCAAGAGTGAATCACTTGAAGCCAGAAAGTTGAGGCTGCATGAGCTATGATCGTGT 1979
   |||||
QY 471 CACCTGCAATTCAGGCTGGGCAAAAGAGACCCCTGCTCAAAAAATTAAGTTAAATA 530
   |||||
Db 1978 CA-CTGCACTCCAGGCTGGGCAACAGTAAAGATCCTGTCTCAAAAAAAGGTCTTA 1920
   |||||
QY 531 ATAA 534
   |||||
Db 1919 AAAA 1916
  
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Search completed: December 21, 2005, 23:57:45
 Job time : 1640 secs

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sequence 106, App
sequence 2, Appli
sequence 12361

sequence 13461, A
sequence 175, Ann

sequence 13359, A
sequence 31 Apr 1

sequence 13461, A
sequence 1 Ann1

sequence	13278, A
sequence	13263, A

sequence 13231, A
sequence 13365, A

sequence 13244, A
sequence 64 Ann1

sequence 13318, A

sequence 13198, A

ANALOG PROBES

	6; Gaps	3;
155989;		
GGCAGCAGTGCGCT	252	
GGCAGCAGTGCGCT		
GGCAGCAGTGCGCT	1348	
TTAGGCGCAGAGGT	312	
TTAGGCGCAGAGGT		
TTAGGCGCAGAGGT	1408	
TTAAATTAATTAAGC	371	
TTAAATTAATTAAGC		
TTTCAAAATTAAGC	1466	
AAGTAGGACTGCTT	431	
GGCAGAGAGAGTTG	1528	
TTGCATTTCAGCCT	487	
TTGCATTTCAGCCT		
TTGCATTTCAGCCT	1587	
TTTATTAATAAATG	547	

Db 1588 GCGTGAAGAGGAGGATCTCTCAATAATAATAATAATAATAATAATAATAATA 1647
Qy 548 TTTAAACCTTAA 559
Db 1648 TTTAATCGCCAA 1659

RESULT 2

US-11-121-086-58
Sequence 58, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138, 6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 58
LENGTH: 180654
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-58

Query Match 7.3%; Score 165.2; DB 7; Length 180654;
Best Local Similarity 70.7%; Pred. No. 4.7e-20;
Matches 263; Conservative 0; Mismatches 103; Indels 6; Gaps 3;

Qy 193 AGATCTGCCCCCAGCCTGTAAGAAATTTTAAGAAATTTCTTGAGGCGCAGGACAGTGCTC 252
Db 161439 ATATTGTCCCTTGCAAAACTCATGTGAAATTTAATCCCAAGCCCGGACACAGTGCTC 161498
Qy 253 ACACCTGTAATTCAGTACTGTGAGAGTCCGAGGTCAAGAGACTGCTTGAGCCAGAGAGT 312
Db 161499 ACGCTGTAAATCCAGCATTTTGGAGAGCCGAGGCGGAGATCACTGAAGTCAAGAGT 161558
Qy 313 TCAAGAGACCTTGAGACACACAGGAGA-CCTGTCACTCAAAAGATTAATAATTAGC 371
Db 161559 TCAAGACCAAGCTGCGCAACATGTGAAACCCCATCTCTCAAAAAATACAAAAATTAGC 161618
Qy 372 CAGGCTTAGAGTCACTCCGTGTGTCCAGCTACTAGGAGGAGAGTGAAGTGAAGTCTT 431
Db 161619 CGGGCGTGTGTGACACCCCTGTGTATCCAGCTACTCGAAGGCTGAGGCGAGAGAGTTG 161678
Qy 432 GT---CCCAAGAGGTCAAGACTGAGTGAAGCTGAGCCAGCCACTGCAATTCAGGCT 487
Db 161679 CTGAGCTTGAGGAGGAGGAGGTGAGTGAAGCCGAGATCGTGCCA-CTGCACTCAGGCT 161737
Qy 488 GGGCAACAAAAGAGACCTGTCTCAAAAAATTAATTAATAATAATAATAATAATAATAG 547
Db 161738 GCGTGAACAAAGCAGATTTCTGTCTCAATAATAATAATAATAATAATAATAATAA 161797
Qy 548 TTTAAACCTTAA 559
Db 161798 TTTAATCGCCAA 161809

RESULT 3

US-10-995-561-13237/c
Sequence 13237, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: C1001559
CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13237
LENGTH: 87672
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-13237

Query Match 7.1%; Score 160.4; DB 6; Length 87672;
Best Local Similarity 70.6%; Pred. No. 2.9e-19;
Matches 243; Conservative 0; Mismatches 96; Indels 5; Gaps 2;

Qy 225 AATTCTTGAGGCGCAGGACAGTGGCTCAACCTGTAATTCAGTACTGTGAGAGTCCGA 284
Db 36715 AAGACCTTCGGGCTGGGACAGATGGCTCAAGCCTGTATCCAGACCTTTGGAGGCGCAA 36656
Qy 285 GGTCAAGAGACTGTTTGAAGCCAGAGATTCAAGAGAGCTTGACAAACAGAGGAGACT 344
Db 36655 AGTGGGTGGATCACTTGAGGTCAAGAGTTTCAAGACCACTTGGCCAAACAGAGCAACC 36596
Qy 345 GTCACTCAAAAGATTAATAATAATTAGCCAGCTTAGTGCTCATCCCTGTGTCCAGCT 404
Db 36595 ATTTCTACTAAAAACAAAAAATTAGCAGGAGCATGTGTGACACAGCTGTATGTCAGCT 36536
Qy 405 ACTAGGAGCAGCAAGTGAAGACTGCTTGT---CCCAAGAGTCAAGACTGCAAGTGAAGT 460
Db 36535 ACTCGGAGGCTGAGAGGAGAGATTCCTTGAACCCAGAGTGTGAGAGTTCCAGTGAAGT 36476
Qy 461 GAGACCCAGCCACTGCATTCAGGCTGGGCAACAAAAGAGACCTGTCTCAAAAAATA 520
Db 36475 GAGATGTGTGCA-CTGTACTCCAGCCCTGGCGCAGAGCAGACTCATCTCAAAAAAAT 36417
Qy 521 AGTTAAATAATAATAATAATAATAATAAGTTTAAACCTTAACACA 564
Db 36416 AAATAATAATAATAATAATAATAAGACCTTCTTCTTAAGTCA 36373

RESULT 4

US-11-112-908-56
Sequence 56, Application US/11112908
Publication No. US20050260659A1
GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR FILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: PatentIn version 3.3
SEQ ID NO 56
LENGTH: 150468
TYPE: DNA
ORGANISM: Homo sapiens
US-11-112-908-56

Query Match 7.0%; Score 159.8; DB 7; Length 150468;
Best Local Similarity 75.4%; Pred. No. 3.9e-19;
Matches 239; Conservative 0; Mismatches 72; Indels 6; Gaps 3;

Qy 235 GCGCAGGACAGTGGCTCAACCTGTAAATTCAGTACTGTGAGAGTCCAGAGTCAAGAGA 294
Db 9823 GCGCAGGACAGTGGCTCAACCTGTAAATTCAGTACTGTGAGAGTCCAGAGTGGAGTGA 9882

QY	295	TTGCTTGAAGCCAGAGATTCAGAGAGAGCTTGAGCAACACAGGAG-CTGTCACTACA	353
Db	9883	TCACCTTAGGTCAGGAGAGTCCGAGACACAGCTGACCAACATGTGTAAACCCCATCTCACT	9942
QY	354	AAGATAATAATTAATGACGAGCCTTAGTGTGCTCATCCCTGTGTGCCAGCTACTAGGAG	413
Db	9943	AAAAATACAAAAATTATGACGAGCGTGTGTGGCGATCCTGTAAATCCACGCTACTCGGAG	10002
QY	414	GCAGAGATGAGA-----CTGCTTGTGCCAGAGAGTCAAGACTGAGATGAGTGAACCCAG	469
Db	10003	ACTGACGTAGAGGAATCTCTTGAACCCAGAGAGGTGAGCTTGACGTGAGCTGAGATTGCG	10062
QY	470	CCACCTGCAATTCAGCTGTGGGCAACAAAAAGAGACCCTGTCTCAAAAAATTAAGTTAAATA	529
Db	10063	CCA-CTGCAATTCATCTGTGGGCAACAGACGAGACTCTGTCTCAAAAAATTAATATAATA	10121
QY	530	AATAATAATAAAAAATA	546
Db	10122	TAAATAATAATAATAAGA	10138

RESULT 5
 US-11-121-086-52/c
 Sequence 52, Application US/11121086
 Publication No. US20050266459A1
 GENERAL INFORMATION:
 APPLICANT: POULSEN, TIM S.
 APPLICANT: NIELSEN, KIRSTEN V.
 TITLE OF INVENTION: NOCLETIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
 FILE REFERENCE: 09138.6000-00000
 CURRENT APPLICATION NUMBER: US/11/121.086
 CURRENT FILING DATE: 2005-05-04
 PRIOR APPLICATION NUMBER: 60/567,570
 PRIOR FILING DATE: 2004-05-04
 NUMBER OF SEQ ID NOS: 107
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 52
 LENGTH: 166639
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-11-121-086-52

Query Match	7.0%	Score 159.8	DB 7	Length 166639
Best Local Similarity	73.8%	Pred. No. 3.9e-19		
Matches 231	Conservative	0	Mismatches 77	Indels 5
			Gaps	2
Qy	235	GGCCGAGCAGCTGCGCTCACCTGTAAATTCAGTACTGTGAGATGCCAGGTCAGAGGA	294	
Db	100677	GGCCGAGCAGCATTGGCTCAGCGCTGTAAATCCAGACCTTTGGGAGGCAGAGGAGCGGA	100618	
Qy	295	CTGCTTGAGGCCAGGAGTTCAAGAGCAGCCTTGACACACAGGAGAGCCTGTCACTACAA	354	
Db	100617	TCACCTTGAGGTGAGAAAGTTCAAGACTAGCGCTGGCCAAATATGGCAAACTGTCTCTACTA	100558	
Qy	355	AGAAATTAATTAATTGACCGAGCTTATGCTGCTCATCCCTGTGGTCCAGCTACTAGGAGAG	414	
Db	100557	AAAAATACAAAATTTAGCCGGGATGGTGGTGAATGGCTGTAGTCCAGCTACTTTGGAGG	100498	
Qy	415	CAGAGTAGGA----CTGCTTGCCAGGAGGTCAGACTGCAAGTAGTGAGCTGAGACCAG	470	
Db	100497	CTGAGGCGAGAGAAATCATCTTGAACCCAGAGAGAGAGGGTGCAATAGACTGAGATGTGC	100438	
Qy	471	CACCTGCATTCCAGCCTGGGGCAACAAAAGAGACCTGTCTCAAAAAATTAAGTTAAATTA	530	
Db	100437	CA-TTGCACTCCAGTCTGGGTGACAGAGAGATCTCCGTCTCAAAAAAAAAAAAAAAAAA	100379	
Qy	531	ATAAATTAATTAATA 543		
Db	100378	AAAAAAAAAAAAAA 100366		

RESULT 6
US-11-112-908-55

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Sequence 55, Application US//11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55
; LENGTH: 193789
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-55

Query Match          7.0%; Score 159.8; DB 7; Length 193789;
Best Local Similarity 75.4%; Pred. No. 46-19;
Matches 239; Conservative 0; Mismatches 72; Indels 6; Gaps 3;

QY      235  GGCAGGACAGAGGGCTCACCTGTAAATTCAGTACGTGTAGAGTCCGAGGTCAGAGAA 294
Db      60008  GGCAGGACAGAGGGCTCACGCTGTGATCCAGACCTTTGGAGGCCAAGGTGGTGA 60067

QY      295  CTGCTTGAAGGCCAGAGATTCAAGAGCAGCCTGAGACAACAGAGAGAGA-CTGTCTACTACA 353
Db      60068  TCACCTTAGGTCAAGAGTCCGAGACCAAGCCTTACCAACATGCTGAACCCACTCTCTACT 60127

QY      354  AAGATTAATTAATTAATTAAGCCAGGCTTAGTGTGCTCATCTCCTGTGCTCCAGACTACTAGGAG 413
Db      60128  AAAAATACAAAAATTAATTAAGCCAGGCGTGTGTCGCATGCTGTAAATCCAGACTACTGGGAG 60187

QY      414  GCAGAAAGTAGA----CTGCTTGTCCCAAGAGAGTCAAGCTGCACTGAGCTGAGACCCAG 469
Db      60188  ACTGACGTAGAGAAATCTCTTGAACCCAGAGAGTGAAGCTTGCACTGAGCTGAGATTGCG 60247

QY      470  CCACTGTCATTCCAGGCTGGGCAACAAAGAAGACCCCTGTCTCAAAAAATAAGTTAAATA 529
Db      60248  CCA-CTGCAATTCATCTCTGGGCAACAGACGAGACTGTCTCAAAAAATAATTAATTAATA 60306

QY      530  AATTAATTAATTAATAATA 546
Db      60307  TAATTAATTAATTAATTAAGA 60323

RESULT 7
US-10-995-561-13262
; Sequence 13262, Application US//10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CI001559
; CURRENT APPLICATION NUMBER: US/10/095,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13262
; LENGTH: 141121
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

```

```

RESULT 7
US-10-995-561-13262
; Sequence 13262, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: C1001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13262
; LENGTH: 141121
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

```

NAME/KEY: misc_feature
LOCATION: (1,...(141121))
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13262

Query Match 7.0%; Score 159; DB 6; Length 141121;

Best Local Similarity 71.4%; Pred. No. 5.3e-19;

Matches 252; Conservative 0; Mismatches 95; Indels 6; Gaps 3;

191 TCAGATCTGCCCCACCCTGTAAGATTTTAAGAGATTTCTTGAAGGCGAGGACAGTGGC 250
10586 TGAGACCTCTGCTCTTACAAAAATTAATAATTAATAATAGGCCAGGTAAAGTGGC 10645
251 TCACACCTGTAATTCAGATCTGAGAGTCCAGAGCTGAGAGCTGAGGCCAGA 310
10646 TCACACCTGTAATCTGATCTTGGAGGCTGAGGAGTGGATGCTGAGCTCAGGA 10705
311 GTTCAAGACGCTTGACCAACACAGAGAG-CTGTCACTACAAAGATTAATAATTA 369
10706 GTTCAAGACGCTTGAGCAACATGTAACCCCATCTATTAACTCAAAAAATTA 10765
370 GCCAGCTTATGCTCATCCCTGTGCTCCAGCTACTAGGAGGACAGAGTAGA---- 425
10766 GCCAGGATGCTGTGACAGCTGTATAGTCCAGCTACTCAGAGGCTGAAAGTGAAGAT 10825
426 CTGCTTGTCCAGAGGTCAGAGCTGAGTGAAGCTGAGCCACCTGACATTCGAGC 485
10826 CGCTGGAATCAGAGGTCAGAGTTCAGTGAAGCTGAGATCAGGCCA-CTACACTCCAGC 10884
486 CTGGGCAACAAAAAGACCTCTCAAAAAATTAATTAATAATTAATA 538
10885 ATGGGCAACAGAGTGAAGCTGTCTCAATTAATAATTAATAATGA 10937

RESULT 8

US-11-121-086-30/c

Sequence 30, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:

APPLICANT: POULSEN, TIM S.

APPLICANT: NIELSEN, KIRSTEN V.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

FILE REFERENCE: 09138, 6000-00000

CURRENT FILING DATE: 2005-05-04

PRIOR APPLICATION NUMBER: 60/567,570

PRIOR FILING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PatentIn version 3.3

SEQ ID NO 30

LENGTH: 158692

TYPE: DNA

ORGANISM: Homo sapiens

US-11-121-086-30

Query Match 7.0%; Score 158.6; DB 7; Length 158692;

Best Local Similarity 74.9%; Pred. No. 6.3e-19;

Matches 239; Conservative 0; Mismatches 74; Indels 6; Gaps 3;

233 GAGGCCAGGCACTGCTCACCTGTAATTTCAAGTCTGTGAGAGTCCAGGTCAGAG 292
155868 GAGGCAAGGCACTGCTCACCTGTAATTTCAAGCCTTTGGAGGAGAGGTTAGGCG 155209
293 GACTGCTTGAAGGAGAGTCAAGAGAGGCTGAGACACAGGAGAGA-CCTGTCACTA 351
155208 GACTGCTTGAAGGAGAGTCAAGAGAGGCTGAGACACAGGAGAGAGAGGAGAGG 155149
352 CAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 411
155148 CAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 155089
412 AGGCAAGTGAAGTCTGTTT-----CCAGAGGTCAAGCTGCAAGTGAAGTGAAGCC 467

155088 AGGCTGAGGTGGAGAGCTGCTTGAAGCCAGAGGTCGAGGCTGAGTGAATCG 155029
468 AGCCACCTGATTCAGAGCTGGGCAACAAAAAGACCTGTCTCAAAAAATTAATTA 527
155028 CACC-CCTGCACTCCAGCTGATGACAGTTCAGACACTGCTCAAAAAA 154970
528 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 546
154969 AAAAAAAGAAAAA 154951

RESULT 9

US-11-112-908-45

Sequence 45, Application US/11112908

Publication No. US20050260659A1

GENERAL INFORMATION:

APPLICANT: Hattie, Cole

TITLE OF INVENTION: Breast Cancer Biomarkers

FILE REFERENCE: 04-164-US

CURRENT FILING DATE: 2005-04-22

PRIOR APPLICATION NUMBER: US 60/564,758

PRIOR FILING DATE: 2004-04-23

PRIOR APPLICATION NUMBER: US 60/575,978

PRIOR FILING DATE: 2004-06-01

PRIOR APPLICATION NUMBER: US 60/631,702

PRIOR FILING DATE: 2004-11-30

PRIOR APPLICATION NUMBER: US 60/633,826

PRIOR FILING DATE: 2004-12-07

NUMBER OF SEQ ID NOS: 511

SOFTWARE: PatentIn version 3.3

SEQ ID NO 45

LENGTH: 182314

TYPE: DNA

ORGANISM: Homo sapiens

US-11-112-908-45

Query Match 7.0%; Score 158.2; DB 7; Length 182314;

Best Local Similarity 69.7%; Pred. No. 7.5e-19;

Matches 260; Conservative 0; Mismatches 103; Indels 10; Gaps 3;

227 TTCTTGAAGCCAGGCAAGTGTCTCACCTGTATTCAGTACTGTGAGTCCAGG 286
20121 TCTCATTAAGCCAAAGTCAAGTGTTCACCTGTATTCAGGCACTTTGGAGAGCTGAGG 20180
287 TCAGAGAGCTGCTTGAAGCCAGAGTTCAGAGAGGCTGAGCAACACAGGAGAC---- 342
20181 TGAAGGATGCTTAAGCCAGAGGTCAGAGAGGCTGAGCAACAAAGTGAAGACCTTG 20240
343 -CTGTCACTACAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 401
20241 TCTTCCAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 20300
402 GCTAAGGAGGAGGAGAGTGAAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGTGA 457
20301 GCTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 20360
458 GCTGAGAGCCAGGCAAGTGTTCAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 517
20361 GCTGTGTTGTGCA-CTTCACTCAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 20419
518 ATAAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 577
20420 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 20479
578 AGAGAGCTTTTA 590
20480 TGAAGAACCTGA 20492

RESULT 10

US-11-121-086-72/c

Sequence 72, Application US/1121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138, 6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 72
LENGTH: 162173
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-72

Query Match 6.9%; Score 157.4; DB 7; Length 162173;
Best Local Similarity 69.6%; Pred. No. 1e-18; Indels 5; Gaps 2;
Matches 243; Conservative 0; Mismatches 101

Qy 217 TTTAAGAGATTCTTGAAGGCGGCGGCGGCTCAGACCTGTATTCTCACTGTGA 276
Db 100622 TATTAATAATAGTAGAGTGGCTGGGCGGCTCAGACCTGTATCCAGCACTTTGG 100563
Qy 277 GAGTCCGAGTTCAGAGCACTGTTAGGCGGAGGTTCAAGAGCACTGCAACAACAG 336
Db 100562 GAGGCGAGGCGGCGGCGGCTCAGACCTGTAGAGGTTCAAGAGCACTGCGCAACATAG 100503
Qy 337 GGAGCCGTGCTACACAAAGATAATTAATTAAGCAGGCTTAAGGCTCATCCCTGTGG 396
Db 100502 TGAAGACTGCTCTAATAAATACAAAATTAAGCCGACATGGGCGGCACTGTGA 100443
Qy 397 TCCGACTACTAGGAGGCGAGAGTAGAGCTGCTGT-----CCGAGAGTCAAGACTGC 452
Db 100442 TCCGAGCTACTTAGAGGCTGATGAGAGGAAATTTTGAACCCGAGAGGTGAGACTTAC 100383
Qy 453 AGTGAGCTGAGACCCAGCCACTGCTTCCAGCTGGGCGCAAAAAGAGACCTGTCTC 512
Db 100382 AGTGAGCCGAGATGTGCGCA-CTGCATCTAGCCCTGGCGATAGAGTGAAGTCCGTTGC 100324
Qy 513 AAAAAATTAAGTTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 561
Db 100323 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATGAGTGAAGTCTCTGAAGC 100275

RESULT 11
US-11-159-597-20/c
Sequence 20, Application US/11159597
Publication No. US20050255559A1
GENERAL INFORMATION:
APPLICANT: Uebele, Victor N.
APPLICANT: Swanson, Richard J.
APPLICANT: Liu, Yuan
APPLICANT: Lagrutka, Armando
TITLE OF INVENTION: NOVEL HUMAN CALCIUM SENSITIVE POTASSIUM
FILE REFERENCE: 20499P
CURRENT APPLICATION NUMBER: US/11/159,597
CURRENT FILING DATE: 2005-06-23
PRIOR APPLICATION NUMBER: US/10/031,691
PRIOR FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US00/19585
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/144,764
PRIOR FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 48000
TYPE: DNA

ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(48000)
OTHER INFORMATION: n = A,T,C or G
US-11-159-597-20

Query Match 6.9%; Score 157.2; DB 7; Length 48000;
Best Local Similarity 67.3%; Pred. No. 9.5e-19;
Matches 253; Conservative 0; Mismatches 118; Indels 5; Gaps 2;

Qy 205 ACCGTGAAGATTTAAGAGATTCTTGAAGGCGGCGGCGGCTCAGACCTGTATT 264
Db 30953 ATCATTAATAAATTAAGATAGATTGTTGGCCAGGTGAGTGGCTATGCTTATTC 30894
Qy 265 CCAGTACTGTGAGAGTCCGAGGTCAGAGACTGCTTGAAGGCGGAGAGTTCAAGACAGC 324
Db 30893 CCAGCACTTGTGGAGGCGGCGGCGGCGGCTCAGACCTGTGAGAGTTTGAACAGC 30834
Qy 325 TGACCAACATGATGAACTGTCTCTTAATAATCAAAATTTAGCCAGGACGTTGC 384
Db 30833 TGACCAACATGATGAACTGTCTCTTAATAATCAAAATTTAGCCAGGACGTTGC 30774
Qy 385 TCATCCCTGTGTCCTCAGCTACTAGGAGGCGGAGAGTAGA-----CTGCTGTCCAGCA 440
Db 30773 ATGGGCTGTATATCAGACTTCTCAGAGAGGCTGAGGCGGAGAAATCGTTGAACCGGGT 30714
Qy 441 GGTCAAGCTCAGTAGTGAAGACCCAGCCACTGCTTCAAGCTGGGCGCAAAAAG 500
Db 30713 GGCAGAGGTTGCACTGAGCCAAATCAATGCGCA-CTGCACCTCAGCTGGGCGAGAGTG 30655
Qy 501 AGACCTGTCTCAAAAATAAGTTAATAATTAATAATTAATAATTAATTAATTAATTA 560
Db 30654 AGACTCACTCAAAAATAAGTTAATAATTAATAATTAATAATTAATAATTAATAATTA 30595
Qy 561 CACATCTCTTTTCA 576
Db 30594 CATGATATGTTTTTA 30579

RESULT 12
US-11-121-086-49
Sequence 49, Application US/1121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138, 6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 49
LENGTH: 159146
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-49

Query Match 6.9%; Score 157.2; DB 7; Length 159146;
Best Local Similarity 69.2%; Pred. No. 1.1e-18;
Matches 274; Conservative 0; Mismatches 113; Indels 9; Gaps 4;

Qy 211 AAAGATTTAAGAGATTCTTGAAGGCGGCGGCGGCTCAGACCTGTATTCCAGTA 270
Db 10462 AATTAATTTCAAGTTAAAGTTAGGCGGCGGCTCAGTGGCTCAACCTGTATCCAGCA 104521
Qy 271 CTGTGAGGTCGAGGTCAGAGACTGTTAGGCGGAGAGTTCAAGAGCACTGAGCA 330
Db 104522 CTTGTGAGACCGAGGTCGAGATCACTGTAGATCAAGAGTTCAAGATGAGCTGGGCA 104581

QY	331	CA - CAGGAGAGACCTGTCACTCAAAAGATTAATAATATAGCCAGGCTTAGTGGTCATC	389
Db	104582	ACATATATGAACCCCGCTCTACTATAAATTCAAAAATTTAGCCAGGCTAGTGGCCACA	1046411
QY	390	CCTGTGTGTCCAGCTACTAGGAGAGCAGAAATGAG- - - CTGCTGTGTCCAGAGGTCA	445
Db	104642	CCTGTAAATCCAGACTCTGTAGGTGTAGGCGCAGGAAATCTTTAAACCCAGAGAGGTGG	1047010
QY	446	AGACTGCAATGAGCTGAGAGCCAGCACCCTGTGCATTCAGCTGTGGGCAACAAAAAGAGACC	505
Db	104702	AGGTTGCAATTAAGCCAGATTCGGGCA - CTGCACCCCAAGCTTGGGCAACAAATGAGACT	1047600
QY	506	CTGTCTCAAAAAATAGTTAAATAA- - - TAAATAATAAAATAGTTTAAACCTTAAACA	562
Db	104761	CTGTCTCAAAAAATAGTTTAAATTAAGAAAGTTGAAAAAATCCCAACACTCA	1048200
QY	563	CATCTTCTTTTCAAAAGAGACTTCTTAAGGACTTC	598
Db	104821	CAGCTAACCTTTCAGAGAACTTCTTGCCAGAAATTC	104856

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RESULT 13
US-11-121-086-13
; Sequence 13, Application US/11121086
; Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138, 6000-00000
CURRENT APPLICATION NUMBER: US/11/121, 086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 13
;
; LENGTH: 191797
;
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-13

Query Match          6.9%; Score 156.8; DB 7; Length 191797;
Best Local Similarity 70.4%; Pred. No. 1.3e-18;
Matches 259; Conservative 0; Mismatches 92; Indels 17; Gaps 3,

QY      211  AAAGATTTAAGAGATTTCCTTGAGGCCAGAGCCAGATGTGCTCAACCTGTAAATCCAGTA 270
DB      127850 AAGTAAGTAAAGAGAAAAGTTAAAGCTGGGCAATGTGGCTCAAGCTGTAAATCCAGCA 127905

QY      271  CTGTGAGAGTCCGAGGTCAGAGAGACCTGTAGAGCCAGAGATTCAAGAGACGCTTGACA 330
DB      127910 CTTTGAGAGGCTGAGATGTGGTGAATTAATGAGATGAGAGGATCAAGACCAAGCTGGCCA 127965

QY      331  ACACAGGAGACCTGTGCATCACTCAAAAGATTAATA-----AATTAGCAGGCTT 378
DB      127970 ACATGATGAATCTGTCTCTTACTTAATAATAAAAAAAAAAATAATAATTAATTAATGCGAGCAT 128025

QY      379  AGTGGCTCATCCCTGTGTGTGCCAGCTACTAGGAGGACAGAGTAGGA----CTGCTGTGC 434
DB      128030 GGTGGTTTCACACTGTAAATCCGAGCTAACCGGAGGCTGAGGTAGGAGAAATCAGTTGAAC 128085

QY      435  CCAAGAGGTCAGACCTGCAGTGAAGCTGAAACCAGATCACTGCATTCAGACCTGGGGAC 494
DB      128090 CCAAGAGGTCAGAGGTTGCAAGTGAAGCTGAAGTCAAGCCA-CTGCACTCCAGCCTGGGGAC 128148

QY      495  AAAAAAGAGACCTGTCTCAAAAAAATAAAGTTAATAATAATAATAATAATAAAGTTAAAC 554
DB      128149 AAGATGAGACTCCATCTCAAAAAAAAAAAAAAAAAAAAAAATAATTTTAAAAAGTTAGATT 128205

QY      555  CCTAAACA 562
DB      128209 TCTTATCA 128216

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RESULT 14
US-11-121-086-9/c
; Sequence 9, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; PRIOR FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 9
; LENGTH: 196200
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-9

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Query Match 6.9%; Score 156; DB 7; Length 196200;
Best Local Similarity 70.4%; Pred. No. 1.8e-18;
Matches 252; Conservative 0; Mismatches 100; Indels 6; Gaps 3;

QY 212 AAGAAATTTAAGAGATTTCTTGAAGCCAGGCACAGTGGCTCACACTGTAAATTCAGATC 271
Db 53744 ATGATTTTAAAAAATTAACCTGAGGGGGGCAAGACATGATGGCTCATGCTGTAAATCCAGCAC 53685
QY 272 TGTGAGAGTCCGAGGTCCAGAGACTCTTGAAGCCACAGAGTTCAAGAGAGCCTGGACAA 331
Db 53684 TTTGGAGAGCTGAGGTGGGGGATCATCTGAAGTTCAGAGTTTCAAGACCAAGCTGGCCAA 53625
QY 332 CACAGGGAGA-CCTGTCACTACAAAGATTAATAATTAGCCAGGCTTAGTGGCTCATCC 390
Db 53624 CATGGTCAAAACCTGTCTCTACTCAAAAATAACAAAATAATCAAGGAGATGATGGGCGATGC 53565
QY 391 CTGGTGTCCAGGCTACTAGGAGAGCAGAAAGTAGA----CTGGTGTCCAGAGAGTCAA 446
Db 53664 CTAAAGTCCAGACTACTTGGAGAGGCTGAGGACAGAGAAATGGCTTACCCCGAGAGGTGA 53505
QY 447 GACTGCAGTAGCTGAGACCAGCCACTGTGACTTCAGGCTTGGGCAACAAAAAGAGACC 506
Db 53504 GGTTGCAGTAGAGAGATTTGTGCCA-ATGCACTTCAGGCTGGGCAACAGATGTAGACTC 53446
QY 507 TGCTCAAAAAATTAAGTTAATAATAATAATAATAATAAAGTTAATACCTTAACACA 564
Db 53445 CATCTCAAAAAATTAATAACAAAATAAAAACTGAAAAGATTACTGCAAAAGCAA 53388

RESULT 15
US-11-121-086-10/c
; Sequence 10, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138,6000-00000
; CURRENT APPLICATION NUMBER: US/11,121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 199321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-10

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Query Match	6.9%	Score 156;	DB 7;	Length 199321;
Best Local Similarity	70.4%;	Pred. No. 1.8e-18;		
Matches 252;	Conservative	0;	Mismatches 100;	Indels 6;
			Gaps	3;

[illegible]

Search completed: December 22, 2005, 00:03:08
Job time : 315 secs

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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIORITY FILING DATE: 2000-04-14
PRIORITY APPLICATION NUMBER: 60/241,755
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 60/237,768
PRIORITY FILING DATE: 2000-10-03
PRIORITY APPLICATION NUMBER: 60/231,498
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15281
LENGTH: 11808
TYPE: DNA
ORGANISM: Human
US-09-949-016-15281

Query Match 89.1%; Score 2022.8; DB 3; Length 11808;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2035; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

233 GAGGCCAGGCAAGTGGCTCAACCTGTAATTCAGTACTGTGAGAGTCCGAGGTACAG 292
1 GAGGCCAGGCAAGTGGCTCAACCTGTAATTCAGTACTGTGAGAGTCCGAGGTACAG 60
293 GACTGCTTGAAGCCAGAGGTTCAAGAGAGCTGTGACAAACAGAGGAACTGTCTACAC 352
61 GACTGCTTGAAGCCAGAGGTTCAAGAGAGCTGTGACAAACAGAGGAACTGTCTACAC 120
353 AAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 412
121 AAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
413 GGCAGAGTGAAGTCTGTTGTCAGAGAGTCAAGAGTCAAGTGAAGTCAAGAGTCAAG 472
181 GGCAGAGTGAAGTCTGTTGTCAGAGAGTCAAGAGTCAAGTGAAGTCAAGAGTCAAG 240
473 CCTGATTCAGAGTCTGTTGTCAGAGAGTCAAGAGTCAAGTGAAGTCAAGAGTCAAG 532
241 CCTGATTCAGAGTCTGTTGTCAGAGAGTCAAGAGTCAAGTGAAGTCAAGAGTCAAG 300
533 AAATATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 592
301 AAATATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 360
593 GACTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 652
361 GACTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
653 GTCTCTTTTGGCAAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 712
421 GTCTCTTTTGGCAAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
713 GACAGCCAGGAGGAGCAATTTTGGTGTGAGGCTTTGATCTGCTGCTGCTGCTGCTGCTG 772
481 GACAGCCAGGAGGAGCAATTTTGGTGTGAGGCTTTGATCTGCTGCTGCTGCTGCTGCTG 540
773 CAATCTCAAGCAATTTTGGTGTGAGGCTTTGATCTGCTGCTGCTGCTGCTGCTGCTG 832
541 CAATCTCAAGCAATTTTGGTGTGAGGCTTTGATCTGCTGCTGCTGCTGCTGCTGCTG 600
833 AAAGCTAGAGAACTGGCGAGGAGGAGTCAAGTGCACAAAGAACTTTATCTTTTC 892
601 AAAGCTAGAGAACTGGCGAGGAGGAGTCAAGTGCACAAAGAACTTTATCTTTTC 660
893 TTTTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 952
661 TTTTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 720
953 CT 1012
721 CT 780

1013 GCAGAAATTAATTCAGGCTTGAATTTGTTTCAAGCTGCTTCTGCGAGGAGCAATCGCTCG 1072
781 GCAGAAATTAATTCAGGCTTGAATTTGTTTCAAGCTGCTTCTGCGAGGAGCAATCGCTCG 840
1073 GCGTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 1132
841 GCGTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 900
1133 TTTCTTGGCAGTCTTCTGCTGTGTAACAACTATGAGGCGCGGCTGACAGGAGTGA 1192
901 TTTCTTGGCAGTCTTCTGCTGTGTAACAACTATGAGGCGCGGCTGACAGGAGTGA 960
1193 AGTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1252
961 AGTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
1253 ATGAGAGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1312
1021 ATGAGAGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080
1313 GGCCTAATTTGTTGCTTTCAAGCATCAATTAATTAATTAATTAATTAATTAATTAATTAAT 1372
1081 GGCCTAATTTGTTGCTTTCAAGCATCAATTAATTAATTAATTAATTAATTAATTAATTAAT 1140
1373 GGCAGACAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1432
1141 GGCAGACAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
1433 CTGAGCTGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1492
1201 CTGAGCTGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
1493 TGTAGAGCTGAGGCTCAAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1552
1261 TGTAGAGCTGAGGCTCAAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
1553 TTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1612
1321 TTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1380
1613 GCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1672
1381 GCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
1673 AGCGGCGGCTGTAACCAATTCAGAGGAGGCGGCTGCGAGGCTCCAGTCCGCTGCTG 1732
1441 AGCGGCGGCTGTAACCAATTCAGAGGAGGCGGCTGCGAGGCTCCAGTCCGCTGCTG 1500
1733 AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1792
1501 AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
1793 GGGCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1852
1561 GGGCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1619
1853 GTCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1912
1620 GTCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1679
1913 TTTGCAATTCACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1972
1680 TTTGCAATTCACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1739
1973 AGGAGTGAACCATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2032
1740 AGGAGTGAACCATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1799
2033 GAGTGAAGAAAGTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2092
1800 GAGTGAAGAAAGTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1859

QY	2093	1860	QY	2153	Db	QY	2213	Db	1980
CCAGAGGCTCCGACACCCAAAGTAGAGCTGCGAGGCGCCGCGCCCGAGAGGCCAC	2152	TTCCAGAGGCTCTCCGACCCCAAGTAGAGGCTGTGGAGGCGCCGCGCCCGAGAGGCTTCAC	1919	CCCGAGGCCCGCCCGAGGCTTAAAGCGCGCCGCGCTGCGAGAGCCCACTGCGGAA	2212	CCCGAGGCCCGCCCGAGGCTTAAAGCGCGCCGCGCTGCGAGAGCCCACTGCGGAA	1979	GCACGAGCTCGCGCGCTCTTGGATTGACTGTCCACGCTCTCCCGGCTGTGTCCAGCGG	2037

```

US-08-846-012A-1
US-BEST 3
Sequence 1, Application US/08846012A
Patent No. 5807740
GENERAL INFORMATION:
APPLICANT: AMARAL, M. Catherine.
APPLICANT: CHEN, Jin-Long
TITLE OF INVENTION: Regulators of UCP2 Gene Expression
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,012A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 736 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-846-012A-1

```

Query Match	21.4%	Score 485;	DB 2;	Length 736;
Best Local Similarity	99.6%	Pred. No. 3.5e-100;		
Matches 507;	Conservative	0;	Mismatches 0;	Indels 2;
			Gaps	2;

Accession	Sequence	Position
Oy	GGGTGGGTAGTTGGCCAGACGTAGGGGGGCTTGAGGCCATTAAGAGAAAGTGCACTTAAAG	1821
Oy	1762	
Db	GGGTGGGTAGTTGGCCAGACGTAGGGGGGCTTGAGGCCATTAAGAGAAAGTGCACTTAAAG	60
Db	1	
Oy	1822 ACACGAGCCCCCGCTGGAACGCTTGTTAAGAAACCGTCTCCGTGAGGAGGCAAGAGTGTGTG	1881
Db	61 ACACGAGCCCCCGCTGGAACGCTTGTTAAGAAACCGTCTCCGTGAGGAGGCAAGAGTGTGTG	119
Oy	1882 ACTGGAACAAGACTTGTCTTGACCGGTCAAGTCTTGCCATCTCTACAGAGGTTTGCCGCCCG	1941
Oy	1802	
Db	120 ACTGGAACAAGACTTGTCTTGACCGGTCAAGTCTTGCCATCTCTACAGAGGTTTGCCGCCCG	179
Oy	1942 AGAGAGTGTGAGGACAGAGCGCGGGAGTGTGCAAGGGAGTGAACCATCTCCGGGAAACGAAGA	2001
Db	180 AGAGAGTGTGAGGACAGAGCGCGGGAGTGTGCAAGGGAGTGAACCATCTCCGGGAAACGAAGA	239

OY	2002	GTAAACCGCGGATGATGGGACCGCAGAAAACGGAGATGTGAGAAAGCATGAGAGAAACCTTA	2061
Db	240	GTAAACCGCGGATGATGGGACCGCAGAAAACGGAGATGTGAGAAAGCATGAGAGAAACCTTA	299
OY	2062	GGCGGGGCGGTCCCGCGGAAAAGGCGGTCTCCAGGAGTCTCGCACCCCAAGTAGAGACT	2121
Db	300	GGCGGGGCGGTCCCGCGGAAAAGGCGGTCTCCAGGAGTCTCGCACCCCAAGTAGAGAG-T	358
OY	2122	GGCAGAGCCCGGACCCCGCCCGCAGAGCCCAACCCCGGAGCCCGCCCGAGAGCTTAAGACCG	2181
Db	359	GGCAGAGCCCGGACCCCGCCCGCAGAGCCCAACCCCGGAGCCCGCCCGAGAGCTTAAGACCG	418
OY	2182	CGCGCGCGCTGCGCGAGACCCCACTGTGGAAGCCCAAGCTGCGCGCGCTTTGGATTGACT	2241
Db	419	CGCGCGCGCTGCGCGAGACCCCACTGTGGAAGCCCAAGCTGCGCGCGCTTTGGATTGACT	478
OY	2242	GTCACAGCTGCGCCCGGCTCGTCCGACGCG	2270
Db	479	GTCACAGCTGCGCCCGGCTCGTCCGACGCG	507

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1      RESULT 4
2      US-09-100-297-1
3      ; Sequence 1, Application US/09100297
4      ; Patent No. 5849514
5      ; GENERAL INFORMATION:
6      ; APPLICANT: AMARAL, M. Catherine.
7      ; APPLICANT: CHEN, Jin-Long
8      ; TITLE OF INVENTION: Regulators of UCP2 Gene Expression
9      ; NUMBER OF SEQUENCES: 16
10     ; CORRESPONDENCE ADDRESS:
11     ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
12     ; STREET: 268 BUSH STREET, SUITE 3200
13     ; CITY: SAN FRANCISCO
14     ; STATE: CALIFORNIA
15     ; COUNTRY: USA
16     ; ZIP: 94104
17     ;
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Floppy disk
20     ; COMPUTER: IBM PC compatible
21     ; OPERATING SYSTEM: PC-DOS/MS-DOS
22     ; SOFTWARE: PatentIn Release #1.0, Version #1.30
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/09/100,297
25     ; FILING DATE:
26     ; CLASSIFICATION:
27     ; PRIOR APPLICATION DATA:
28     ; APPLICATION NUMBER: 08/846,012
29     ; FILING DATE:
30     ; ATTORNEY/AGENT INFORMATION:
31     ; NAME: OSMAN, RICHARD A
32     ; REGISTRATION NUMBER: 36,627
33     ; REFERENCE/DOCKET NUMBER: T97-003
34     ; TELECOMMUNICATION INFORMATION:
35     ; TELEPHONE: (415) 343-4341
36     ; TELEFAX: (415) 343-4342
37     ; INFORMATION FOR SEQ ID NO: 1:
38     ; SEQUENCE CHARACTERISTICS:
39     ; LENGTH: 736 base pairs
40     ; TYPE: nucleic acid
41     ; STRANDEDNESS: double
42     ; TOPOLOGY: linear
43     ; MOLECULE TYPE: cDNA
44     ;
45     ; US-09-100-297-1

```

Query Match	21.4%	Score 485, DB 2;	Length 726;
Best Local Similarity	99.6%	Pred. NC. 3.5e-100;	
Matches 507; Conservative	0;	Mismatches 0;	Indels 2; Gaps 2;

QY 1762 GGGTGGGTACTTTGCGCCAGCGTAGGGGCGCTGGGCGCCATAAAGAGAAAGTGCACTTAAAG 1821

Db 1 GGGTGGGTAGTTTGCCCAAGCGTAGGGGCGCTGGGCGCCATAAAGAGAGAGTGCACTTAAAG 60

Oy	1822	CCACGCGCCCCCTGGACGCTTGTTGAACCGCTCTGGCTGGAGAGCAAGAGGTGTG	1881
Db	61	ACACGCGCCCCCTGGACCGC-TGTTGAACCGCTCTGGCTGGAGAGCAAGAGGTGTG	119
Oy	1882	ACTGGAACAAGCTTGTGTTCTGGCGGTCACTTGTGCATCTTCACAGAGGTTGGCGGCCG	1941
Db	120	ACTGGAACAAGCTTGTGTTCTGGCGGTCACTTGTGCATCTTCACAGAGGTTGGCGGCCG	179
Oy	1942	AGAGAGTGTAGGCGAGGCGCGGGAGTGGCAAGGAGTGAACCATCTCGGGGAAACGAAGA	2001
Db	180	AGAGAGTGTAGGCGAGGCGCGGGAGTGGCAAGGAGTGAACCATCTCGGGGAAACGAAGA	239
Oy	2002	GTAACCGCGGTGATGGAGACGCAACGGAACCGGAGTGGAGAAAGTCATGAGAGAACCTTA	2061
Db	240	GTAACCGCGGTGATGGAGACGCAACGGAACCGGAGTGGAGAAAGTCATGAGAGAACCTTA	299
Oy	2062	GCGCGGGCGGTCTCCCGCGGAAAGCGGTGCTTCAGAGGTCCTCCGCAACCCAGTAGAGCT	2121
Db	300	GCGCGGGCGGTCTCCCGCGGAAAGCGGTGCTTCAGAGGTCCTCCGCAACCCAGTAGAGAG-T	358
Oy	2122	GGCAGGCGCGGCGCGCGCGGACCCCACTCCGAGGCGCGCGCGCGCGAGGCTTAAAGCG	2181
Db	359	GGCAGGCGCGGCGCGCGCGGACCCCACTCCGAGGCGCGCGCGCGCGAGGCTTAAAGCG	418
Oy	2182	CGCGCGCGCTTCGCGCGGAGCCCACTGCGAAGCCCAAGCTGCGCGGCTTGGGATTGACT	2241
Db	419	CGCGCGCGCTTCGCGCGGAGCCCACTGCGAAGCCCAAGCTGCGCGGCTTGGGATTGACT	478
Oy	2242	GTCACGCTCGCGCGGCTCGTCCGACGGG	2270
Db	479	GTCACGCTCGCGCGGCTCGTCCGACGGG	507

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RESULT 5
US-09-949-016-176561/c
; Sequence 176561, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176561
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-176561

Query Match          7.5%; Score 170.4; DB 3; Length 601;
Best Local Similarity 74.7%; Pred. No. 4,2e-29;
Matches 254; Conservative 0; Mismatches 81; Indels 5; Gaps 3;

QY      TTTAAGAAATTTCTTGAGGCGAGGACAGGTGCTCACACCTGTAATTCCAGTACTGTGA 276
      |||||||
DB      TTTTAAATTAATTAATTCGGGCGCGAGGTGCTCACACCTGTAATTCAGACCTTTGG 541
      |||||||

QY      GAGTCGAGGTGAGAGGACTGCTTTGAGGCGCAGAGTTTCAAGGACGAGCTTGACAAACAG 336
      |||||||
DB      GAGGCGGAGGTGGGTGCTCACCTGAGGCGCAGGAGTTTCAAGGACCAACCTTGCCAAACAG 481
      |||||||

QY      GGAGG-CCGTGTCACTTCAAGAAGATAATTAATTAGCCAGGCTTAAGTGGCTCATCCTGTG 395
      |||||||

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[illegible]

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RESULT 6
US-09-949-016-16780/C
; Sequence 16780, Application US/09949016
; Patent No. 6812319
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16780
; LENGTH: 35493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(35493)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16780

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Query Match	7.58	Score 170.4	DB 3	Length 35493
Best Local Similarity	74.7%	Pred. No. 1.8e-28		
Matches 254	Conservative	0	Mismatches 81	Indels 5
				Gaps 3
QY	217	TTTAAAGAAATTTCTTGAGCCGAGGACAGGTGCTCACACTGTATATTCAGTACTGTGA	276	
Db	12792	TTTTAAATATATTTATCGGGGCCAGGGCAGTGGCTCACACTGTATATCCACGACTTTGG	12733	
QY	277	GAGTCGAGGCTCAGAGGACTGCTTGAAGCCAGGAGTTCAAAGACGACTTGAACAACAG	336	
Db	12732	GAGGCCGAGGTGGGTGGCTCACTCGAGGCCAGGAGTTCAAAGACCACTTGGCCAAACAG	12672	
QY	337	CGAATCCTTCTACTCAAAAGATTAATTAATTAGCCAGGCTTATGTCCTCATTCCTGTG	395	
Db	12672	CGAAACCCCATCTCCATATAAAATTAATAAAATTAGCCGAGGCTCATGAGGCTCTGGA	12613	
QY	396	GTCCACGACTCTAAGGAGGAGGAGA--AGTAGGACTCTTGTCCGAGGAGGTCAAGACTGC	452	
Db	12612	ATCCCACTCTACGAGAGGCTGAGGCGAGAGAAATTCCTGAACTCGGAGGCGAGGCTGC	12555	
QY	453	AGTAGCTGAACCCAGCCACTGTCAATTCAGGCTTGGGCAACAAAAGAAGACCTGTGTCTC	512	
Db	12552	ATTGAGCTGAGATCATGCCA-CTGCCTTCAGGCTGGGCAACAAACGAGACTCTCATCTC	12494	
QY	513	AAAAAATTAAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	552	
Db	12493	AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	12454	

RESULT 7
US-09-949-016-15382/c
; Sequence 15382, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 15382
; LENGTH: 37292
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(37292)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15382

Query Match 7.4%; Score 168.4; DB 3; Length 37292;
Best Local Similarity 63.2%; Pred. No. 5.2e-26;
Matches 345; Conservative 0; Mismatches 186; Indels 15; Gaps 5;

QY 5 GATGTGCGGCGCTGAGCTCCCAAGTGTGAGATTGAGCGGCTGAGGCACTTCACTG 64
DB 31797 GATGTGCGGCGCTGAGCTCCCAAGTGTGAGATTGAGCGGCTGAGGCACTTCACTG 31738
QY 65 CTACAAGTTTCAAAATGATTTATGATGACCATATCTTCAAGTTGTTCACAGGA 124
DB 31737 C-----CTGAGCACTGAGGGTTTCAATTCACAGTTTCCCATGTTCTGAGGGGT 31685
QY 125 CATCTTATGACTTGAAGCAAGCTGCTAAATTCCAAGGTGAGGCTTTGATGTCTATG 184
DB 31684 TGCCGTGAGGGCTGTGCACTGAGGAAAGATGTGAGATGATC-TCAGTCCCTCTTC 31626
QY 185 GATTGTGAGTGTGCGGCTGAGGAAAGATTTAAGAAATTTCTTGAAGCGACGAC 244
DB 31625 AAGTCCCTTCTATCTGTGCTTCCCTATGCAATTCCTAAG--TCTTCAGGCTGGGCT 31568
QY 245 AGTGTGCTCACTGTGTAATTCAGTACTGTGAGAGTCCGAGGTGAGAGACTGCTTGA 304
DB 31567 GGTGTGCTATGCTATATATCCAGCAAGTTTGGAGGCTGAGGTGAGAGATTTGCTTGA 31508
QY 305 CCAAGAGTTCAAGAGAGAGCTGAGCAACAGAGAGAGCTGTCACTACAAAGATTAATA 364
DB 31507 CTTGAGATTGACAGCAAGCTGAGCAACATTAAGAGACCTGTCTCAAAAAATTAAAA 31448
QY 365 AATTAGCAGGCTTATGAGTCTATCCCTGTGATCCAGCTACTAGGAGGAGAGTATG 424
DB 31447 AATTAGCAGGCTTATGAGTCTATCCCTGTGATCCAGCTACTAGGAGGAGTATG 31388
QY 425 A-----TGCTTGTCCAGAGAGTCAAGCTGAGTGAAGCTGAGCCAGCCACTGACT 480
DB 31387 AGGACCGATTGAGCTGAGGAGTGAAGGCTGAGGAGGCTGATGAGCA-CTGCACT 31329
QY 481 CCAAGCTGAGGCAAGAAAGAGAGCTGTCTCAAAAAATTAATTAATAATAATA 540
DB 31328 CCAAGCTGAGGCAAGAAAGAGAGCTGTCTCAAAAAATTAATAATAATAATAATA 31269
QY 541 AAAATA 546
DB 31268 AAAATA 31263

RESULT 8
US-09-949-016-16674/c
; Sequence 16674, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 16674
; LENGTH: 126237
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16674

Query Match 7.4%; Score 167.4; DB 3; Length 126237;
Best Local Similarity 70.1%; Pred. No. 1.4e-27;
Matches 253; Conservative 0; Mismatches 106; Indels 2; Gaps 2;

QY 178 TCTATGAGATTGCTCAGATTCGCCCACTTAAAGATTTAAGAGATTTCTTGAAGC 237
DB 21667 TCCCTTGAAGCATCAGGCTGACCAAGCTATTTATTCCTATTTAAAGTAAATAGGC 21608
QY 238 CAGGCAAGGCTCAGCTCAGCTGTAATTCAGTACTGTGAGAGCCGAGGTCAAGGACTG 237
DB 21607 CAGGTGAGGCTCAGCTCAGCTGTAATTCAGTACTGTGAGAGCCGAGGTCAAGGACTG 21548
QY 298 CTTGAGGCAAGGCTCAGGCTGAGCAACAGAGGAG-CTGTCACTACAAAG 356
DB 21547 CATGAGCCCGGAGTTTGAACCAAGTCTGGGCAACAGAGGAGACCCATCTTACAAAC 21488
QY 357 AATTAATTAATTAAGCAGGCTTATGAGTCTATCCCTGTGATCCAGCTACTAGGAGGCA 416
DB 21487 AAACAAAAATTAAGCTGAGGATGATGATGATGATGATGATGATGATGATGATGAT 21428
QY 417 GAAGTGAAGCTGCTGTGCTGAGAGGCTGAGAGCTGAGAGGCTGAGAGGCTGAGAGGCT 476
DB 21427 GAGGAGAGCTGCTGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 21369
QY 477 CATTCAAGCTGAGCAACAAAGAGAGCTGTCTCAAAAAATTAATTAATAATAATA 536
DB 21368 CATTCAAGCTGAGCAACAAAGAGAGCTGTCTCTGAGAGGCTGAGAGGCTGAGAGGCT 21309
QY 537 A 537
DB 21308 A 21308

RESULT 9
US-09-949-016-16675/c
; Sequence 16675, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

Query Match	7.4%	Score 167;	DB 3;	Length 16230;
Best Local Similarity	73.6%;	Pred. No. 8e-28;		
Matches 254; Conservative	0;	Mismatches 85;	Indels 6;	Gaps 3

	Query Match	Best Local Similarity	7.3% ; Score 165.2 ; DB 3 ;	Length 99370 ;			
	Matches 240 ;	Conservative 0 ;	Mismatches 83 ;	Indels 5 ;			
				Gaps 2 ;			
QY	223	AGAAATTTCTTTGAGGCCACAGCACA	GTGGCTCA	CACTGTGTAATTCAGTA	CTGTGAAGATCC	282	
Db	66639	ATAATTTTGCA	CAGGCCACGGTGCA	GTGGCTCA	CAACGTGTAATTCACA	CACATTTTGGAGGGCC	66698
QY	283	GAGSTCAGAGGAC	CTGCTTTGAGGCCAGAGATTC	CAAGACAGC	CTGACACACAGGGAGA-	341	
Db	66669	AAGGTGGCAGAGAT	CACTAATAGTCC	AGAGATTC	CAAGACAGCCTGAC	CAACATATGGCAAAAC	66758
QY	342	CTGTGCTCA	CTCAAAAGATTAATTAATTAATTA	ATGCGCAGGCTTA	TGGCTCATCCCTGTGGTCCCA	401	
Db	66759	CTGTGCTCTCA	CAATTAATAACAAAATTAATTA	ATGCGCAGGCAATGGTGCTTA	TGGCTGTGGTCCCA	66818	
QY	402	GCTACTAGGAGGAGCAGAA	GTAGA-----	CTGCTTTGTC	CCAGAGAGGTCA	AGACTGACAGTGA	457
Db	66819	GCTACTAGGAGAGGT	GATGCTGGGAGGATCA	CTTGAACCA	CGAAGACAGAGGTT	GCAGTGA	66878
QY	458	GCTGAGACCCAGCACA	CTTGATTTCC	AGCTCTGGGCA	CAAAAAGACACCTGTGTT	CAAAAA	517
Db	66879	GCTGAGATATCATG	CCCATCTGACCTT	TAGCTCGGGGAA	CAAGACAGACCCGTGTCT	CAAAAA	66938

QY 518 ATAGTTAAATTAATAATAATAAAT 545
Db 66939 AAAAAAAAAAACCAACCCCAAAAT 66966

RESULT 12
US-09-949-016-17540
Sequence 17540, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14, 755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 17540
LENGTH: 99370
TYPE: DNA
ORGANISM: Human
US-09-949-016-17540

Query Match 7.3%; Score 165.2; DB 3; Length 99370;
Best Local Similarity 73.2%; Pred. No. 4e-27;
Matches 240; Conservative 0; Mismatches 83; Indels 5; Gaps 2;

QY 223 AGAATTTCTTGAAGCCGACGACAGTGGCTTCACTGTAATTCAGTACTGTGAAGTCC 282
Db 66639 ATATTGTGACAGGCGAGGTGCTGAGTGTCAAGCTGAATTCAGCACTTTGGAGAGCC 66698
QY 283 GAGGTGAGAGGAGCTGTTGAGGCGAGGAGTCAAGAGAGGCTGGAACAACAGAGGAGA- 341
Db 66699 AAGGTGAGAGGATCATATTAATTCAGAGGTTCAAGAGGCTGGAACAACAGAGGAGA- 66758
QY 342 CCTGTCACTACAAAGAAATTAATAATTAAGCCAGGCTTAAGTGGCTCATCTCCGTGTCCTCA 401
Db 66759 CCTGTCTTACATAATAATAATAAATTAGCCAGGAGTGTGCTTAAGCTGTGTCCTCA 66818
QY 402 GCTACTAGGAGGCGAGAGTGA---CTGCTTGTCCAGAGAGTCAAGCTGCAATGA 457
Db 66819 GCTACTAGGAGGCTGAGGTGAGAGATCACTGAACCCAGAGAGAGAGGTTGCAATGA 66878
QY 458 GCTGAGAGCCAGCCAGCTGATTCAGGCTGGGCAACAAAGAGACCTGTCTCAAAA 517
Db 66879 GCTGAGATCATGCCACTGCTGAGCTGGGAAACAGAGAGAGCCCTGTCTCAAAA 66938
QY 518 ATAGTTAAATTAATAATAATAAAT 545
Db 66939 AAAAAAAAAAACCAACCCCAAAAT 66966

RESULT 13
US-09-949-016-27232/c
Sequence 27232, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 27232
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-27232

Query Match 7.2%; Score 164.2; DB 3; Length 601;
Best Local Similarity 59.7%; Pred. No. 1e-27;
Matches 330; Conservative 1; Mismatches 214; Indels 8; Gaps 3;

QY 6 ATTCGCGCGCTCAGCTTCCCAAGGCTGGGATTCGAGGCGGAGCCACTCAGCTGCG 65
Db 588 ATCTGCTGCTCAGCTCAGGCTCAAGAGTGTAGATTCAGGCGAGGCACTGTGCGAGG 529
QY 66 TACAAGT---TTCAAAATACATTTATCTAGTACCCATACATTCCTCAGTTGTCCAG 122
Db 528 CCTCATGACTTTTAAAAAACAATTAAAAAGAAATAGAACTTGTGTAATAAGTAAATG 469
QY 123 GACATCTTATGACTGAGCAAGCTGCTAAATTCAGAGGTGAGCGTTGTAT 182
Db 468 GACAGAAATTTGAATTAATATATGATTCATTAATAGAAAGATATTTGTAATCTGAT 409
QY 183 AGAATGCTCAGATTCGCCCCCAGCTGAAAGAAATTTAAGAAATTTCTGAGGCGAGG 242
Db 408 TCAAAATAGTATTTCTGACCATATGAAATTAATTTTAAATTAATTAATTTCTGCGAGG 349
QY 243 ACAATGCTCAGACTGTATTTCCAGTACTGTGAGAGTCCGAGGTCAAGAGTCTGTTGA 302
Db 348 ACGGTGCTATGCTGTATATCCAGACTTCGAGAGCGGAGAGGTAATCACTGA 269
QY 303 GGCAGAGTTCAAGAGCAGCTGAGCAACAGAGAGACTGTCACTACAAAGATTA 352
Db 288 GGTCAAGAGTTCAAGACAGCTGATCAATCAACAAACCCATCTCTATAAAATAC 229
QY 363 TAAATAGCAGGCTTATGAGTCTATCCCTGTGCTCCAGCTACTAGGAGGAGAGTA 422
Db 228 AAAATAGCGGAGTGTGACATGTCTGATATCCAGCTACTGTGGAGGCTGAGGCA 169
QY 423 GGA---CTGCTTGTCCCAAGAGTCAAGACTGCAAGTGAAGTCAAGCCAGCA-CCTGC 477
Db 168 GGAATATCGCTTGAACCCGAGAGGCGAGGTTGCAAGTGAAGTCAAGTCCATGTTGC 109
QY 478 ATTCAGCTGGGCAACAAAGAGACCTGTCTCAAAAATAGTAAATTAATAATA 537
Db 108 ACTCAGCTGGGCAACAGAGAACTCATCTCAAAAAAAAAAAAAAAAAATTATTGA 49
QY 538 ATAAATAGTTT 550
Db 48 TTCGATTAATGT 36

RESULT 14
US-09-949-016-160756/c
Sequence 160756, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498

;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 160756
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-160756

Query Match 7.2%; Score 164.2; DB 3; Length 601;
Best Local Similarity 59.7%; Pred. No. 1e-27;
Matches 330; Conservative 1; Mismatches 214; Indels 8; Gaps 3;

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Oy 6 ATCTGCGCGCTCCAGCCCTCCCAAGTGTGGGATTTGAGCGGCGGACCCACCTGAGC 65
Db 588 ATCTGCGCTCCAGCCCTCCCAAGTGTGGGATTTGAGCGGCGGACCCACCTGAGC 529
Oy 66 TACAAGT---TTTCAAAATACATTTATCTAGTACCCATATCTTCAGTTTGTCCAG 122
Db 528 CCTCATGATCTTTTAAAAAACAATTAAAAAGAAATGAACTTGTAAATAGTAAAAATG 469
Oy 123 GACATCTTATGACTGAGCAAGCTGTAAATCCAAAGGTGACCGCTTTGTATGTCTAT 182
Db 468 GACAGAAATTTGAATATATATGATTCATATTAATAGAACAGTATTTGATCTGTAT 409
Oy 183 AGGATTGCTCAGATCTGCCCCCACCCTGAAAGAAATTTAAGAGAAATTTGAGCGCAGG 242
Db 408 TCAATATGATTTCTTAGCCATATGAAATTAATTTTAAATTTATTTTCTGCGCAGGC 349
Oy 243 ACAGTGGCTCACACCTGTATTCAGTACTGTGAGAGTCCGAGTCCAGAGACTGCTTGA 302
Db 348 ACGGTGGCTCATGCTGTATATCCAGCACTTCGGAAGCGGAGSGTGAATACCTGA 289
Oy 303 GCGCAGAGTTCAAGAGCAAGCTGGAACAACAGGAGAACTGTCTACATCAAAAGATAA 362
Db 288 GGTGAGGATTCAGAACACAGCTGTATCAACAGAAACCCCATCTATCAAAAATAC 229
Oy 363 TAAATTACCGAGGCTTAACTGCTCATCCCTGTGTCAGGCTTACAGGAGGCAAGATA 422
Db 228 AAAATTAGGGGGGAGGAGGAGCAATGTGTAAATCCAGTACTTGGAGGCTAGAGGA 169
Oy 423 GGA---CTGCTTGTCCAGAGAGTCAAGACTGCAAGTGAAGTGAAGCCAGCA--CTGC 477
Db 168 GGAGAAATGCTTGAACCGGGAGGAGGAGGTTGCAGTGAGTGAATGTGCTGATGTTGC 109
Oy 478 ATTCAAGCTGGGCAACAAAAGAAACCTGTCTCAAAAAATTAATTAATTAATA 537
Db 108 ACTCCAGCTGGGCAACAAAGCAAGAACTCATCTCAAAAAAATTAATTAATGA 49
Oy 538 ATAAATAATGTTT 550
Db 48 TTCTGAATATATGT 36
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RESULT 15
US-09-949-016-13576
; Sequence 13576, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 13576
;; LENGTH: 63783
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-13576

Query Match 7.2%; Score 164.2; DB 3; Length 63783;
Best Local Similarity 66.7%; Pred. No. 5.7e-27;
Matches 266; Conservative 0; Mismatches 128; Indels 5; Gaps 2;

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Oy 205 ACCCTGAAAGATTTAAGAGATTTCTTGAAGCCAGCAAGTGGCTCAGACCTGTAAT 264
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Oy 265 CCAGTACTGTAGAGCTCCAGAGTCAAGAGACTGTGAGGCGCAGAGTTCAAGAGCAGCC 324
Db 35978 CCAGCACTTGGAGGCGGAGGTGGTGAATCAGTGAAGTCAAGAGTTCAAGGCGCAGCC 36037
Oy 325 TGACAAACAGAGAGACCTGTCACTACAAAGATTAATTAATTAAGCCAGCTTATGAGC 384
Db 36038 TGCCAAACATGTGAACCCCATCTCTAATAAATTAATTAAGCCAGGATGTAGC 36097
Oy 385 TCATCCCTGTGTCCAGCTACTAGGAGGCAAGTGA---CTGCTGTCCAGGA 440
Db 36098 AGGCACTTGTAGTCTAGCTACTCGAGAGGCTGAAGCAAGAAATCACTGAACCCAGGA 36157
Oy 441 GGTCAAGCTGAGTGAAGTGAACCCAGCCTGCAATTCAGGCTGGGCAACAAAG 500
Db 36158 GCGAGAGGTTGCAGTGAGCTGAGGCAATGCCA--TTGCACTCAGCTGGGCAACAGAGCA 36216
Oy 501 AGACCTGTCTCAAAAAATTAAGTAAATTAATTAATTAATTAATTAATTAATTAATTA 560
Db 36217 AGATCCATCTCAAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 36276
Oy 561 CACATCTTCTTTTCAAGAGAGACTTCTTAAGAGCTTCA 599
Db 36277 TCTTATTTACTTAATTAAGTAAATTAATTAAGTAAATTAATTAATTAATTAATTA 36315
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Job time : 425 secs

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